UNIVERSITÄT
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# ANNUAL REPORT 2020
# Institute of Veterinary Bacteriology

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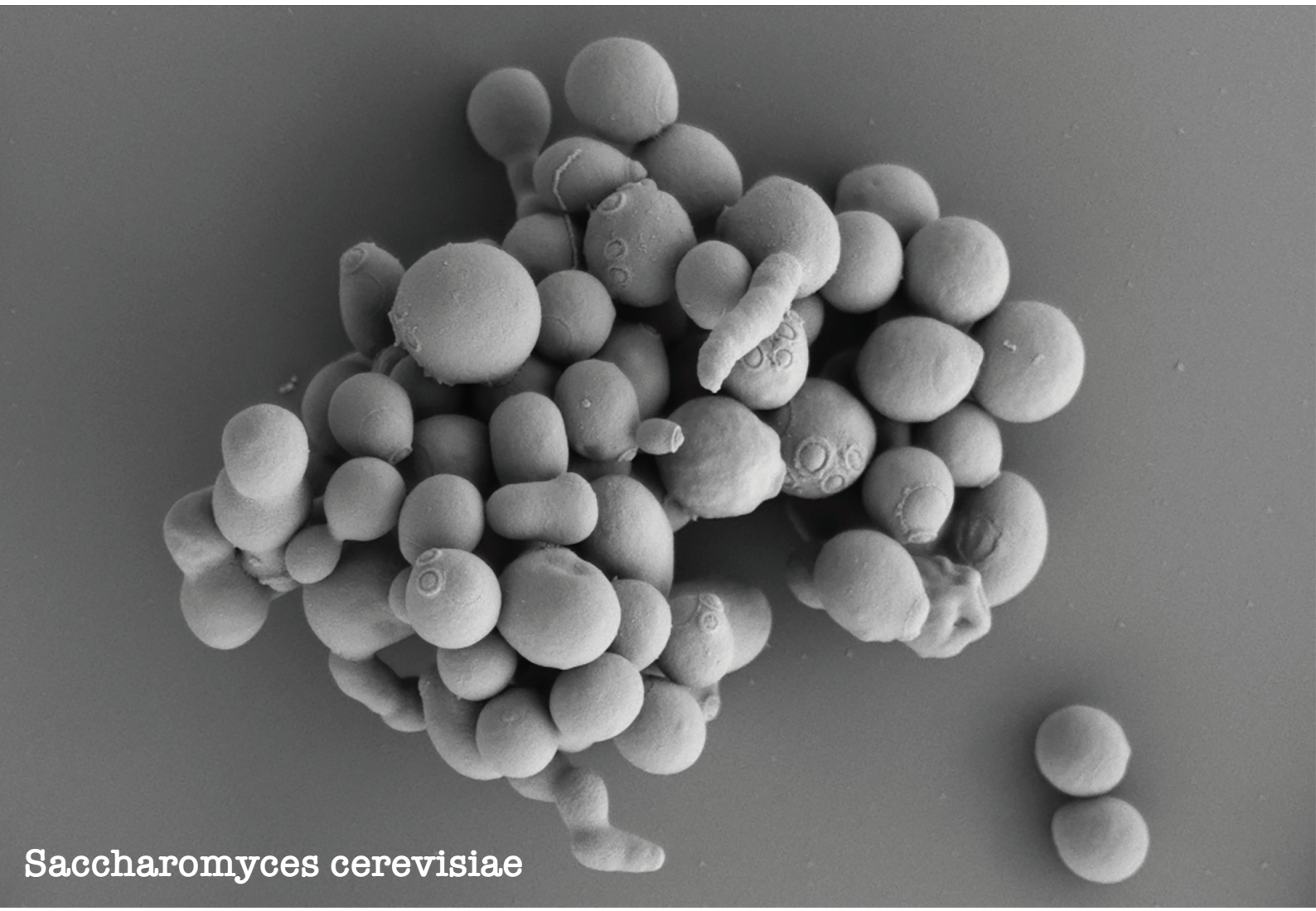

Saccharomyces cerevisiae

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# 1 Preface

The Institute of Veterinary Bacteriology is delighted to distribute its Annual Report summarizing the activities and publications of 2020. It features the achievements of our staff, students and collaborators.

The COVID-19 pandemic shaped the year 2020 in many different aspects. We had to switch most of the teaching to an online format and to adjust the staffing concept of our diagnostic service team and research team to minimize the risk of infection at work, which was mastered successfully. I would like to thank our staff for their devotion regarding the many new tasks and for their spirit to keep teaching, research and diagnostic services at the highest level.

A collaboration with the group of Prof. Volker Thiel from the Institute of Virology and Immunology, which was already initiated in 2018 enabled us to be part of the team of scientists that firstly reconstructed the deadly SARS-CoV-2 virus worldwide. This work was published in the journal Nature and had a great impact worldwide and with respect to media coverage. Concerning our postgraduate education, we established as the first institution in Switzerland a training center for the recently established European College of Veterinary Microbiology (ECVM). Jörg Jores and Gudrun Overesch are recognised de facto ECVM diplomates.

2020 marked the beginning of an independent new ISO 17025:2017 accreditation of the ZOBA, which was successfully mastered by our quality management team and ZOBA team.

Finally, we contributed to the provision of diagnostic services to the university, private practitioners and the Federal Food Safety and Veterinary Office (FSVO) as reference functions and monitoring of antibiotic resistance. I thank all members of the institute, its partners, and customers who made 2020 despite the COVID-19 pandemic a very successful year for veterinary bacteriology in Bern.

Bern, in December 2021 Jörg Jores

# 2 Research Units

## 2.1 Host-Pathogen Interactions

### 2.1.1 Complete Genome Sequences of Four *Brucella suis* Strains Isolated from Swiss Wild Boars

*Publication:* Hatice Akarsu, Isabelle Brodard, Sonja Kittl, Gudrun Overesch, and Joerg Jores (2020) Microbial Resource Announcements, 9: e01048-20, DOI: 10.1128/MRA.01048-20
*Collaborators:* N/A
*Abstract*: We present the complete genomes of four *Brucella suis* biovar 2 isolates that were obtained from wild boars in Switzerland in 2008 and 2009. Genomes were sequenced with PacBio technology, contained two chromosomes each, had a genome size of 3.3 Mbp, and contained more than 3,225 genes per genome.

### 2.1.2 Contagious Bovine and Caprine Pleuropneumonia: a research community's recommendations for the development of better vaccines

*Publication:*Joerg Jores, Cynthia Baldwin, Alain Blanchard, Glenn Browning, Angie Colston, Volker Gerdts, Danny Goovaerts, Martin Heller, Nick Juleff, Fabien Labroussaa, Anne Liljander, Geoffrey Muuka, Vishvanath Nene, Ran Nir-Paz, Flavio Sacchini, Artur Summerfield, François Thiaucourt, Hermann Unger, Sanjay Vashee, Xiumei Wang and Jeremy Salt (2020) NPJ Vaccines, 5: 66, DOI: 10.1038/s41541-020-00214-2
*Collaborators:* University of Massachusetts Amherst, Amherst, USA; INRAE, Universite de Bordeaux, UMR 1332 de Biologie du Fruit et Pathologie, 33882 Villenave d'Ornon, France ; Asia-Pacific Centre for Animal Health, Melbourne Veterinary School, University of Melbourne, Parkville, VIC 3010 Australia; GALVmed, Doherty Building, Pentlands Science Park, Bush Loan, Penicuik, Edinburgh, EH26 0PZ Scotland UK; Vaccine and Infectious Disease Organization-International Vaccine Centre, University of Saskatchewan, Saskatoon, SK Canada; Friedrich-Loeffler-Institute - Federal Research Institute for Animal Health, Jena, Germany; Bill & Melinda Gates Foundation, Seattle, USA; International Livestock Research Institute, Nairobi, Kenya; Central Veterinary Research Institute, Lusaka, Zambia; Hadassah-Hebrew University Medical Center, Jerusalem, Israel; Istituto Zooprofilattico Sperimentale Dell'Abruzzo e Del Molise G. Caporale, Teramo, Italy; Institute of Virology and Immunology, Mittelhausern, Switzerland; Centre de cooperation internationale en recherche agronomique pour le developpement (CIRAD), Montpellier, France; Animal Production and Health Section, Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, Vienna, Austria.
J. Craig Venter Institute, Rockville, USA; Harbin Veterinary Research Institute, Chinese Academy of Agricultural Sciences (CAAS), Harbin, China.
*Abstract*: Contagious bovine pleuropneumonia (CBPP) and contagious caprine pleuropneumonia (CCPP) are major infectious diseases of ruminants caused by mycoplasmas in Africa and Asia. In contrast with the limited pathology in the respiratory tract of humans

infected with mycoplasmas, CBPP and CCPP are devastating diseases associated with high morbidity and mortality. Beyond their obvious impact on animal health, CBPP and CCPP negatively impact the livelihood and wellbeing of a substantial proportion of livestock-dependent people affecting their culture, economy, trade and nutrition. The causative agents of CBPP and CCPP are Mycoplasma mycoides subspecies mycoides and Mycoplasma capricolum subspecies capripneumoniae, respectively, which have been eradicated in most of the developed world. The current vaccines used for disease control consist of a live attenuated CBPP vaccine and a bacterin vaccine for CCPP, which were developed in the 1960s and 1980s, respectively. Both of these vaccines have many limitations, so better vaccines are urgently needed to improve disease control. In this article the research community prioritized biomedical research needs related to challenge models, rational vaccine design and protective immune responses. Therefore, we scrutinized the current vaccines as well as the challenge-, pathogenicity- and immunity models. We highlight research gaps and provide recommendations towards developing safer and more efficacious vaccines against CBPP and CCPP.

### 2.1.3 Differential innate immune responses induced by *Mycoplasma hyopneumoniae* and *Mycoplasma hyorhinis* in various types of antigen presenting cells

*Publication:* Bettina Trueeb, Roman Braun, Gael Auray, Peter Kuhnert, Artur Summerfield (2020) Veterinary Microbiology, 240:108541, DOI: 10.1016/j.vetmic.2019.108541
*Collaborators:* Institute of Virology and Immunology, Switzerland.
*Abstract: Mycoplasma (M.) hyopneumoniae* is the etiological agent of enzootic pneumonia in pigs and is closely related to *M. hyorhinis*, which can be isolated from the healthy mucosal surfaces of the upper respiratory tract. In rare cases it can also cause arthritis and polyserositis. Since the innate immune system is an important first line of defense and promotes adaptive immune responses, we characterized the innate immune response of various antigen presenting cells (APCs) to *M. hyopneumoniae* and *M. hyorhinis*, which differ in their pathogenicity in vivo. Porcine peripheral blood mononuclear cells were infected with different multiplicities of infection (MOI) of live and inactivated porcine mycoplasmas. Both *Mycoplasma* species induced strong tumour necrosis factor (TNF) responses in monocytes, with a stronger activation by *M. hyorhinis*. This higher stimulatory activity was also confirmed for CD40 upregulation. Conventional and plasmacytoid dendritic cells (cDC and pDC, respectively) did not or poorly respond to mycoplasmas in terms of TNF expression but more efficiently in terms of CD40 upregulation. Again, these responses were generally stronger with *M. hyorhinis* than with *M. hyopneumoniae*. Both *Mycoplasma* species also activated B cells in terms of CD25 upregulation, proliferation, and IgM secretion. Interestingly, while the induction of CD25 and in particular proliferation was higher with *M. hyorhinis*, the IgM secretion did not differ between the two species with the exception of the highest dose of *M. hyopneumoniae*,which appeared to suppress IgM responses. Taken together, our results provide a comparative analysis

of innate immune response with different porcine APCs and demonstrate *Mycoplasma* species-dependent differences, which could relate to their different pathogenicity *in vivo*.

### 2.1.4 *Treponema phagedenis* (ex Noguchi 1912) Brumpt 1922 sp. nov., nom. rev., isolated from bovine digital dermatitis

*Publication:* Peter Kuhnert, Isabelle Brodard, Maher Alsaaod, Adrian Steiner, Michael H. Stoffel, Joerg Jores (2020) International Journal of Systematic and Evolutionary Microbiology, 70: 2115–2123, DOI: 10.1099/ijsem.0.004027

*Collaborators:* Clinic for Ruminants, Vetsuisse Faculty, University of Bern, Bern, Switzerland; Division of Veterinary Anatomy, Vetsuisse Faculty, University of Bern, Bern, Switzerland.

*Abstract*: '*Treponema phagedenis*' was originally described in 1912 by Noguchi but the name was not validly published and no type strain was designated. The taxon was not included in the Approved Lists of Bacterial Names and hence has no standing in nomenclature. Six *Treponema* strains positive in a '*T. phagedenis*' phylogroup-specific PCR test were isolated from digital dermatitis (DD) lesions of cattle and further characterized and compared with the human strain 'T. phagedenis' ATCC 27087. Results of phenotypic and genotypic analyses including API ZYM, VITEK2, MALDI-TOF and electron microscopy, as well as whole genome sequence data, respectively, showed that they form a cluster of species identity. Moreover, this species identity was shared with '*T. phagedenis*'-like strains reported in the literature to be regularly isolated from bovine DD. High average nucleotide identity values between the genomes of bovine and human '*T. phagedenis*' were observed. Slight genomic as well as phenotypic variations allowed us to differentiate bovine from human isolates, indicating host adaptation. Based on the fact that this species is regularly isolated from bovine DD and that the name is well dispersed in the literature, we propose the species *Treponema phagedenis* sp. nov., nom. rev. The species can phenotypically and genetically be identified and is clearly separated from other *Treponema* species. The valid species designation will allow to further explore its role in bovine DD. The type strain for *Treponema phagedenis* sp. nov., nom. rev. is B43.1(T) (=DSM 110455(T)=NCTC 14362(T)) isolated from a bovine DD lesion in Switzerland.

### 2.1.5 The prevalence of *Dichelobacter nodosus* in clinically footrot-free sheep flocks: A comparison of elimination concepts

*Publication:* Alinta Kraft, Heinz Strobel, Johanna Hilke, Adrian Steiner, Peter Kuhnert (2020) BMC Veterinary Research, 16:21, DOI: 10.1186/s12917-020-2243-8

*Collaborators:* Clinic for Ruminants, Vetsuisse Faculty, University of Bern, Bern, Switzerland; Schafpraxis, Stoffenried, Germany.

*Abstract:* Background: Ovine footrot caused by *Dichelobacter nodosus* (*D nodosus*) is an infectious disease affecting sheep worldwide. Switzerland plans a nationwide footrot eradication program, based on PCR-testing of interdigital swab samples. The aim of this study was to test for the presence of *D nodosus* in clinically footrot-free sheep flocks which had been subjected to different treatment strategies, to assess whether they were feasible for the

eradication process, especially focussing on antimicrobial flock treatments. Clinical scoring and PCR-results were compared. Ten farms had used hoof bathing and hoof trimming without causing bleeding, ten had used individual treatments and flock vaccines to gain the free status and ten had become free through whole-flock systemic macrolide treatment. For every farm, three risk-based collected pool samples were analysed for the occurrence of virulent and benign *D nodosus* by PCR detection of *aprV2/aprB2*.

Results: Six flocks from any treatment group tested positive for *aprB2* in all pools. Clinical signs were absent at the time of sampling, but some flocks had experienced non-progressive interdigital inflammation previously. Two flocks tested *aprV2*-positive in the high-risk pool. One of them underwent a progressive footrot outbreak shortly after sampling. Individual retesting indicated, that virulent *D nodosus* most likely was reintroduced by a recently purchased ram. In the second flock, a ram was tested positive and treated before clinical signs occurred.

Conclusions: All treatment strategies eliminated the causative agent and were found to be suitable for implementation in the PCR-based eradication process. PCR-testing proved to be more sensitive than visual scoring, as it also detected clinically healthy carriers. It will be of benefit as a diagnostic tool in elimination and surveillance programs.

### 2.1.6 *In vitro* and *ex vivo* testing of alternative disinfectants for use in footbaths against virulent *Dichelobacter nodosus* to replace formaldehyde, zinc sulfate and copper sulfate

*Publication:* Tobias Hidber, Urs Pauli, Adrian Steiner, Peter Kuhnert (2020) PloS ONE, 15:e0229066, DOI: 10.1371/journal.pone.0229066

*Collaborators:* Clinic for Ruminants, Vetsuisse Faculty, University of Bern, Bern, Switzerland; Institute of Virology and Immunology, Switzerland.

*Abstract:* A footbath-based control program for ovine footrot, a contagious disease caused by *Dichelobacter nodosus*, will be implemented in Switzerland. The currently used footbath disinfectants formaldehyde, zinc sulfate and copper sulfate are carcinogenic or environmental pollutants. Hence, the aim of this study was to identify alternative disinfectants, which are highly effective, non-carcinogenic, environmentally acceptable, inexpensive, available as concentrate and suitable for licensing. The antimicrobial effect of a series of potential chemicals such as lactic acid, propionic acid, hydrogen peroxide, sodium hypochlorite, octenidine dihydrochloride, chlorocresol, Ampholyt 20 and the registered biocide DESINTEC® Hoof Care Special D (Desintec) were investigated by culture based in vitro testing. The microcidal effect of various Desintec concentrations were then compared against routinely used 4% formaldehyde and 10% zinc sulfate in ex vivo assays on sheep feet from slaughter. For this purpose a newly established PMA (propidium monoazid) real-time PCR using the improved dye PMAxx™ was applied that allows discrimination of viable and dead *D. nodosus*. In the ex vivo experiments, 4% formaldehyde was significantly more effective than 10% zinc sulfate and

was chosen as positive control for assessing the new disinfectant. The disinfectant effect of Desintec in a minimal concentration of 6% was equally effective as 4% formaldehyde, meaning that it offers a comparable antimicrobial effect against virulent *D. nodosus*. In conclusion, Desintec is a promising disinfectant for replacing formaldehyde, copper sulfate and zinc sulfate in footbaths against footrot.

### 2.1.7 Foot health and prevalence of *Dichelobacter nodosus* in 11 ungulate species at Berne Animal Park

*Publication:* Stefan Hoby, Adrian Steiner, Peter Kuhnert, Rebecca Furtado Jost, Susanne Guthruf, Katja Schönbächler, Maher Alsaaod (2020) Schweizer Archiv für Tierheilkunde, 162:675-681, DOI: 10.17236/sat00277

*Collaborators:* Bern Animal Park, Bern, Switzerland; Clinic for Ruminants, Vetsuisse Faculty, University of Bern, Bern, Switzerland.

*Abstract: Dichelobacter nodosus* (*D. nodosus*) is the etiological agent of ovine footrot affecting mainly sheep worldwide, but also free-ranging wild ungulates such as Alpine ibex (*Capra ibex ibex*) and mufflon (*Ovis orientalis orientalis*). A nationwide ovine footrot eradication program is planned for the years to come, based on polymerase chain reaction (PCR)-testing of interdigital swab samples and regular footbathing. In this cross-sectional study, we clinically evaluated the foot health and analysed presence of *D. nodosus* in 11 different even-toed ungulate species (mainly European species) during a 13 months (2018-2019) period in Berne Animal Park. The foot lesions were scored for any clinical signs of pathologies as described in cattle and simultaneously for clinical signs of footrot as described for sheep, using a scale from 0 to 5 (while 0 describes clinically healthy feet and 5 loss of the horn capsule). From a total of 53 animals, 4-feet swab samples were taken from the interdigital cleft and subjected to real-time PCR assays to detect *D. nodosus* at animal level. Foot lesions were detected in five different species. In 3/5 muskoxen (*Ovibos moschatus wardi*), 7/12 Cretan wild goats (*Capra hircus cretica*) and 2/3 dwarf goats (*Capra hircus aegagrus*), they mainly consisted of white line disease, whereas in 9/10 European bison, dermatitis of the interdigital cleft was diagnosed. 1/3 alpaca was diagnosed with chorioptic mange of the heel area. None of the examined animals showed clinical signs of footrot (score 0), and neither benign (*aprB2*-positive) nor virulent (*aprV2*-positive) *D. nodosus* were detected in any of the samples. This study provides additional information to facilitate an efficient ovine footrot control program in Switzerland and suggests that captive wild even-toed ungulates do not pose a risk to the planned footrot control program.

### 2.1.8 Identification of *Photorhabdus* symbionts by MALDI-TOF mass spectrometry

*Publication:* Virginia Hill, Peter Kuhnert, Matthias Erb, Ricardo Machado (2020) Microbiology, 166:522-530, DOI: 10.1099/mic.0.000905

*Collaborators:* Institute of Plant Sciences, University of Bern, Switzerland; Experimental Biology Research Group, University of Neuchatel, Switzerland.

*Abstract:* Species of the bacterial genus *Photorhabus* live in a symbiotic relationship with *Heterorhabditis* entomopathogenic nematodes. Besides their use as biological control agents against agricultural pests, some *Photorhabdus* species are also a source of natural products and are of medical interest due to their ability to cause tissue infections and subcutaneous lesions in humans. Given the diversity of *Photorhabdus* species, rapid and reliable methods to resolve this genus to the species level are needed. In this study, we evaluated the potential of matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) for the identification of *Photorhabdus* species. To this end, we established a collection of 54 isolates consisting of type strains and multiple field strains that belong to each of the validly described species and subspecies of this genus. Reference spectra for the strains were generated and used to complement a currently available database. The extended reference database was then used for identification based on the direct transfer sample preparation method and the protein fingerprint of single colonies. High-level discrimination of distantly related species was observed. However, lower discrimination was observed with some of the most closely related species and subspecies. Our results therefore suggest that MALDI-TOF MS can be used to correctly identify *Photorhabdus* strains at the genus and species level, but has limited resolution power for closely related species and subspecies. Our study demonstrates the suitability and limitations of MALDI-TOF-based identification methods for assessment of the taxonomic position and identification of *Photorhabdus* isolates.

### 2.1.9 Imaging findings of abdominal arterial pseudoaneurysms caused by systemic mycosis in three dogs

*Publication:* Simona Morabito, Swan Specchi, Edoardo Auriemma, Silvia Ferro, Peter Kuhnert, Eric Zini (2020) Journal of Small Animal Practice, 61:300-307, DOI: 10.1111/jsap.13116

*Collaborators:* Clinic for Small Animal Internal Medicine, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland; Department of Imaging, Animal Health Trust, Newmarket, UK; Department of Diagnostic Imaging, Istituto Veterinario di Novara, Granozzo con Monticello, Italy.

*Abstract:* Objectives: To describe multidetector CT and ultrasonographic characteristics of abdominal arterial pseudoaneurysms (segmental dilatations of an artery with a ruptured *tunica intima*) arising secondary to systemic mycosis in dogs.

Materials and Methods: Retrospective study on dogs with confirmed histological diagnosis of a fungal pseudoaneurysm and the availability of multidetector CT or ultrasound images.

Results:At the time of admission, the three dogs included in this study demonstrated segmental arterial dilation, irregular arterial wall thickening, and increased echogenicity or attenuation within the local perivascular fat on ultrasound and multidetector CT images. Follow-up examinations revealed progressive increase in arterial wall thickening and saccular dilation with formation of a pseudoaneurysm in affected vessels of two dogs.

Clinical Significance: Multidetector CT and ultrasonography can be useful imaging modalities in the diagnosis and monitoring of abdominal arterial pseudoaneurysms caused by systemic mycosis.

### 2.1.10 Vertebral fracture due to *Actinobacillus pleuropneumoniae* osteomyelitis in a weaner

*Publication:* Felix Giebels, Urs Geissbühler, Anna Oevermann, Alex Grahofer, Philipp Olias, Peter Kuhnert, Arianna Maiolini, Veronika Stein (2020) BMC Veterinary Research, 16:438-444, DOI: 10.1186/s12917-020-02656-1

*Collaborators:* Division of Clinical Neurology and Division of Clinical Radiology and Clinic for Swine, Department of Clinical Veterinary Medicine, Division of Neurological Sciences, Department of Clinical Research and Veterinary Public Health, Institute of Animal Pathology, Vetsuisse Faculty, University of Bern, Switzerland.

*Abstract:* Background: Osteomyelitis is relatively frequent in young pigs and a few bacterial species have been postulated to be potential causative agents. Although *Actinobacillus* (*A.*) *pleuropneumoniae* has been sporadically described to cause osteomyelitis, typically, actinobacillosis is characterized by respiratory symptoms. Nevertheless, subclinical infections are a challenging problem in pig herds. To the authors' knowledge, this is the first case description that reports clinical, diagnostic imaging, pathological and histopathological findings of vertebral osteomyelitis in a pig and first describes *A. pleuropneumoniae* as the causative agent identified by advanced molecular methods.

Case presentation: An eight-week-old female weaner was presented with a non-ambulatory tetraparesis. The neurological signs were consistent with a lesion in the C6-T2 spinal cord segments. Imaging studies revealed a collapse of the seventh cervical vertebral body (C7) with a well demarcated extradural space-occupying mass ventrally within the vertebral canal severely compressing the spinal cord. Post-mortem examination identified an abscess and osteomyelitis of C7 and associated meningitis and neuritis with subsequent pathological fracture of C7 and compression of the spinal cord. In the microbiological analysis, *A. pleuropneumoniae* was identified using PCR and DNA sequence analysis.

Conclusions: *A. pleuropneumoniae* can be responsible for chronic vertebral abscess formation with subsequent pathological fracture and spinal cord compression in pigs.

### 2.1.11 Complete Genome Sequence of *Mycoplasma feriruminatoris* Strain IVB14/OD_0535, Isolated from an Alpine Ibex in a Swiss Zoo

*Publication:* Fabien Labroussaaa, Andreas Thomann, Pamela Nicholson, Laurent Falquet* and Joerg Jores* (2020) Microbiology Resource Announcements, 9: e01528-19, DOI: 10.1128/MRA.01528-19, *equal contribution

*Collaborators:* Biochemistry Unit, University of Fribourg and Swiss Institute of Bioinformatics, Fribourg, Switzerland.

*Abstract*: *Mycoplasma feriruminatoris* is a fast-growing and genetically tractable mycoplasma species. We sequenced the Swiss strain IVB14/OD_0535, isolated from an Alpine ibex. This strain has a circular genome of 1,027,435 bp with a G+C content of 24.3%. It encodes 835 open reading frames (ORFs), 2 rRNA operons, and 30 tRNAs.

### 2.1.12 Antimicrobial resistant and extended-spectrum beta-lactamase (ESBL) producing *Escherichia coli* isolated from fecal samples of African dromedary camels

*Publication:* Magdalena Nüesch-Inderbinen, Patrick Kindle, Melinda Baschera, Anne Liljander, Joerg Jores, Victor Max Corman, Roger Stephan (2020) Scientific African, 7: e00274
*Collaborators:* Institute for Food Safety and Hygiene, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland; International Livestock Research Institute, PO Box 30709, 00100 Nairobi, Kenya; Charite-Universitatsmedizin Berlin, Corporate Member of Freie Universitat Berlin, Humboldt-Universitat zu Berlin, and Berlin Institute of Health, Institute of Virology, Berlin, Germany; German Centre for Infection Research, Berlin, Germany.
*Abstract*: This study was conducted to determine the distribution of antimicrobial resistance among *Escherichia coli* isolated from feces of healthy dromedary camels in Kenya. A total of 162 fecal samples were cultivated for *E. coli*. Samples were also subcultivated to detect *E. coli* with extended-spectrum g-lactamases (ESBLs). Antimicrobial susceptibility testing (AST) was performed by disk diffusion using a panel of 16 antimicrobials. In addition, isolates were screened for the presence of the plasmid-mediated colistin resistance genes mcr-1 to mcr-5.
Samples from 20 (12.4%) of the camels contained antimicrobial resistant (AMR) *E. coli*, and 85% of the AMR isolates were multidrug resistant (MDR). The highest frequency of resistance was observed to tetracycline (11.7%), followed by ampicillin and streptomycin (both 10.5%), and sulfamethoxazole/trimethoprim (9.9%). Two (1.2%) of the isolates showed intermediate resistance to cefazolin and streptomycin, respectively. All the isolates were susceptible to amoxycillin/clavulanic acid, ciprofloxacin, fosfomycin, aztreonam and kanamycin, and 86.4% of the isolates were susceptible to all 16 antimicrobials used in this study. The prevalence of fecal carriage of ESBL producing *E. coli* was 0.6%. PCR and amplicon sequencing showed that the ESBL producer belonged to *E. coli* phylogenetic group A, sequence type (ST) 48, and harbored blactx-ma 5. None of the isolates contained mcr genes. The results indicate that dromedary camels in Kenya may be reservoirs of AMR *E. coli*, including ESBL producers, that could potentially be transmitted to humans by direct contact or via the food chain.

### 2.1.13 Reproduction of contagious bovine pleuropneumonia via aerosol-based challenge with *Mycoplasma mycoides* subsp. *mycoides*

*Publication:* Flavio Sacchinia, Anne Liljander, Martin Heller, Jane E Poole, Horst Posthaus, Elise Schieck, and Joerg Jores (2020) Acta Veterinaria Scandinavica, 62: 62
*Collaborators:* International Livestock Research Institute, Old Naivasha Road, PO Box 30709, Nairobi, 00100, Kenya; Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G.

Caporale", Via Campo Boario, 64100, Teramo, Italy; Friedrich-Loeffler-Institute-Federal Research Institute for Animal Health, Naumburger Str. 96a, 07743, Jena, Germany; Institute of Animal Pathology, Department of Infectious Diseases and Pathobiology, Vetsuisse Faculty, University of Bern, Langassstrasse 122, CH-3012, Bern, Switzerland; COMPATH, Vetsuisse Faculty & Faculty of Medicine, University of Bern, Langassstrasse 122, CH-3012, Bern, Switzerland.

*Abstract*: Contagious bovine pleuropneumonia (CBPP) is a respiratory disease caused by *Mycoplasma mycoides* subsp. *mycoides*. Infection occurs via *Mycoplasma*-containing droplets and therefore requires close contact between animals. The current infection models are suboptimal and based on intratracheal installation of mycoplasmas or in-contact infection. This work tested the infection of adult cattle via aerosols containing live mycoplasmas mimicking the infection of cattle in the field. Therefore, we infected six cattle with aerosolized *Mycoplasma mycoides* subsp. *mycoides* strain Afadé over seven consecutive days with altogether 10(9) colony forming units. All animals seroconverted between 11-24 days post infection and five out of six animals showed typical CBPP lesions. One animal did not show any lung lesions at necropsy, while another animal had to be euthanized at 25 days post infection because it reached endpoint criteria. Seroconversion confirmed successful infection and the spectrum of clinical and lesions observed mirrors epidemiological models and the field situation, in which only a fraction of animals suffers from acute clinical disease post infection.

### 2.1.14 Rapid reconstruction of SARS-CoV-2 using a synthetic genomics platform

*Publication*: Tran Thi Nhu Thao[@], Fabien Labroussaa[@], Nadine Ebert[@], Philip V'kovski, Hanspeter Stalder, Jasmine Portmann, Jenna Kelly, Silvio Steiner, Melle Holwerda, Annika Kratzel, Mitra Gultom, Laura Laloli, Linda Hüsser, Manon Wider, Stephanie Pfaender, Dagny Hirt, Valentina Cippà, Silvia Crespo-Pomar, Simon Schröder, Doreen Muth, Daniela Niemeyer, Victor M. Corman, Marcel A. Müller, Christian Drosten, Ronald Dijkman, Joerg Jores*, Volker Thiel*, Nature, DOI: https://doi.org/10.1038/s41586-020-2294-9, [@] equal contribution, *equal supervision

*Collaborators:* Institute of Virology and Immunology, IFIK, Bern, Charite Berlin

*Abstract*: Reverse genetics has been an indispensable tool to gain insights into viral pathogenesis and vaccine development. The genomes of large RNA viruses, such as those from coronaviruses, are cumbersome to clone and manipulate in Escherichia coli owing to the size and occasional instability of the genome(1-3). Therefore, an alternative rapid and robust reverse-genetics platform for RNA viruses would benefit the research community. Here we show the full functionality of a yeast-based synthetic genomics platform to genetically reconstruct diverse RNA viruses, including members of the Coronaviridae, Flaviviridae and Pneumoviridae families. Viral subgenomic fragments were generated using viral isolates, cloned viral DNA, clinical samples or synthetic DNA, and these fragments were then reassembled in one step in Saccharomyces cerevisiae using transformation-associated

recombination cloning to maintain the genome as a yeast artificial chromosome. T7 RNA polymerase was then used to generate infectious RNA to rescue viable virus. Using this platform, we were able to engineer and generate chemically synthesized clones of the virus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)(4), which has caused the recent pandemic of coronavirus disease (COVID-19), in only a week after receipt of the synthetic DNA fragments. The technical advance that we describe here facilitates rapid responses to emerging viruses as it enables the real-time generation and functional characterization of evolving RNA virus variants during an outbreak.

## 2.2 Molecular and Bacterial Epidemiology and Infectious Diseases

### 2.2.1 OXA-181-Producing Extraintestinal Pathogenic *Escherichia coli* Sequence Type 410 Isolated from a Dog in Portugal.

*Publication:* Michael Brilhante, Juliana Menezes, Adriana Belas, Claudia Feudi, Stefan Schwarz, Constança Pomba, Vincent Perreten. Antimicrob Agents Chemother. 2020 Mar 24;64(4):e02298-19.

*Collaborators:* Centre for Interdisciplinary Research in Animal Health (CIISA), Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Portugal. Institute of Microbiology and Epizootics, Centre for Infection Medicine, Department of Veterinary Medicine, Freie Universität Berlin, Berlin, Germany. Graduate School of Cellular and Biomedical Sciences, University of Bern, Bern, Switzerland.

*Abstract*: Two multidrug-resistant and carbapenemase-producing *Escherichia coli* clones of sequence type 410 were isolated from fecal samples of a dog with skin infection on admission to an animal hospital in Portugal and 1 month after discharge. Whole-genome sequencing revealed a 126,409-bp Col156/IncFIA/IncFII multidrug resistance plasmid and a 51,479-bp IncX3 *bla*$_{\text{OXA-181}}$-containing plasmid. The chromosome and plasmids carried virulence genes characteristic for uropathogenic *E. coli*, indicating that dogs may carry multidrug-resistant *E. coli* isolates related to those causing urinary tract infections in humans.

### 2.2.2 *Staphylococcus ursi* sp. nov., a new member of the *'Staphylococcus intermedius* group' isolated from healthy black bears

*Publication:* Vincent Perreten, Stephen A Kania, David Bemis. Int J Syst Evol Microbiol. 2020 Aug;70(8):4637-4645.

*Collaborators:* Department of Biomedical and Diagnostic Sciences, University of Tennessee College of Veterinary Medicine, Knoxville, Tennessee, USA

*Abstract*: Six *Staphylococcus* strains were isolated from healthy black bears (*Ursus americanus*) in the Great Smoky Mountains National Park, Tennessee, USA. Phylogenetic analysis based on complete genome, 16S rRNA, *dnaJ*, *hsp60*, *rpoB* and *sodA* genes, and MALDI-TOF-MS main spectral profiles revealed that the strains belonged to one species and showed the closest relatedness to members of the *'Staphylococcus intermedius group'* (SIG),

which include *Staphylococcus intermedius, Staphylococcus pseudintermedius, Staphylococcus delphini and Staphyloccoccus cornubiensis*. The strains were positive in SIG-specific and negative in individual species-specific PCR assays for the nuc gene. The strains can be differentiated from the other SIG species by the absence of sucrose fermentation, from *S. intermedius* DSM 20373$^T$, *S. pseudintermedius* CCUG 49543$^T$ and *S. cornubiensis* DSM 105366$^T$ by the absence of methyl β-d-glucopyranoside fermentation and from *S. delphini* DSM 20771$^T$ by fermentation of trehalose. DNA relatedness of the type strain MI 10-1553$^T$ with the type strains of *S. delphini, S. pseudintermedius, S. intermedius* and *S. cornubiensis* was ≤48.2 % by digital DNA-DNA hybridization and ≤92.3 % by average nucleotide identity calculations. Iso-C15:0, anteiso-C15 : 0 and anteiso-C17 : 0 were the most common fatty acids. Polar lipids consisted of phosphadidylglycerols, phospholipids, glycolipid, diphosphatidylglycerol and aminophospholipid. Cell-wall peptidoglycan was of type A3α l-Lys-Gly3 (Ser; similar to A11.2 and A11.3). The respiratory quinone belonged to menaquinone 7 (MK-7). The G+C content of MI 10-1553$^T$ was 39.3 mol%. The isolated strains represent a novel species of the genus *Staphylococcus*, for which we propose the name *Staphylococcus ursi* sp. nov. The type strain is MI 10-1553$^T$ (=ATCC TSD-55$^T$=CCOS 1900$^T$).

### 2.2.3 Impact of the early-life skin microbiota on the development of canine atopic dermatitis in a high-risk breed birth cohort

*Publication:* Sabrina Rodriguez-Campos, Ana Rostaher, Lena Zwickl, Niels Fischer, Isabelle Brodard, Sarah Vidal, Bernd W Brandt, Claude Favrot, Vincent Perreten. Sci Rep. 2020 Jan 23;10(1):1044.

*Collaborators:* Bacteriology and Mycology Unit, Faculty of Veterinary Medicine, Norwegian University of Life Sciences, Oslo, Norway. Clinic for Small Animal Internal Medicine, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland. Gnubiotics Sciences SA, Microbiome Research, StartLab/Biopôle, Epalinges, Switzerland. Department of Preventive Dentistry, Academic Centre for Dentistry Amsterdam (ACTA), University of Amsterdam and Vrije Universiteit Amsterdam, Amsterdam, The Netherlands.

*Abstract*: Canine atopic dermatitis (CAD) is a prevalent inflammatory skin disease of dogs worldwide. Certain breeds such as the West Highland White Terriers (WHWT) are predisposed to suffer from CAD. Microbial dysbiosis is known to play a significant role in the pathogenesis of the disease, which is similar to its human counterpart, atopic dermatitis (AD). To date, no large cohort-study has been conducted in a predisposed dog breed to study the impact of the early-life microbiota on the development of CAD, as well as the possible implication of factors such as hygiene and access to the outdoors. In this study skin samples of 143 WHWT, including 109 puppies up to three weeks old and 34 parent dogs, from 17 breeders, were subjected to 16S rRNA gene and ITS2 amplicon sequencing to disclose the bacterial and fungal oral and skin microbiota, respectively. The oral samples served as a control group to confirm differences between haired and mucosal surfaces. The cutaneous microbiota differed between sample sites

and age of the dogs. The season of sampling, geographical origin as well as hygiene status of the household and the access to the outdoors shaped the skin microbiota of the puppies significantly. However, we found that the individual early-life microbiota did not predispose for the later development of CAD.

### 2.2.4 The Novel Macrolide Resistance Genes *mef*(D), *msr*(F), and *msr*(H) Are Present on Resistance Islands in *Macrococcus canis*, *Macrococcus caseolyticus*, and *Staphylococcus aureus*

*Publication:* Sybille Schwendener, Valentina Donà, Vincent Perreten. Antimicrob Agents Chemother. 2020 Apr 21;64(5):e00160-20.

*Abstract*: Chromosomal resistance islands containing the methicillin resistance gene *mecD* (McRI$_{mecD}$ ) have been reported in *Macrococcus caseolyticus* Here, we identified novel macrolide resistance genes in *Macrococcus canis* on similar elements, called McRI$_{msr}$ These elements were also integrated into the 3' end of the 30S ribosomal protein S9 gene (*rpsI*), delimited by characteristic attachment (*att*) sites, and carried a related site-specific integrase gene (*int*) at the 5' end. They carried novel macrolide resistance genes belonging to the *msr* family of ABC subfamily F (ABC-F)-type ribosomal protection protein [*msr*(F) and *msr*(H)] and the macrolide efflux *mef* family [*mef*(D)]. Highly related *mef*(D)-*msr*(F) fragments were found on diverse McRI$_{msr}$ elements in *M. canis*, *M. caseolyticus*, and *Staphylococcus aureus* Another McRI$_{msr}$ -like element identified in an *M. canis* strain lacked the classical *att* site at the 3' end and carried the *msr*(H) gene but no neighboring *mef* gene. The expression of the novel resistance genes in *S. aureus* resulted in a low-to-moderate increase in the MIC of erythromycin but not streptogramin B. In the *mef*(D)-*msr*(F) operon, the *msr*(F) gene was shown to be the crucial determinant for macrolide resistance. The detection of circular forms of McRI$_{msr}$ and the *mef*(D)-*msr*(F) fragment suggested mobility of both the island and the resistance gene subunit. The discovery of McRI$_{msr}$ in different *Macrococcus* species and *S. aureus* indicates that these islands have a potential for dissemination of antibiotic resistance within the *Staphylococcaceae* family.

### 2.2.5 Environmental dissemination of carbapenemase-producing Enterobacteriaceae in rivers in Switzerland

*Publication:* Stephanie Bleichenbacher, Marc J.A. Stevens, Katrin Zurfluh, Vincent Perreten, Andrea Endimian, Roger Stephan, Magdalena Nüesch-Inderbinen. Environ Pollut. 2020 Oct;265(Pt B):115081.

*Collaborators:* Institute for Food Safety and Hygiene, Vetsuisse Faculty, University of Zurich, Winterthurerstrasse 272, 8057, Zurich, Switzerland. Institute for Infectious Diseases, University of Bern, Friedbühlstrasse 51, 3001, Bern, Switzerland. Institute for Food Safety and Hygiene, Vetsuisse Faculty, University of Zurich, Winterthurerstrasse 272, 8057, Zurich, Switzerland.

*Abstract*: The aquatic environment takes on a key role in the dissemination of antimicrobial-resistant Enterobacteriaceae. This study assesses the occurrence of carbapenemase-producing Enterobacteriaceae (CPE) in freshwater samples from rivers, inland canals, and streams throughout Switzerland, and characterizes the isolated strains using phenotypic and NGS-based genotypic methods. CPE producing KPC-2 (n = 2), KPC-3 (n = 1), NDM-5 (n = 3), OXA-48 (n = 3), OXA-181 (n = 6), and VIM-1 (n = 2) were detected in 17/164 of the water samples. Seven *Escherichia coli* had sequence types (STs) that belonged to extra-intestinal pathogenic clonal lineages ST38, ST73, ST167, ST410, and ST648. The majority (16/17) of the carbapenemase genes were located on plasmids, including the widespread IncC (n = 1), IncFIIA (n = 1), and IncFIIB plasmids (n = 4), the epidemic IncL (n = 1) and IncX3 (n = 5) plasmids, a rare Col156 plasmid (n = 1), and the mosaic IncFIB, IncR, and IncQ plasmids (n = 3). Plasmids were composed of elements that were identical to those of resistance plasmids retrieved from clinical and veterinary isolates locally and worldwide. Our data show environmental dissemination of high-risk CPE clones in Switzerland. Epidemic and mosaic-like plasmids carrying clinically relevant carbapenemase genes are replicating and evolving pollutants of river ecosystems, representing a threat to public health and environmental integrity.

### 2.2.6 Employees of Swiss veterinary clinics colonized with epidemic clones of carbapenemase-producing *Escherichia coli*

*Publication:* Andrea Endimiani, Michael Brilhante, Odette J Bernasconi, Vincent Perreten, Janne S Schmidt, Valentina Dazio, Aurélien Nigg, Stefanie Gobeli Brawand, Stefan P Kuster, Simone Schuller, Barbara Willi. J Antimicrob Chemother. 2020 Mar 1;75(3):766-768.

*Collaborators:* Institute for Infectious Diseases, University of Bern, Bern, Switzerland. Graduate School of Cellular and Biomedical Sciences, University of Bern, Bern, Switzerland. Clinic for Small Animal Internal Medicine, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland. Division of Small Animal Internal Medicine, Department of Clinical Veterinary Medicine, University of Bern, Bern, Switzerland. Division of Infectious Diseases and Hospital Epidemiology, University and University Hospital of Zurich, Zurich, Switzerland.

*Abstract*: Between June and October 2018, a total of 108 employees of three Swiss veterinary clinics (A, *n*=46; B, *n*=37; and C, *n*=21) and one private practice (*n*=4) voluntarily self-collected their stools. Two employees (1.9%) were shown to be colonized at the gut level with CPE; one subject at clinic A carried ST410-OXA-181-*Ec* and one subject at clinic B carried ST167-NDM-5-*Ec*. ST410-OXA-181-*Ec* carried $bla_{\text{OXA-181}}$ and *qnrS1* in a 51 kb IncX3 plasmid, while $bla_{\text{CMY-42}}$ was in a 47 kb IncI1 element. ST167-NDM-5-*Ec* possessed three main plasmids: a 99 kb IncFII/FIA/FIB plasmid harbouring $bla_{\text{NDM-5}}$, *aac(3)-IIa*, *aadA2*, *dfrA12*, *mph*(A), *sul1* and *tet*(A); a 71 kb IncFII plasmid with $bla_{\text{CMY-2}}$ and *erm*(B); and a 115 kb IncI1 plasmid possessing $bla_{\text{TEM-30}}$, *aadA1*, *floR*, *sul1/2* and *dfrA1* resistance genes. This study revealed that the diffusion of very successful international epidemic CPE clones in companion animal veterinary clinics not only compromised the outcome of infected animals, but

emphasized that people working with pets can be colonized. These subjects might also contribute to the transmission and further expansion of these life-threatening bacteria to healthy people in the community.

### 2.2.7 PFM-like enzymes are a novel family of subclass B2 metallo-β-lactamases from *Pseudomonas synxantha* belonging to the *Pseudomonas fluorescens* complex

*Publication:* Laurent Poirel, Mattia Palmieri, Michael Brilhante, Amandine Masseron, Vincent Perreten, Patrice Nordmann. Antimicrob Agents Chemother. 2020 Jan 27;64(2):e01700-19.

*Collaborators:* Microbiology Unit, Department of Medicine, Faculty of Science, University of Fribourg, Fribourg, Switzerland INSERM European Unit (IAME, France), University of Fribourg, Fribourg, Switzerland. Swiss National Reference Center for Emerging Antibiotic Resistance (NARA), University of Fribourg, Fribourg, Switzerland. Microbiology Unit, Department of Medicine, Faculty of Science, University of Fribourg, Fribourg, Switzerland. bioMérieux, Data Analytics Unit, La Balme Les Grottes, France. Institute for Microbiology, University of Lausanne and University Hospital Centre, Lausanne, Switzerland.

*Abstract*: A carbapenem-resistant *Pseudomonas synxantha* isolate recovered from chicken meat produced the novel carbapenemase PFM-1. That subclass B2 metallo-β-lactamase shared 71% amino acid identity with β-lactamase Sfh-1 from *Serratia fonticola* The $bla_{\text{PFM-1}}$ gene was chromosomally located and likely acquired. Variants of PFM-1 sharing 90% to 92% amino acid identity were identified in bacterial species belonging to the *Pseudomonas fluorescens* complex, including *Pseudomonas libanensis* (PFM-2) and *Pseudomonas fluorescens* (PFM-3), highlighting that these species constitute reservoirs of PFM-like encoding genes.

### 2.2.8 Effects of the novel concept 'outdoor veal calf' on antimicrobial use, mortality and weight gain in Switzerland

*Publication:* Jens Becker, Gertraud Schüpbach-Regula, Adrian Steiner, Vincent Perreten, Dominik Wüthrich, Anna Hausherr, Mireille Meylan. Prev Vet Med. 2020 Mar;176:104907.

*Collaborators*: Clinic for Ruminants Vetsuisse-Faculty, University of Bern, Switzerland. Veterinary Public Health Institute, Vetsuisse-Faculty, University of Bern, Switzerland. Clinic for Ruminants Vetsuisse-Faculty, University of Bern, Switzerland; Institute of Veterinary Bacteriology, Vetsuisse-Faculty, University of Bern, Switzerland. Clinic for Ruminants Vetsuisse-Faculty, University of Bern, Switzerland.

*Abstract*: The aim of the intervention study 'outdoor veal calf' was to evaluate a novel concept for calf fattening which aimed at reducing antimicrobial use without compromising animal health. Management practices such as commingling of calves from multiple birth farms, crowding, and suboptimal barn climate are responsible for high antimicrobial use and mortality in the veal calf population. The risk of selecting bacteria resistant to antimicrobials and of economic losses is accordingly elevated. The 'outdoor veal calf' concept, implemented in nineteen intervention farms (IF), is based on three main measures: 1. purchased calves are transported directly from neighboring birth farms to the fattening facility instead of

commingling calves in livestock dealer trucks; 2. each calf is vaccinated against pneumonia after arrival and completes a three-week quarantine in an individual hutch; and 3. the calves spend the rest of the fattening period in outdoor hutches in groups not exceeding 10 calves. The covered and bedded paddock and the group hutches provide shelter from cold weather and direct sunshine, constant access to fresh air is warranted. Nineteen conventional calf fattening operations of similar size served as controls (CF). Every farm was visited once a month for a one-year period, and data regarding animal health, treatments, and production parameters were collected. Treatment intensity was assessed by use of the defined daily dose method (TIDDD in days per animal year), and calf mortality and daily weight gain were recorded in both farm groups. Mean TIDDD was 5.3-fold lower in IF compared to CF (5.9 ± 6.5 vs. 31.5 ± 27.4 days per animal year; $p < 0.001$). Mortality was 2.1-fold lower in IF than in CF (3.1% ± 2.3 vs. 6.3 % ± 4.9; $p = 0.020$). Average daily gain did not differ between groups (1.29 ± 0.17 kg/day in IF vs. 1.35 ± 0.16 kg/day in CF; $p = 0.244$). A drastic reduction in antimicrobial use and mortality was achieved in the novel 'outdoor veal calf' system without compromising animal health. The principles of risk reduction used in designing the system can be used to improve management and animal health, decrease the need for antimicrobial treatments and thus selection pressure on bacteria in veal operations.

### 2.2.9 Investigating the use of bacteriophages as a new decolonization strategy for intestinal carriage of CTX-M-15-producing ST131 *Escherichia coli*: An in vitro continuous culture system model

*Publication*. Odette J Bernasconi, Edgar I Campos-Madueno, Valentina Donà, Vincent Perreten, Alessandra Carattoli, Andrea Endimiani. J Glob Antimicrob Resist. 2020 Sep;22:664-671.

*Collaborators:* Institute for Infectious Diseases, University of Bern, Bern, Switzerland. Institute for Infectious Diseases, University of Bern, Bern, Switzerland. Department of Molecular Medicine, Sapienza University of Rome, Rome, Italy. Institute for Infectious Diseases, University of Bern, Bern, Switzerland.

*Abstract*: We investigated the use of bacteriophages as a strategy to decolonize intestinal carriers of multidrug-resistant *Escherichia coli*. A fermentor was used as a continuous culture system for 48h. Two different pools of faeces (studies I and II) obtained from volunteers were spiked with a CTX-M-15-producing ST131 *E. coli* (strain 4901.28) susceptible to bacteriophages and challenged with three doses of INTESTI Bacteriophage cocktail administered at 2, 6 and 10h after the inoculum. Bacterial typing was performed by implementing microdilution panels, spot test, rep-PCR and whole-genome sequencing (including cgMLST and single-nucleotide variant analysis) obtained using Nanopore and Illumina platforms. In study I, bacteriophages decreased the numbers of 4901.28 dramatically (≤101CFU/mL after 6h). In contrast, during study II, a phage-resistant mutant of 4901.28 persisted in the continuous culture (104CFU/mL at 48h). Whole-genome sequencing revealed

the presence of two additional plasmids in the mutant as well as 11 single-nucleotide variants, including one chromosomal in a glycosyltransferase family 2 protein that is responsible for the transfer of sugars to polysaccharides and lipids. In both studies, the commensal *E. coli* population remained unchanged by the phage treatment maintaining itself at 108CFU/mL. Our data indicates that bacteriophage cocktails may be implemented to decolonize some intestinal carriers. However, the individual microbiota composition may have an impact on the development of phage resistance. Mechanisms underlying this phenomenon are likely to be various and complex. Further in vivo studies and protein expression experiments are needed to confirm our observations and hypotheses.

### 2.2.10 Poor infection prevention and control standards are associated with environmental contamination with carbapenemase-producing Enterobacterales and other multidrug-resistant bacteria in Swiss companion animal clinics

*Publication.* Janne S Schmidt, Stefan P Kuster, Aurélien Nigg, Valentina Dazio, Michael Brilhante, Helene Rohrbach, Odette J Bernasconi, Thomas Büdel, Edgar I Campos-Madueno, Stefanie Gobeli Brawand, Simone Schuller, Andrea Endimiani, Vincent Perreten, Barbara Willi. Antimicrob Resist Infect Control. 2020 Jun 23;9(1):93.

*Collaborators:* Clinic for Small Animal Internal Medicine, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland. Division of Infectious Diseases and Hospital Epidemiology, University and University Hospital of Zurich, Zurich, Switzerland. Division of Small Animal Internal Medicine, Department of Clinical Veterinary Medicine, Vetsuisse Faculty, University of Bern, Bern, Switzerland. Graduate School of Cellular and Biomedical Sciences, University of Bern, Bern, Switzerland. Small Animal Clinic, Department of Clinical Veterinary Medicine, Vetsuisse Faculty, University of Bern, Bern, Switzerland. Institute for Infectious Diseases, Faculty of Medicine, University of Bern, Bern, Switzerland. Clinic for Small Animal Internal Medicine, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland. Intensive medical care in companion animal clinics could pose a risk for the selection and dissemination of multidrug-resistant organisms (MDROs). Infection prevention and control (IPC) concepts are key measures to reduce the spread of MDROs, but data on IPC standards in companion animal clinics is sparse. The study assessed IPC standards in seven companion animal clinics and practices in Switzerland by structured IPC audits and combined results with environmental MDRO contamination and MDRO carriage of the personnel. IPC audits were held between August 2018 and January 2019. The observations in 34 IPC areas were scored based on predefined criteria (not fulfilled/partially fulfilled/fulfilled = score 0/1/2). Environmental swabs and nasal and stool samples from veterinary personnel were tested for methicillin-resistant (MR) staphylococci and macrococci and for colistin-resistant, extended-spectrum β-lactamase- and carbapenemase-producing (CP) Enterobacterales (CPE). Species was identified by MALDI-TOF MS, antimicrobial resistance determined by microdilution and β-lactam resistance gene detection, and genetic relatedness assessed by REP-/ERIC-PCR and multilocus

sequence typing. Of a maximum total IPC score of 68, the institutions reached a median (range) score of 33 (19-55). MDROs were detected in median (range) 8.2% (0-33.3%) of the sampling sites. Clinics with low IPC standards showed extensive environmental contamination, i.e. of intensive care units, consultation rooms and utensils. CPE were detected in two clinics; one of them showed extensive contamination with CP *Klebsiella pneumoniae* (ST11, *bla*$_{\text{OXA-48}}$) and MR *Staphylococcus pseudintermedius* (ST551, mecA). Despite low IPC scores, environmental contamination with MDROs was low in primary opinion practices. Three employees were colonized with *Escherichia coli* ST131 (*bla*$_{\text{CTX-M-15}}$, *bla*$_{\text{CTX-M-27}}$, *bla*$_{\text{CTX-M-14}}$). Two employees carried CP *E. coli* closely related to environmental (ST410, *bla*$_{\text{OXA-181}}$) and patient-derived isolates (ST167, *bla*$_{\text{NDM-5}}$). MR *Staphylococcus aureus* (ST225, *mecA*) and MR *S. pseudintermedius* (ST551, *mecA*) of the same sequence types and with similar resistance profiles were found in employees and the environment in two clinics. The study indicates that IPC standards in companion animal clinics are variable and that insufficient IPC standards could contribute to the evolution of MDROs which can be transferred between the environment and working personnel. The implementation of IPC concepts in companion animal clinics should urgently be promoted.

# 3 ZOBA – Centre for Zoonoses, Bacterial Epizootics and Antimicrobial Resistance

In ZOBA encompasses the two subdivisions (i) 'Diagnostic Services and Epizootic Surveillance'and (ii) 'Reference Laboratories and Antimicrobial Resistance Monitoring'. The two subdivisons analysed a total of 27862 samples. Details are shown in Table 1.

Table 1: Number of investigated samples listed per unit of the two subdivisions

| Subdivision | Unit | Number of samples |
|---|---|---|
| Diagnostic Services and Epizootic Surveillance | Clinical material and mycology | 2880 |
| | Necropsy material, abortion and feaces | 3560 |
| | Molecular diagnostics (PCR incl. qPCR) | 1674 |
| | Bovine mastitis | 3177 |
| | Serology | 2568 |
| | Antibiograms for diagnostics | 1546 |
| Reference Laboratories and Resistance Monitoring | Antimicrobial resistance monitoring (detection) | 3137 |
| | Antimicrobial resistance monitoring (MIC*) | 8852 |
| | Reference laboratories | 468 |

* Minimal inhibitory concentration

## 3.1 Diagnostic Services and Epizootic Surveillance (Notifiable Animal Diseases)

Methods:

| | |
|---|---|
| Micr | Microscopic examination |
| IF | Immunofluorescence |
| Cult | Culture |
| ELISA | Antibody detection by Enzyme-Linked Immunosorbent Assay |
| RBT | Antibody detection by Rose Bengal test |
| CFT | Antibody detection by complement fixation test |
| MAT | Antibody detection by the microscopic agglutination test |
| LF | Antibody detection by lateral flow test |
| PCR | Polymerase chain reaction |

SEQ Sequencing

ST Serotyping (* in human reference laboratory)

### 3.1.1 Highly infectious epizootics

Table 2: Number of samples investigated related to highly infectious epizootics

| Epizootic | Agent | Method | Host | Total | Negative | Suspicious | Positive |
|---|---|---|---|---|---|---|---|
| **Contagious Bovine** | *Mycoplasma* | Cult | **Cattle** | 0 | 0 | 0 | 0 |
| **Pleuropneumonia** | *mycoides* subsp. | PCR | | 0 | 0 | 0 | 0 |
| | *mycoides* | ELISA | | 0 | 0 | 0 | 0 |

### 3.1.2 Epizootics to be eradicated

Table 3: Number of samples investigated related to epizootics to be eradicated

| Epizootic | Agent | Method | Host | Total | Negative | Suspicious | Positive |
|---|---|---|---|---|---|---|---|
| **Anthrax** | *Bacillus anthracis* | Micr | **Cattle** | 7 | 7 | 0 | 0 |
| | | Cult | | 7 | 7 | 0 | 0 |
| | *Bacillus anthracis* | Micr | **Bison** | 1 | 1 | 0 | 0 |
| | | Cult | | 1 | 1 | 0 | 0 |
| **Brucellosis** | *Brucella abortus* | Micr | **Cattle** | 83 | 81 | 2 | 0 |
| | | RBT | | 2 | 1 | 0 | 1 |
| | | ELISA | | 810 | 808 | 0 | 2 |
| | | CFT | | 2 | 1 | 0 | 1 |
| | *Brucella melitensis* | Micr | **Sheep/goat** | 15 | 15 | 0 | 0 |
| | | ELISA | | 117 | 114 | 0 | 3 |
| | | CFT | | 0 | 0 | 0 | 0 |
| | | RBT | | 6 | 6 | 0 | 0 |
| | *Brucella abortus /* | Micr | **Others** | 43 | 43 | 0 | 0 |
| | *Brucella melitensis* | ELISA | | 17 | 16 | 0 | 1 |
| | | CFT | | 2 | 2 | 0 | 0 |
| | | RBT | | 45 | 44 | 0 | 1 |
| | *Brucella suis* | Micr | **Pig** | 39 | 39 | 0 | 0 |
| | | RBT | | 707 | 701 | 0 | 6 |

| Epizootic | Agent | Method | Host | Total | Negative | Suspicious | Positive |
|---|---|---|---|---|---|---|---|
| **Brucellosis** | | ELISA | **Pig** | 139 | 134 | 0 | 5 |
| | * anticomplementary | CFT | | 12 | 5 | 5* | 2 |
| | *Brucella ovis* (epizootic to be controlled) | ELISA | **Sheep** | 42 | 38 | 0 | 4 |
| | *Brucella canis* (no epizootic) | Micr | **Dog** | 21 | 21 | 0 | 0 |
| | | LF | | 35 | 35 | 0 | 0 |
| **Bovine genital Campylo-bacteriosis** | *Campylobacter fetus* subspecies *venerealis* | Cult | **Cattle** | 794 | 794 | 0 | 0 |
| | | PCR | | 181 | 181 | 0 | 0 |
| **Sproadic *Campylobacter* abortion** | *Campylobacter fetus* subspecies *fetus* (no epizootic) | Cult | **Ruminats** | 9 | 9 | 0 | 0 |
| | | PCR | | 2 | 2 | 0 | 0 |
| **Glanders** | *Burkholderia mallei* | CFT | **Horse** | 0 | 0 | 0 | 0 |
| | | Cult | | 0 | 0 | 0 | 0 |

### 3.1.3 Epizootics to be controlled

Table 4: Number of samples investigated related to epizootics to be controlled

| Epizootic | Agent | Method | Host | Total | Negative | Suspicious | Positive |
|---|---|---|---|---|---|---|---|
| **Leptospirosis** | *L.* Australis | MAT | **Cattle** | 585 | 585 | 0 | 0 |
| | | | **Dog** | 75 | 58 | 14 | 3 |
| | | | **Horse** | 5 | 4 | 1 | 0 |
| | | | **Pig** | 11 | 11 | 0 | 0 |
| | | | **Others** | 8 | 8 | 0 | 0 |
| | *L.* Autumnalis | MAT | **Dog** | 75 | 70 | 4 | 1 |
| | | | **Horse** | 5 | 5 | 0 | 0 |
| | | | **Others** | 2 | 2 | 0 | 0 |
| | *L.* Ballum | MAT | **Cattle** | 83 | 83 | 0 | 0 |
| | | | **Pig** | 9 | 9 | 0 | 0 |
| | | | **Others** | 7 | 7 | 0 | 0 |
| | *L.* Bataviae | MAT | **Dog** | 75 | 74 | 1 | 0 |
| | | | **Others** | 4 | 4 | 0 | 0 |

| Epizootic | Agent | Method | Host | Total | Negative | Suspicious | Positive |
|---|---|---|---|---|---|---|---|
| **Leptospirosis** | *L.* Bratislava | MAT | **Dog** | 75 | 69 | 4 | 2 |
| | | | **Pig** | 11 | 11 | 0 | 0 |
| | | | **Others** | 10 | 9 | 1 | 0 |
| | *L.* Canicola | MAT | **Cattle** | 588 | 588 | 0 | 0 |
| | | | **Dog** | 75 | 69 | 5 | 1 |
| | | | **Pig** | 11 | 11 | 0 | 0 |
| | | | **Others** | 13 | 13 | 0 | 0 |
| | *L.* Copenhageni | MAT | **Dog** | 53 | 44 | 4 | 5 |
| | | | **Others** | 8 | 8 | 0 | 0 |
| | *L.* Grippotyphosa | MAT | **Cattle** | 588 | 587 | 1 | 0 |
| | | | **Dog** | 76 | 70 | 4 | 2 |
| | | | **Pig** | 11 | 11 | 0 | 0 |
| | | | **Others** | 13 | 12 | 1 | 0 |
| | *L.* Hardjo | MAT | **Cattle** | 607 | 577 | 22 | 8 |
| | | | **Dog** | 75 | 75 | 0 | 0 |
| | | | **Others** | 8 | 7 | 0 | 1 |
| | *L.* Icterohaemo-rrhagiae | MAT | **Cattle** | 588 | 588 | 0 | 0 |
| | | | **Dog** | 75 | 72 | 1 | 2 |
| | | | **Pig** | 13 | 13 | 0 | 0 |
| | | | **Others** | 13 | 13 | 0 | 0 |
| | *L.* Pomona | MAT | **Cattle** | 585 | 585 | 0 | 0 |
| | | | **Dog** | 75 | 71 | 3 | 1 |
| | | | **Pig** | 11 | 11 | 0 | 0 |
| | | | **Others** | 13 | 13 | 0 | 0 |
| | *L.* Pyrogenes | MAT | **Dog** | 75 | 74 | 1 | 0 |
| | | | **Others** | 7 | 7 | 0 | 0 |
| | *L.* Sejroe | MAT | **Cattle** | 592 | 572 | 19 | 1 |
| | | | **Dog** | 24 | 24 | 0 | 0 |
| | | | **Others** | 7 | 6 | 1 | 0 |
| | *L.* Tarassovi | MAT | **Cattle** | 83 | 82 | 1 | 0 |
| | | | **Dog** | 75 | 75 | 0 | 0 |
| | | | **Pig** | 11 | 11 | 0 | 0 |

| Epizootic | Agent | Method | Host | Total | Negative | Suspicious | Positive |
|---|---|---|---|---|---|---|---|
| **Leptospirosis** | | MAT | **Others** | 13 | 13 | 0 | 0 |
| | *Leptopsira* spp. (pathogen) | MAT Eye | **Horse** | 21 | 18 | 3 | 0 |
| | *Leptopsira* spp. (pathogen) | PCR | **Beaver** | 17 | 12 | 0 | 5 |
| | | | **Cattle** | 8 | 8 | 0 | 0 |
| | | | **Pig** | 3 | 3 | 0 | 0 |
| | | | **Dog** | 4 | 4 | 0 | 0 |
| | | | **Horse** | 1 | 1 | 0 | 0 |
| | | | **Others** | 7 | 7 | 0 | 0 |
| **Salmonellosis** | *Salmonella* spp. | Cult/ST | **Alpaca** | 4 | 4 | 0 | 0 |
| | | | **Ape** | 9 | 9 | 0 | 0 |
| | | | **Beaver** | 2 | 2 | 0 | 0 |
| | | | **Bird** | 71 | 70 | | 1 |
| | *S. enterica* subsp. *houtenae* 44:z4,z32: - | | | | | | 1 |
| | | | **Bison** | 1 | 1 | 0 | 0 |
| | | | **Cat** | 39 | 36 | 0 | 3 |
| | *S.* Enteritidis | | | | | | 1 |
| | *S.* Typhimurium | | | | | | 1 |
| | *S.* Typhimurium, monophasic variant (4,12 : i : -) | | | | | | 1 |
| | | | **Cattle** | 487 | 341 | 0 | 146 |
| | *S.* Enteritidis | | | | | | 12 |
| | *S.* Typhimurium | | | | | | 3 |
| | *S.* Typhimurium, monophasic variant (4,12 : i : -) | | | | | | 131 |
| | | | **Chamois** | 4 | 4 | 0 | 0 |
| | | | **Chicken** | 11 | 11 | 0 | 0 |
| | | | **Deer** | 4 | 4 | 0 | 0 |
| | | | **Dog** | 61 | 61 | 0 | 0 |
| | | | **Donkey** | 4 | 4 | 0 | 0 |
| | | | **Fox** | 5 | 3 | 0 | 2 |

| Epizootic | Agent | Method | Host | Total | Negative | Suspicious | Positive |
|---|---|---|---|---|---|---|---|
| **Salmonellosis** | *S.* Enteritidis | | **Fox** | | | | 1 |
| | *S.* Typhimurium | | | | | | 1 |
| | | | **Goat** | 10 | 10 | 0 | 0 |
| | | | **Hedgehog** | 8 | 7 | 0 | 1 |
| | *S.* Enteritidis | | | | | | 1 |
| | | | **Horse** | 38 | 38 | 0 | 0 |
| | | | **Mouse** | 10 | 9 | 0 | 1 |
| | *S. enterica* subsp. *houtenae* 44:z4,z32:- | | | | | | 1 |
| | | | **Pigeon** | 4 | 4 | 0 | 0 |
| | | | **Rabbit** | 6 | 5 | 0 | 1 |
| | *S. enterica* subsp. *diarizonae* 61: k: 1,5,7 | | | | | | 1 |
| | | | **Reptil** | 13 | 10 | 0 | 3 |
| | *S. enterica* subsp. *diarizonae* rough:k:-* | | | | | | 1 |
| | *S. enterica* subsp. *enterica* rough:d:1,2 | | | | | | 1 |
| | *S. enterica* subsp. *houtenae* 11:z4,z32:- | | | | | | 1 |
| | | | **Sheep** | 99 | 96 | 0 | 3 |
| | *S. enterica* subsp. *diarizonae* 61: k: 1,5,7 | | | | | | 3 |
| | | | **Snake** | 7 | 5 | 0 | 2 |
| | *S. enterica* subsp. *diarizonae* 11:l,v: z | | | | | | 1 |
| | *S. enterica* subsp. *diarizonae* 48: i: z* | | | | | | 1 |
| | | | **Pig** | 87 | 87 | 0 | 0 |
| | | | **Tortoise** | 9 | 7 | 0 | 2 |
| | *S. enterica* subsp. *enterica* rough:d:1,2 | | | | | | 1 |
| | *S.* Typhimurium | | | | | | 1 |
| | | | **Wild boar** | 2 | 2 | 0 | 0 |
| | | | **Zoo animal** | 55 | 55 | 0 | 0 |
| | | | **Total** | **1050** | | | **163** |

| Epizootic | Agent | Method | Host | Total | Negative | Suspicious | Positive |
|---|---|---|---|---|---|---|---|
| **Contagious** | *Taylorella* | Cult | **Horse** | 559 | 546 | 13* | 0 |
| **equine metritis** | *equigenitalis* | | **Donkey** | 6 | 3 | 3* | 0 |
| *highly contaminated sample | | PCR | **Horse** | 1 | 1 | 0 | 0 |
| ' | | | **Donkey** | 9 | 9 | 0 | 0 |
| **Enzootic pneumonia in swine** | *Mycoplasma hyopneumoniae* | PCR Lung (pooled) | **Pig** | 71 | 61 | 0 | 10 |
| | | PCR Lung (single) | | 14 | 7 | 0 | 7 |
| | | PCR Nasal swabs (pooled) | | 47 | 46 | 0 | 1 |
| | | PCR Nasal swabs (single) | | 5 | 3 | 0 | 2 |
| | | PCR Project (single)t | | 60 | 60 | 0 | 0 |
| | | PCR Lung (single) | **Wild boar** | 4 | 2 | 0 | 2 |
| | | MLST | **Pig** | 7 | 0 | 0 | 7 |
| | | MLST | **Wild boar** | 2 | 0 | 0 | 2 |
| | | ELISA | **Pig** | 202 | 200 | 1 | 1 |
| **Swine actinobacillosis** | *Actinobacillus pleuropneumoniae* | Cult/PCR | **Pig** | 146 | 101 | 6 | 47 |
| | I BD +II CA, Serotyp 7,12 | | | | | | 17 |
| | I BD+II CA+III CA+BD, Serotyp 2 | | | | | | 8 |
| | I BD + II CA, Serotyp 2 | | | | | | 8 |
| | ICA + BD, Serotyp 10 | | | | | | 2 |

| Epizootic | Agent | Method | Host | Total | Negative | Suspicious | Positive |
|---|---|---|---|---|---|---|---|
| **Swine actinobacillosis** | II CA+IIICA+BD, Serotyp 3 | Cult/PCR | **Pig** | | | | 12 |
| | | ELISA ApxIV | **Pig** | 3 | 0 | 1 | 2 |

### 3.1.4 Epizootics to be Monitored

Table 5: Number of samples investigated related to epizootics to be monitored

| Epizootic | Agent | Method | Host | Total | Negative | Suspicious | Positive |
|---|---|---|---|---|---|---|---|
| **Campylobac-teriosis** | *C. jejuni / C. coli* | Cult | **Dog** | 73 | 67 | 0 | 6 |
| **Campylobac-teriosis** | *C. jejuni / C. coli* | | **Cat** | 35 | 29 | 0 | 6 |
| | | | **Others** | 49 | 45 | 0 | 4 |
| **Listeriosis** | *Listeria monocytogenes* | Cult | **Ruminants** | 6 | 5 | 0 | 1 |
| | | | **Others** | 31 | 20 | 0 | 11 |
| **Yersiniosis** | *Yersinia enterocolitica* | Cult | **Cattle/Pig** | 1 | 0 | 0 | 1 |
| | | | **Others** | 38 | 35 | 0 | 3 |
| | *Yersinia pseudotuberculosis* | Cult | **Hare** | 1 | 0 | 0 | 1 |
| | | | **Others** | 18 | 14 | 0 | 4 |
| **Caseous lymphadenitis in sheep/goat** | *Corynebacterium pseudotuberculosis* | Cult | **Goat** | 3 | 1 | 0 | 2 |
| | | | **Sheep** | 4 | 2 | 0 | 2 |
| **Enzootic abortion in ewes (chlamydiosis)** | *Chlamydia abortus* | Micr | **Sheep** | 11 | 11 | 0 | 0 |
| | | ELISA | | 75 | 54 | 0 | 21 |
| | | PCR | | 1 | 1 | 0 | 0 |
| | | Micr | **Goat** | 4 | 4 | 0 | 0 |
| | | ELISA | | 4 | 4 | 0 | 0 |
| | | PCR | | 2 | 2 | 0 | 0 |
| | | Micr | **Cattle** | 37 | 36 | 1 | 0 |
| | | ELISA | | 0 | 0 | 0 | 0 |
| | | PCR | | 16 | 16 | 0 | 0 |
| | | Micr | **Others** | 7 | 7 | 0 | 0 |
| | | ELISA | | 11 | 8 | 1 | 2 |
| | | PCR | | 6 | 6 | 0 | 0 |

| Epizootic | Agent | Method | Host | Total | Negative | Suspicious | Positive |
|---|---|---|---|---|---|---|---|
| **Psittacosis** | *Chlamydia psittaci* | PCR | **Bird** | 8 | 5 | 0 | 3 |
| | | Micr | | 22 | 22 | 0 | 0 |
| **Tularaemia** | *Francisella* | Cult | **Hare** | 29 | 17 | 0 | 12 |
| | *tularensis* | PCR | | 13 | 9 | 0 | 4 |
| | | Cult | **Others** | 8 | 8 | 0 | 0 |
| | | PCR | | 7 | 7 | 0 | 0 |
| **Blackleg** | *Clostridium* | IF | **Ruminant** | 6 | 6 | 0 | 0 |
| | *chauvoei* | Cult | | 6 | 5 | 0 | 1 |
| **Coxiellosis** | *Coxiella burnetii* | Micr | **Cattle** | 81 | 79 | 2 | 0 |
| | | ELISA | | 20 | 14 | 1 | 5 |
| | | PCR | | 20 | 20 | 0 | 0 |
| | | Micr | **Sheep** | 11 | 11 | 0 | 0 |
| | | ELISA | | 46 | 46 | 0 | 0 |
| | | PCR | **Sheep** | 1 | 0 | 0 | 1 |
| | | Micr | **Goat** | 4 | 4 | 0 | 0 |
| | | ELISA | | 1 | 1 | 0 | 0 |
| | | PCR | | 4 | 4 | 0 | 0 |
| | | Micr | **Others** | 7 | 7 | 0 | 0 |
| | | ELISA | | 11 | 11 | 0 | 0 |
| | | PCR | | 3 | 3 | 0 | 0 |

### 3.1.5 Epizootics planned to be eradicated in the future

Table 5: Number of samples investigated

| Epizootics | Method | Host | Agent | Total | Negative | Suspicious | Positive |
|---|---|---|---|---|---|---|---|
| **Foot rot** | PCR (single or pool) | **Sheep** | *benigne D.nodosus* | 40 | 40 | 0 | 0 |
| | | | *virulent D.nodosus* | 41 | 33 | 0 | 8 |
| | PCR (single or pool) | **Cattle** | *benigne D.nodosus* | 0 | 0 | 0 | 0 |
| | | | *virulent D.nodosus* | 0 | 0 | 0 | 0 |

| Epizootics | Method | Host | Agent | Total | Negative | Suspicious | Positive |
|---|---|---|---|---|---|---|---|
| **Foot rot** | PCR (single or pool) | **Goat** | *benigne D.nodosus* | 1 | 0 | 0 | 1 |
| | | | *virulent D.nodosus* | 1 | 1 | 0 | 0 |

## 3.2 Reference Laboratories and Resistance Monitoring

### 3.2.1 Antimicrobial resistance monitoring for food producing animals and meat thereof

The program follows the specifications laid down in the decision 2013/652/EU on the monitoring and reporting of antimicrobial resistance in zoonotic and commensal bacteria in Europe. Caecal samples from broilers were collected at slaughter and cultured for indicator *E. coli*, *Campylobacter* spp., extended spectrum beta-lactamases (ESBLs) and carbapenemases producing *E. coli.* Moreover, fresh meat thereof from retail was analysed for ESBLs and carbapenemases producing *E. coli*. Isolated strains and all *Salmonella enterica* subspecies *enterica* strains from livestock, provided either from diagnostics and reference function, were tested for antimicrobial susceptibility. Minimal Inhibitory Concentration (MIC) determination was performed by the broth microdilution method.

Results of this antimicrobial resistance monitoring get published in the biannual Swiss antibiotic resistance report, Federal Office of Public Health (FOPH) and Federal Food Safety and Veterinary Office (FSVO). Moreover, annually a summary of the results are published in the ARCH-Vet reports, published by the Federal Food Safety and Veterinary Office (FSVO). On the European level the results are listed in the European summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food, European Food Safety Authority and European Centre for Disease Prevention and Control.

The numbers of analyses that are part of the 2020 antimicrobial resistance monitoring are displayed in tables 6a to 6e.

Table 6a: Number of analyses on ESBL/pAmpC producing *E. coli*

| Matrix | Number of analyses |
|---|---|
| broiler caecal samples | 612 |
| chicken meat samples | 296 |
| **Total** | **908** |

Table 6b: Number of analyses on carbapenemases producing *E. coli*

| Matrix | Number of analyses |
|---|---|
| broiler caecal samples | 612 |
| chicken meat samples | 296 |
| **Total** | **908** |

Table 6c: Number of analyses on indicator *E. coli*

| Matrix | Number of analyses |
|---|---|
| broiler caecal samples | 217 |
| **Total** | **217** |

Table 6d: Number of analyses on *Campylobacter* spp.

| Matrix | Number of analyses |
|---|---|
| broiler caecal samples | 808 |
| chicken meat samples | 296 |
| **Total** | **1104** |

Table 6e: Number of analyses on *Salmonella enterica* subspecies *enterica*

| Salmonella serovar | Number of analyses |
|---|---|
| *S.* Enteritidis | 20 |
| *S.* Typhimurium | 40 |
| *S.* Typhimurium, monophasic variant | 21 |
| other serovars | 57 |
| **Total** | **138** |

### 3.2.2 Confirmation of results from other laboratories (exclusive typing for *Salmonella* spp. and *Actinobacillus pleuropneumoniae*)

Table 7: Number of analyses for confirmation of results from other laboratories (exclusive typing for *Salmonella* spp. and *Actinobacillus pleuropneumoniae*)

| Epizootic | Method | Animal | Total | Negative | Suspicious | Positive |
|---|---|---|---|---|---|---|
| **Anthrax** | Micr | **Cattle** | 0 | 0 | 0 | 0 |
| | Cult | | 0 | 0 | 0 | 0 |
| **Glanders** | Cult | **Horse** | 0 | 0 | 0 | 0 |
| | CFT | **Horse** | 0 | 0 | 0 | 0 |
| **Bovine brucellosis** | ELISA | **Cattle** | 21 | 15 | 3 | 3 |
| | RBT | | 21 | 18 | 0 | 3 |
| | CFT | | 21 | 16 | 3 | 2 |
| | CULT | | 4 | 4 | 0 | 0 |
| | PCR | | 4 | 4 | 0 | 0 |
| **Caprine and ovine brucellosis** | ELISA | **Sheep/ goat** | 0 | 0 | 0 | 0 |
| | RBT | | 0 | 0 | 0 | 0 |
| | CFT | | 0 | 0 | 0 | 0 |
| | PCR | | 0 | 0 | 0 | 0 |
| **Porcine brucellosis** | ELISA | **Swine** | 0 | 0 | 0 | 0 |
| | RBT | | 0 | 0 | 0 | 0 |
| | CFT | | 0 | 0 | 0 | 0 |
| | CULT | | 2 | 2 | 0 | 0 |
| | PCR | | 2 | 2 | 0 | 0 |
| **Canine brucellosis** | LF | **Dog** | 0 | 0 | 0 | 0 |
| | Micr | | 0 | 0 | 0 | 0 |
| | Cult | | 0 | 0 | 0 | 0 |
| | Direct PCR | | 0 | 0 | 0 | 0 |
| **Ovine epididymitis (*Brucella ovis*)** | ELISA | **Sheep** | 1 | 0 | 0 | 1 |
| **Bovine genital campylobacteriosis** | CULT | **Cattle** | 3 | 3 | 0 | 0 |
| **Swine actinobacillosis** | ELISA ApxIV | **Swine** | 0 | 0 | 0 | 0 |
| | Cult | | 44 | 1 | 0 | 43 |
| | PCR | | 43 | 0 | 0 | 43 |

| Epizootic | Method | Animal | Total | Negative | Suspicious | Positive |
|---|---|---|---|---|---|---|
| **Contagious equine metritis** | Cult | **Horse** | 1 | 0 | 1* | 0 |
| *highly contaminated | PCR | | 0 | 0 | 0 | 0 |
| **Blackleg** | IF | **Cattle** | 1 | 0 | 0 | 1 |
| | Cult | | 2 | 0 | 0 | 2 |
| **Enzootic pneumonia in swine*** | ELISA | **Swine** | 20 | 1 | 0 | 19 |
| | PCR Dubosson | | 10 | 10 | 0 | 0 |
| ***EP Diagnostic evaluation | PCR Strait* | | 10 | 10 | 0 | 0 |
| **Tularaemia** | ID | | 0 | 0 | 0 | 0 |
| **Yersiniosis** | ID | **Dog** | 1 | 0 | 0 | 1 |
| **Antimicrobial resistance** | ID, MIC | **Diverse** | 4 | 0 | 0 | 4 |

### 3.2.3 Serotyping of *Salmonella* sp.

Table 8: Number of *Salmonella* spp. isolates for serotyping

| Serovar | Animal | Number |
|---|---|---|
| *S.* Abortusovis | Sheep | 3 |
| *S.* Albany | Chicken | 7 |
| | Dog | 1 |
| | Turkey | 19 |
| *S.* Anatum | Chicken | 4 |
| *S.* Braenderup | Chicken | 3 |
| *S.* Bredeney | Pig | 1 |
| *S.* Coeln | Cattle | 1 |
| *S.* Eboko | Dog | 1 |
| *S.* Enteritidis | Cattle | 5 |
| | Chicken | 17 |
| | Dog | 3 |
| *S.* Gallinarum Biovar Gallinarum | Chicken | 1 |
| *S.* Goladcoat | Chicken | 2 |
| *S.* Hessarek | Chicken | 1 |
| *S.* Jerusalem | Chicken | 7 |
| *S.* Kedougou | Snake | 1 |
| *S.* Kisarawe | Lizard | 1 |
| *S.* Kottbus | Chicken | 3 |
| *S.* Livingstone | Chicken | 1 |
| *S.* Llandoff* | Chicken | 1 |
| *S.* Mbandaka | Chicken | 4 |
| *S.* Muenchen | Bird | 1 |
| *S.* Napoli | Chicken | 1 |
| | Cat | 1 |
| *S.* Nigeria | Horse | 1 |
| *S.* Nyborg | Lizard | 1 |
| *S.* Oranienburg | Lizard | 1 |
| | Frog | 1 |
| *S.* Richmond | Tortoise | 1 |
| *S.* Rissen | Chicken | 1 |

| Serovar | Animal | Number |
|---|---|---|
| *S.* Schwarzengrund | Cattle | 1 |
| *S.* Telelkebir | Lizard | 1 |
| *S.* Tennessee | Chicken | 3 |
| | Guinea pig | 1 |
| | Lizard | 1 |
| *S.* Typhimurium | Cattle | 18 |
| | Chicken | 20 |
| | Bison | 1 |
| | Dog | 1 |
| | Tortoise | 1 |
| | Pig | 1 |
| | Pigeon | 3 |
| *S.* Typhimurium, monophasic variant (4,12 : i : -) | Cattle | 5 |
| | Chicken | 15 |
| *S.* Veneziana | Goose | 1 |
| | Horse | 1 |
| *S.* Welikade | Chicken | 1 |
| *S. enterica* subsp. *arizonae* -41:z4,z23:-* | Lizard | 1 |
| | Mouse | 1 |
| | Snake | 1 |
| *S. enterica* subsp. *enterica* 13,23:i:- | Chicken | 2 |
| *S. enterica* subsp. *enterica* 6,8:-:- | Dog | 2 |
| *S. enterica* subsp. *enterica* rauh:b:l,w | Chicken | 1 |
| *S. enterica* subsp. *enterica* rauh:g,p:- | Deer | 1 |
| *S. enterica* subsp. *diarizonae* 38:r:z* | Chicken | 1 |
| *S. enterica* subsp. *diarizonae* 47:l,v:z | Snake | 1 |
| *S. enterica* subsp. *diarizonae* 48:k:z35* | Snake | 1 |
| *S. enterica* subsp. *diarizonae* 48:k:z53* | Snake | 1 |
| *S. enterica* subsp. *diarizonae* 50:k:z | Snake | 1 |
| *S. enterica* subsp. *diarizonae* 61:-:1,5,7 | Chicken | 1 |
| *S. enterica* subsp. *diarizonae* 65:z10:e,n,x,z15 | Snake | 1 |
| *S. enterica* subsp. *diarizonae* rauh:z10:z35* | Snake | 1 |
| *S. enterica* subsp. *diarizonae* 50:r:z35* | Snake | 1 |
| *S. enterica* subsp. *diarizonae* 53:k:e,n,x,z15 | Chameleon | 3 |

| Serovar | Animal | Number |
|---|---|---|
| *S. enterica* subsp. *diarizonae* 53:k:e,n,,z15 | Chameleon | 1 |
| *S. enterica* subsp. *diarizonae* 53:z10:z35* | Sloth | 3 |
| *S. enterica* subsp. *diarizonae* 61:k:1,5,7 | Sheep | 2 |
| | Chicken | 1 |
| *S. enterica* subsp. *houtenae* 38:z4,z23:-* | Snake | 1 |
| *S. enterica* subsp. *houtenae* 40:z4,z23:-* | Chicken | 1 |
| *S. enterica* subsp. *salamae* 58:l,z13,z28:z6 | Dog | 1 |
| No *Salmonella* | | 2 |
| | **Total** | **207** |

* serotyping in human reference laboratory

### 3.2.4 Swine actinobacillosis: PCR based identification of *Actinobacillus pleuropneumoniae* by *apx* toxin gene typing and *cps2* gene detection

Table 9: Number of *Actinobacillus pleuropneumoniae* (APP) isolates for typing received from other laboratories

| Biovar | apx group | Serotype | Number |
|---|---|---|---|
| Biovar I | apx group: I BD + II CA | 7,12 | 31 |
| Biovar I | apx group: I BD + II CA + III CA + BD<br>*cps*2 gene positive | 2 | 1 |
| Biovar I | apx group: II CA + III CA + BD | 3 | 5 |
| Biovar I | apx group: III CA + BD<br>*other variant of serotype 3* | 3 | 1 |
| Biovar II | apx group: I BD + II CA<br>*cps*2 gene positive | 2 | 5 |
| No APP | - | - | 1 |
| | | **Total** | **44** |

### 3.2.5 Leptospirosis Diagnostics for Humans

Table 10: Number of samples investigated related to humane medicine

| Zoonosis | Agent | Method | Host | Total | Negative | Suspicious | Positive |
|---|---|---|---|---|---|---|---|
| **Leptospirosis** | *L.* Altodouro | MAT | **Human** | 1 | 1 | 0 | 0 |
| | *L.* Andaman | | | 4 | 3 | 1 | 0 |
| | *L.* Australis | | | 4 | 3 | 0 | 1 |
| | *L.* Autumnalis | | | 4 | 3 | 1 | 0 |
| | *L.* Ballum | | | 4 | 4 | 0 | 0 |
| | *L.* Bataviae | | | 4 | 3 | 1 | 0 |
| | *L.* Bratislava | | | 4 | 3 | 1 | 0 |
| | *L.* Canicola | | | 4 | 3 | 0 | 1 |
| | *L.* Celledoni | | | 4 | 4 | 0 | 0 |
| | *L.* Copenhageni | | | 4 | 3 | 0 | 1 |
| | *L.* Cynopetri | | | 4 | 4 | 0 | 0 |
| | *L.* Grippotyphosa | | | 4 | 4 | 0 | 0 |
| | *L.* Hardjo | | | 4 | 4 | 0 | 0 |
| | *L.* Hebdomalis | | | 4 | 4 | 0 | 0 |
| | *L.* Icterohaemo-rrhagiae | | | 4 | 3 | 0 | 1 |
| | *L.* Javanica | | | 4 | 3 | 1 | 0 |
| | *L.* Panama | | | 4 | 4 | 0 | 0 |
| | *L.* Patoc | | | 3 | 3 | 0 | 0 |
| | *L.* Pomona | | | 4 | 4 | 0 | 0 |
| | *L.* Pyrogenes | | | 4 | 3 | 1 | 0 |
| | *L.* Sejroe | | | 4 | 3 | 1 | 0 |
| | *L.* Shermani | | | 4 | 3 | 1 | 0 |
| | *L.* Tarassovi | | | 4 | 4 | 0 | 0 |
| | pathogene Leptospiren | PCR | **Human** | 9 | 8 | 0 | 1 |

### 3.2.6 Organisation of Proficiency Testing for approved laboratories

As Swiss national reference laboratory for a broad range of zoonotic or epizootic diseases and antimicrobial resistance the ZOBA is responsible for the diagnostic quality of the approved laboratories in Switzerland. For this purpose the ZOBA organized proficiency testings for these laboratories, which are mandatory for the approval by the Federal Food Safety and Veterinary Office. The proficiency testings conducted in 2020 are listed in Table 11.

Table 11: Proficiency testings for approved laboratories organised by the ZOBA in 2020

| Target | Method | Number of samples | Number of laboratories |
|---|---|---|---|
| Anthrax microscopy | Micr | 10 | 2 |
| Brucellosis microscopy | Micr | 15 | 8 |
| Brucellosis serology | ELISA | 10 | 9 |

## 3.3 Research Activities

### 3.3.1 Methicillin-resistant *Staphylococcus aureus* strains in Swiss pigs and their relation to isolates from farmers and veterinarians.

*Publication:* Sonja Kittl, Isabelle Brodard , Dagmar Heim, Patrizia Andina-Pfister, Gudrun Overesch. Appl Environ Microbiol. 2020 Feb 18;86(5). pii: e01865-19. doi: 10.1128/AEM.01865-19

*Collaborators:* Federal Food Safety and Veterinary Office, Bern, Switzerland, Gesellschaft Schweizer Tierärztinnen und Tierärzte GST, Bern, Switzerland

*Abstract*: Methicillin-resistant *Staphylococcus aureus* (MRSA) has emerged over the last decades as a One Health problem with an increasing prevalence in various animal species. The most notable animals are pigs, as asymptomatic carriers, and horses, where there is often an association with infections. The current study looked at the course of MRSA prevalence in Swiss livestock since 2009, with a special focus on pigs, followed by screening of veterinarians and farmers. Livestock isolates were obtained from the Swiss monitoring program and then characterized by *spa* typing. Concentrating on the year 2017, we analyzed the prevalence of MRSA in Swiss veterinarians and farmers, followed by whole-genome sequencing of selected human and animal strains. The phylogeny was assessed by applying core-genome multilocus sequence typing (MLST) and single-nucleotide polymorphism (SNP) analyses, followed by screening for resistance genes and virulence factors. The prevalence of MRSA in Swiss pigs showed a dramatic increase from 2% in 2009 to 44% in 2017. Isolates almost consistently belonged to clonal complex 398 (CC398), split between *spa* types t011 and t034. The higher prevalence was mainly due to an increase in t011. *Spa* type t034 strains from farmers were found to be closely associated with porcine t034 strains. The same could be shown for t011

strains from horses and veterinarians. *spa* type t034 strains had a high number of additional resistance genes, and two strains had acquired the immune evasion cluster. However, all but one of the pig t011 strains clustered in a separate group. Thus, the increase in pig t011 strains does not directly translate to humans.

### 3.3.2 *Clostridium perfringens*-Associated Necrotic Enteritis-Like Disease in Coconut Lorikeets (Trichoglossus haematodus)

*Publication*: Llorenç Grau-Roma, Mauricio Navarro, Sohvi Blatter , Christian Wenker, Sonja Kittl, Francisco A Uzal, Horst Posthaus Vet Pathol. 2021 Mar;58(2):423-427. doi: 10.1177/0300985820971788. Epub 2020 Nov 19.

*Collaborators*: Institute of Veterinary Pathology, University of Bern, Bern Switzerland

*Abstract*: Several outbreaks of necrotic enteritis-like disease in lorikeets, from which *Clostridium perfringens* was consistently isolated, are described. All lorikeets had acute, segmental, or multifocal fibrinonecrotizing inflammatory lesions in the small and/or the large intestine, with intralesional gram-positive rods. The gene encoding *C. perfringens* alpha toxin was detected by PCR (polymerase chain reaction) on formalin-fixed, paraffin-embedded (FFPE) tissues in 20 out of 24 affected lorikeets (83%), but it was not amplified from samples of any of 10 control lorikeets ($P < .0001$). The second most prevalent *C. perfringens* toxin gene detected was the beta toxin gene, which was found in FFPE from 7 out of 24 affected lorikeets (29%). The other toxin genes were detected inconsistently and in a relatively low number of samples. These cases seem to be associated with *C. perfringens*, although the specific type involved could not be determined.

### *3.3.3 Clostridium perfringens* type C necrotic enteritis in pigs: diagnosis, pathogenesis, and prevention

*Publication:* Horst Posthaus, Sonja Kittl, Basma Tarek, Julia Bruggisser J Vet Diagn Invest. 2020 Mar;32(2):203-212. doi: 10.1177/1040638719900180. Epub 2020 Jan 20.

*Collaborators*: Institute of Veterinary Pathology, University of Bern, Bern Switzerland

*Abstract*: *Clostridium perfringens* type C causes severe and lethal necrotic enteritis (NE) in newborn piglets. NE is diagnosed through a combination of pathology and bacteriologic investigations. The hallmark lesion of NE is deep, segmental mucosal necrosis with marked hemorrhage of the small intestine. *C. perfringens* can be isolated from intestinal samples in acute cases but it is more challenging to identify pathogenic strains in subacute-to-chronic cases. Toxinotyping or genotyping is required to differentiate *C. perfringens* type C from commensal type A strains. Recent research has extended our knowledge about the pathogenesis of the disease, although important aspects remain to be determined. The pathogenesis involves rapid overgrowth of *C. perfringens* type C in the small intestine, inhibition of beta-toxin (CPB) degradation by trypsin inhibitors in the colostrum of sows, and most likely initial damage to the

small intestinal epithelial barrier. CPB itself acts primarily on vascular endothelial cells in the mucosa and can also inhibit platelet function. Prevention of the disease is achieved by immunization of pregnant sows with *C. perfringens* type C toxoid vaccines, combined with proper sanitation on farms. For the implementation of prevention strategies, it is important to differentiate between disease-free and pathogen-free status of a herd. The latter is more challenging to maintain, given that *C. perfringens* type C can persist for a long time in the environment and in the intestinal tract of adult animals and thus can be distributed via clinically and bacteriologically inapparent carrier animals.

### 3.3.4 *Campylobacter jejuni* from canine and bovine cases of campylobacteriosis express high antimicrobial resistance rates against (fluoro)quinolones and tetracyclines.

*Publication*: Sarah Moser, Helena Seth-Smith, Adrian Egli, Sonja Kittl, Gudrun Overesch. Pathogens. 2020 Aug 23;9(9):691

*Collaborators:* University Hospital Basel, 4001 Basel, Switzerland

*Abstract*: *Campylobacter* (*C.*) spp. from poultry is the main source of foodborne human campylobacteriosis, but diseased pets and cattle shedding *Campylobacter* spp. may contribute sporadically as a source of human infection. As fluoroquinolones are one of the drugs of choice for the treatment of severe human campylobacteriosis, the resistance rates of *C. jejuni* and *C. coli* from poultry against antibiotics, including fluoroquinolones, are monitored within the European program on antimicrobial resistance (AMR) in livestock. However, much less is published on the AMR rates of *C. jejuni* and *C. coli* from pets and cattle. Therefore, *C. jejuni* and *C. coli* isolated from diseased animals were tested phenotypically for AMR, and associated AMR genes or mutations were identified by whole genome sequencing. High rates of resistance to (fluoro)quinolones (41%) and tetracyclines (61.1%) were found in *C. jejuni* (n = 29/66). (Fluoro)quinolone resistance was associated with the known point mutation in the quinolone resistance-determining region (QRDR) of gyrA, and tetracycline resistance was mostly caused by the tet(O) gene. These high rates of resistance, especially to critically important antibiotics in *C. jejuni* and *C. coli,* are worrisome not only in veterinary medicine. Efforts to preserve the efficacy of important antimicrobial treatment options in human and veterinary medicine have to be strengthened in the future.

### *3.3.5* Abortions and stillbirths caused by *Coxiella burnetii* in goats.

*Publication:* Miriam Heinzelmann, Sabrina Rodriguez-Campos, Sonja Kittl, Patrik Zanolari, Gabriela Hirsbrunner. Schweiz Arch Tierheilkd. 2020 Oct;162(10):625-633. doi: 10.17236/sat00275.

*Collaborators*: Clinic for Ruminants, Vetsuisse Faculty, University of Bern, Bern, Switzerland

*Abstract*: Coxiellosis, caused by the bacterium *Coxiella burnetii*, is a reportable disease in animals and humans in Switzerland. The number of cases in farm animals and humans has risen continuously in recent years. The aim of this work was to investigate abortions and stillbirths in goats with a focus on *C. burnetii*, to identify excretory routes which pose a zoonotic risk and the excretion time after an acute infection. Besides the submitted fetuses, does were screened

with a serological antibody test. In addition, excretion via milk, faeces and vaginal mucus were investigated in dams with fetuses tested positive for *C. burnetii* at 14-day intervals. *C. burnetii* were isolated in 8 cases (3× in the placenta, 2× in the abomasum, 3× in the placenta and abomasum) of 13 examined stillbirths/abortions. Ten abomasums of goat kids and 8 placentas were examined using modified Ziehl-Neelsen staining (ZN) according to Stamp simultaneously with a real-time PCR. Four of 18 samples were false negative using modified ZN staining according to Stamp in contrast to real-time PCR. Seven does had serum antibodies against *Coxiella*. The excretion of *C. burnetii* persisted for 63 days in the milk, for 96 days in the vaginal mucus and for 96 respectively 114 days in two does monitored extensively. Intermittent excretion could also be observed in the milk during these 63 days. The present study showed that confirmation of disease, respectively transmission cannot be based on a single test. Only combined serological antibody test and real-time PCR examinations of birth material, milk, feces and vaginal mucus can result in a conclusive diagnosis. In addition, the examination using modified ZN staining according to Stamp is less sensitive and specific than the real-time PCR examination.

### *3.3.6* Assessing *Campylobacter* colonization of broiler herds *ante mortem* and monitoring *Campylobacter* contamination *post mortem* by qPCR

*Publication*: Gudrun Overesch, Katrin Haas, Peter Kuhnert. 2020. Pathogens. 2020 Sep 10;9(9):742, DOI: 10.3390/pathogens9090742

*Collaborators:* Institute of Veterinary Bacteriology, University of Bern, Bern, Switzerland

*Abstract*: Human campylobacteriosis is the most prevalent zoonosis, with chicken and meat contributing substantially to the number of cases. Measures to avoid or at least reduce exposure by meat contaminated with *Campylobacter* (*C.*) spp. are needed. With regard to the process hygiene criterion introduced in 2018 for *Campylobacter* spp. on broiler carcasses, we evaluated the performance of a recently developed quantitative real-time PCR (qPCR) for *C. jejuni/coli* on random caecal samples and chicken meat. With the qPCR on pooled caecal samples not only *C. jejuni/coli* positive (69.6%) versus negative broiler herds (30.4%) were identified, but herds highly colonized with *C. jejuni/coli* (39.4%) could also be identified. From the chicken meat samples, 8.0% were positive for *C. jejuni/coli*. by qPCR and 0.7% by enumeration (>10 cfu/g) compared to 58.3% using cultural enrichment. Given the higher sensitivity, the qPCR method could replace the currently used enumeration method to assess the process hygiene criterion for *Campylobacter* spp. on broiler carcasses. Moreover, with the qPCR, a reliable identification of *C. jejuni/coli* colonized incoming broiler herds a few days before slaughter is feasible, which provides important information to optimize slaughter processes. Finally, identifying and monitoring herds with high C. jejuni/coli colonization rates could help to individually improve biosecurity measures at farm level, eventually reducing the *C. jejuni/coli* load on chicken meat.

### 3.3.7 First European report of *Francisella tularensis* subsp. *holarctica* isolation from a

**domestic cat**

*Publication:* Sonja Kittl, Thierry Francey, Isabelle Brodard, Francesco C Origgi, Stéphanie Borel, Marie-Pierre Ryser-Degiorgis, Ariane Schweighauser, Joerg Jores.Vet Res. 2020 Aug 31;51(1):109. doi: 10.1186/s13567-020-00834-5.

*Collaborators*: Clinic for Small Animals, Vetsuisse Faculty, University of Bern, Bern, Switzerland

*Abstract*: *Francisella tularensis* subsp. *holarctica* is a select agent causing life-threatening tularemia. It has been isolated from humans and animals, mainly lagomorphs and rodents, rarely other wild carnivore species. Increasing numbers of human tularemia cases have been reported during the last 5 years in Switzerland. Here we report the first isolation of *Francisella tularensis* subsp. *holarctica* from a domestic cat in Europe and compare its genome sequence with other Swiss isolates. The cat isolate shows a close phylogenetic relationship with a contemporary hare isolate from close geographic proximity, indicating a possible epidemiological link.

### 3.3.8 Prevalence and antimicrobial resistance of opportunistic pathogens associated with bovine respiratory disease isolated from nasopharyngeal swabs of veal calves in Switzerland.

*Publication:* Lutz Schönecker, Petra Schnyder, Gertraud Schüpbach-Regula, Mireille Meylan, Gudrun Overesch. Prev Vet Med. 2020 Oct 20;185:10518

*Collaborators:* Clinic for Ruminants, Vetsuisse Faculty, University of Bern, Bern, Switzerland, Veterinary Public Health Institute, Vetsuisse Faculty, University of Bern, Bern, Switzerland

*Abstract*: The composition of the bacterial flora in the calf nasopharynx might influence the risk of bovine respiratory disease (BRD). The aims of the present study were, firstly, to investigate the prevalence of bacteria potentially involved in BRD in the nasopharynx of veal calves and to identify associated risk factors for their presence, and, secondly, to provide data on antimicrobial resistance levels in these bacteria.

Deep nasopharyngeal swabs were collected from veal calves on 12 Swiss farms over a period of one year by non-random, but systematic sampling for isolation of *Pasteurellaceae* and *Mycoplasma* (*M.*) *bovis* and *dispar*. Associations of potential risk factors with occurrence of these bacteria were tested in multivariable mixed logistic regression analyses, based on information gained from extensive questionnaires completed with the farmers. Antimicrobial susceptibility testing was performed for *Pasteurellaceae* by broth microdilution method to obtain minimal inhibitory concentrations (MIC).

*Pasteurellaceae,* including *Pasteurella* (*P.*) *multocida, Mannheimia* (*M.*) *haemolytica,* Bisgaard Taxon 39 and *Histophilus* (*H.*) *somni,* were almost twice as prevalent as *M. bovis* and dispar in this study. Continuous stocking was a risk factor for the presence of *Pasteurellaceae*, especially when calves originated from more than six suppliers. In young calves (≤ 91 days),

feeding of California Mastitis Test (CMT) positive milk was an additional risk factor for the presence of *Pasteurellaceae* whereas transport of calves by farmers and livestock traders (as opposed to transport only by farmers) increased the risk in older calves (> 91 days). Risk factors for the presence of *M. bovis/dispar* were higher number of calves per drinking nipple in young calves and no access to an outside pen and feeding of CMT positive milk in older calves, respectively. While further research will have to investigate the observed associations in more detail, this suggests that management can play an important role in the prevalence of nasopharyngeal bacteria with a potential subsequent involvement in BRD. Antimicrobial resistance differed between the three bacterial species tested in this study and was highest to oxytetracycline and spectinomycin in *P. multocida*, oxytetracycline and penicillin in *M. haemolytica* and ampicillin and penicillin in *H. somni*. Only two European VetCAST breakpoints (for florfenicol in *P. multocida* and *M. haemolytica*) have been published to date matching the MIC distribution of the present isolate populations well, in contrast to certain commonly applied American Clinical and Laboratory Institute interpretive criteria. This highlights the potential for further refinement of clinical breakpoints in veterinary medicine.

# 4 Teaching Obligations

## 4.1 Bacteriology Lecture Series

| | |
|---|---|
| General Bacteriology and Mycology: | 26 x 45 min |
| Clinical Bacteriology and Mycology: | 26 x 45 min |
| Blood parasites | 1 x 45 min |

## 4.2 Organ Specific Lectures

| | |
|---|---|
| Blood/Laboratory/Immune system: | 1 x 45 min |
| Skin and Thermoregulation: | 1 x 45 min |

## 4.3 Clinical Topics

| | |
|---|---|
| Population Medicine: | 8 x 45 min |

## 4.4 Hands on Courses

| | |
|---|---|
| Practical Course in Bacteriology: | 48 x 45 min |
| Practical Course in Microbial and Immunological Diagnostics: | 56 x 45 min |

# 5 Publications

## 5.1 Peer-Reviewed Publications


1. Akarsu H., Brodard I., Kittl S., Overesch G., Jores J., Complete Genome Sequences of Four *Brucella suis* Strains Isolated from Swiss Wild Boars. *Microbiol Resour Announc* **9** (2020).
2. Arduser F., Moore-Jones G., Gobeli Brawand S., Durr S., Steiner A., Ryser-Degiorgis M. P., Zanolari P., *Dichelobacter nodosus* in sheep, cattle, goats and South American camelids in Switzerland-Assessing prevalence in potential hosts in order to design targeted disease control measures. *Prev Vet Med* **178**, 104688 (2020).
3. Becker J., Schupbach-Regula G., Steiner A., Perreten V., Wuthrich D., Hausherr A., Meylan M., Effects of the novel concept 'outdoor veal calf' on antimicrobial use, mortality and weight gain in Switzerland. *Prev Vet Med* **176**, 104907 (2020).
4. Bernasconi O. J., Campos-Madueno E. I., Dona V., Perreten V., Carattoli A., Endimiani A., Investigating the use of bacteriophages as a new decolonization strategy for intestinal carriage of CTX-M-15-producing ST131 *Escherichia coli*: An *in vitro* continuous culture system model. *J Glob Antimicrob Resist* **22**, 664-671 (2020).
5. Bleichenbacher S., Stevens M. J. A., Zurfluh K., Perreten V., Endimiani A., Stephan R., Nuesch-Inderbinen M., Environmental dissemination of carbapenemase-producing *Enterobacteriaceae* in rivers in Switzerland. *Environ Pollut* **265**, 115081 (2020).
6. Brilhante M., Menezes J., Belas A., Feudi C., Schwarz S., Pomba C., Perreten V., OXA-181-Producing Extraintestinal Pathogenic *Escherichia coli* Sequence Type 410 Isolated from a Dog in Portugal. *Antimicrob Agents Chemother* **64** (2020).
7. Duquesne F., Merlin A., Perez-Cobo I., Sedlak K., Melzer F., Overesch G., Fretin D., Iwaniak W., Breuil M. F., Wernery U., Hicks J., Aguero-Garcia M., Frias-Serrano N., San Miguel-Ibanez E., Patrasova E., Waldvogel A. S., Szulowski K., Joseph M., Jeeba J., Shanty J., Varghese P., Hans A., Petry S., Overview of spatio-temporal distribution inferred by multi-locus sequence typing of *Taylorella equigenitalis* isolated worldwide from 1977 to 2018 in *equidae*. *Vet Microbiol* **242**, 108597 (2020).
8. Egli A., Koch D., Danuser J., Hendriksen R. S., Driesen S., Schmid D. C., Neher R., Mausezahl M., Seth-Smith H. M. B., Bloemberg G., Tschudin-Sutter S., Endimiani A., Perreten V., Greub G., Schrenzel J., Stephan R., Symposium report: One Health meets sequencing. *Microbes Infect* **22**, 1-7 (2020).

9. Endimiani A., Brilhante M., Bernasconi O. J., Perreten V., Schmidt J. S., Dazio V., Nigg A., Gobeli Brawand S., Kuster S. P., Schuller S., Willi B., Employees of Swiss veterinary clinics colonized with epidemic clones of carbapenemase-producing *Escherichia coli*. *J Antimicrob Chemother* **75**, 766-768 (2020).
10. Fritschi J., Marti H., Seth-Smith H. M. B., Aeby S., Greub G., Meli M. L., Hofmann-Lehmann R., Muhldorfer K., Stokar-Regenscheit N., Wiederkehr D., Pilo P., Van Den Broek P. R., Borel N., Prevalence and phylogeny of *Chlamydiae* and hemotropic mycoplasma species in captive and free-living bats. *BMC Microbiol* **20**, 182 (2020).
11. Giebels F., Geissbuhler U., Oevermann A., Grahofer A., Olias P., Kuhnert P., Maiolini A., Stein V. M., Vertebral fracture due to *Actinobacillus pleuropneumoniae* osteomyelitis in a weaner. *BMC Vet Res* **16**, 438 (2020).
12. Hidber T., Pauli U., Steiner A., Kuhnert P., *In vitro* and *ex vivo* testing of alternative disinfectants to currently used more harmful substances in footbaths against *Dichelobacter nodosus*. *PLoS One* **15**, e0229066 (2020).
13. Hill V., Kuhnert P., Erb M., Machado R. A. R., Identification of *Photorhabdus* symbionts by MALDI-TOF MS. *Microbiology* **166**, 522-530 (2020).
14. Hoby S., Steiner A., Kuhnert P., Furtado Jost R., Guthruf S., Schonbachler K., Alsaaod M., Foot health and prevalence of *Dichelobacter nodosus* in 11 ungulate species at Berne Animal Park. *Schweiz Arch Tierheilkd* **162**, 675-681 (2020).
15. Jores J., Baldwin C., Blanchard A., Browning G. F., Colston A., Gerdts V., Goovaerts D., Heller M., Juleff N., Labroussaa F., Liljander A., Muuka G., Nene V., Nir-Paz R., Sacchini F., Summerfield A., Thiaucourt F., Unger H., Vashee S., Wang X., Salt J., Contagious Bovine and Caprine Pleuropneumonia: a research community's recommendations for the development of better vaccines. *NPJ Vaccines* **5**, 66 (2020).
16. Kauer R. V., Koch M. C., Schonecker L., Becker J., Holwerda M., Glaus A. N., Hierweger M. M., Werder S., Dijkman R., Meylan M., Seuberlich T., Fecal Shedding of Bovine Astrovirus CH13/NeuroS1 in Veal Calves. *J Clin Microbiol* **58** (2020).
17. Kittl S., Brodard I., Heim D., Andina-Pfister P., Overesch G., Methicillin-Resistant *Staphylococcus aureus* Strains in Swiss Pigs and Their Relation to Isolates from Farmers and Veterinarians. *Appl Environ Microbiol* **86** (2020).
18. Kittl S., Francey T., Brodard I., Origgi F. C., Borel S., Ryser-Degiorgis M. P., Schweighauser A., Jores J., First European report of *Francisella tularensis* subsp. *holarctica* isolation from a domestic cat. *Vet Res* **51**, 109 (2020).

19. Kraft A. F., Strobel H., Hilke J., Steiner A., Kuhnert P., The prevalence of *Dichelobacter nodosus* in clinically footrot-free sheep flocks: a comparative field study on elimination strategies. *BMC Vet Res* **16**, 21 (2020).
20. Kuhnert P., Brodard I., Alsaaod M., Steiner A., Stoffel M. H., Jores J., *Treponema phagedenis* (ex Noguchi 1912) Brumpt 1922 sp. nov., nom. rev., isolated from bovine digital dermatitis. *Int J Syst Evol Microbiol* **70**, 2115-2123 (2020).
21. Labroussaa F., Thomann A., Nicholson P., Falquet L., Jores J., Complete Genome Sequence of *Mycoplasma feriruminatoris* Strain IVB14/OD_0535, Isolated from an Alpine Ibex in a Swiss Zoo. *Microbiol Resour Announc* **9** (2020).
22. Moore-Jones G., Arduser F., Durr S., Gobeli Brawand S., Steiner A., Zanolari P., Ryser-Degiorgis M. P., Identifying maintenance hosts for infection with *Dichelobacter nodosus* in free-ranging wild ruminants in Switzerland: A prevalence study. *PLoS One* **15**, e0219805 (2020).
23. Morabito S., Specchi S., Auriemma E., Ferro S., Kuhnert P., Zini E., Computed tomographic and ultrasonographic findings of abdominal arterial pseudoaneurysms caused by systemic mycosis in dogs. *J Small Anim Pract* **61**, 300-307 (2020).
24. Moser S., Seth-Smith H., Egli A., Kittl S., Overesch G., *Campylobacter jejuni* from Canine and Bovine Cases of Campylobacteriosis Express High Antimicrobial Resistance Rates against (Fluoro)quinolones and Tetracyclines. *Pathogens* **9** (2020).
25. Nuesch-Inderbinen M., Kindle P., Baschera M., Liljander A., Jores J., Corman V. M., Stephan R., Antimicrobial resistant and extended-spectrum beta-lactamase (ESBL) producing *Escherichia coli* isolated from fecal samples of African dromedary camels. *Sci Afr* **7** (2020).
26. Overesch G., Haas K., Kuhnert P., Assessing *Campylobacter* Colonization of Broiler Herds Ante Mortem and Monitoring *Campylobacter* Contamination Post Mortem by qPCR. *Pathogens* **9** (2020).
27. Perreten V., Kania S. A., Bemis D., *Staphylococcus ursi* sp. nov., a new member of the '*Staphylococcus intermedius* group' isolated from healthy black bears. *Int J Syst Evol Microbiol* **70**, 4637-4645 (2020).
28. Poirel L., Palmieri M., Brilhante M., Masseron A., Perreten V., Nordmann P., PFM-Like Enzymes Are a Novel Family of Subclass B2 Metallo-beta-Lactamases from *Pseudomonas synxantha* Belonging to the *Pseudomonas fluorescens* Complex. *Antimicrob Agents Chemother* **64** (2020).

29. Posthaus H., Kittl S., Tarek B., Bruggisser J., *Clostridium perfringens* type C necrotic enteritis in pigs: diagnosis, pathogenesis, and prevention. *J Vet Diagn Invest* **32**, 203-212 (2020).
30. Register K. B., Lysnyansky I., Jelinski M. D., Boatwright W. D., Waldner M., Bayles D. O., Pilo P., Alt D. P., Comparison of Two Multilocus Sequence Typing Schemes for *Mycoplasma bovis* and Revision of the PubMLST Reference Method. *J Clin Microbiol* **58** (2020).
31. Rodriguez-Campos S., Rostaher A., Zwickl L., Fischer N., Brodard I., Vidal S., Brandt B. W., Favrot C., Perreten V., Impact of the early-life skin microbiota on the development of canine atopic dermatitis in a high-risk breed birth cohort. *Sci Rep* **10**, 1044 (2020).
32. Sacchini F., Liljander A. M., Heller M., Poole E. J., Posthaus H., Schieck E., Jores J., Reproduction of contagious bovine pleuropneumonia via aerosol-based challenge with *Mycoplasma mycoides* subsp. *mycoides*. *Acta Vet Scand* **62**, 62 (2020).
33. Schmidt J. S., Kuster S. P., Nigg A., Dazio V., Brilhante M., Rohrbach H., Bernasconi O. J., Budel T., Campos-Madueno E. I., Gobeli Brawand S., Schuller S., Endimiani A., Perreten V., Willi B., Poor infection prevention and control standards are associated with environmental contamination with carbapenemase-producing *Enterobacterales* and other multidrug-resistant bacteria in Swiss companion animal clinics. *Antimicrob Resist Infect Control* **9**, 93 (2020).
34. Schönecker L., Schnyder P., Schupbach-Regula G., Meylan M., Overesch G., Prevalence and antimicrobial resistance of opportunistic pathogens associated with bovine respiratory disease isolated from nasopharyngeal swabs of veal calves in Switzerland. *Prev Vet Med* **185**, 105182 (2020).
35. Schwendener S., Dona V., Perreten V., The Novel Macrolide Resistance Genes *mef*(D), *msr*(F), and *msr*(H) Are Present on Resistance Islands in *Macrococcus canis*, *Macrococcus caseolyticus*, and *Staphylococcus aureus*. *Antimicrob Agents Chemother* **64** (2020).
36. Thi Nhu Thao T., Labroussaa F., Ebert N., V'Kovski P., Stalder H., Portmann J., Kelly J., Steiner S., Holwerda M., Kratzel A., Gultom M., Schmied K., Laloli L., Husser L., Wider M., Pfaender S., Hirt D., Cippa V., Crespo-Pomar S., Schroder S., Muth D., Niemeyer D., Corman V. M., Muller M. A., Drosten C., Dijkman R., Jores J., Thiel V., Rapid reconstruction of SARS-CoV-2 using a synthetic genomics platform. *Nature* **582**, 561-565 (2020).

37. Trueeb B. S., Braun R. O., Auray G., Kuhnert P., Summerfield A., Differential innate immune responses induced by *Mycoplasma hyopneumoniae* and *Mycoplasma hyorhinis* in various types of antigen presenting cells. *Vet Microbiol* **240**, 108541 (2020).

### 5.2 Book Chapters

- Tran Thi Nhu Thao*, Fabien Labroussaa*, Nadine Ebert, Joerg Jores*, Volker Thiel*, Chapter 13: In-yeast assembly of coronavirus infectious cDNA clones using a synthetic genomics pipeline, to be published in the book: Coronaviruses - Methods and Protocols, Editors: Helena Maier, Erica Bickerton, Paul Britton, Springer (New York), Volume 2203, *equal contribution
- Peter Kuhnert and Jörg Jores, Title: *Mycoplasma hyopneumoniae* pathogenicity: the known and the unknown, in the book: Mycoplasmas in Swine, Editors: Dominiek Maes, Marina Sibilia & Maria Pieters, Acco (Belgium), 2020, ISBN: 978-94-6379-796-2, Pages: 73-86
- Peter Kuhnert and Bozena Korczak *Nicoletella* In: *Bergey's Manual of Systematics of Archaea and Bacteria*, ed W.B. Whitman, John Wiley, Chichester, UK, 2020, https://doi.org/10.1002/9781118960608.gbm01853
- Peter Kuhnert, Henrik Christensen, Magne Bisgaard, Bozena Korczak. *Frederiksenia* In: *Bergey's Manual of Systematics of Archaea and Bacteria*, ed W.B. Whitman, John Wiley, Chichester, UK, 2020, https://doi.org/10.1002/9781118960608.gbm01847
- Henrik Christensen, Magne Bisgaard, Peter Kuhnert *Necropsobacter* In: *Bergey's Manual of Systematics of Archaea and Bacteria*, ed W.B. Whitman, John Wiley, Chichester, UK, 2020, https://doi.org/10.1002/9781118960608.gbm01852
- Henrik Christensen, Peter Kuhnert, Hans-Jürgen Busse, Pat Blackall, Magne Bisgaard, Niels Norskov-Lauritsen *Pasteurellaceae* In: *Bergey's Manual of Systematics of Archaea and Bacteria*, ed W.B. Whitman, John Wiley, Chichester, UK, 2020, https://doi.org/10.1002/9781118960608.fbm00230.pub2

### 5.3 Other Publications

- «Ein Klon geht um die Welt» by Volker Thiel & Jörg Jores, PIPETTE – SWISS LABORATORY MEDICINE | WWW. SULM.CH, Nr. 2, Page 16-7 | May, 2020
- Federal Office of Public Health and Federal Food Safety and Veterinary Office. Swiss Antibiotic Resistance Report 2020. Usage of Antibiotics and Occurrence of Antibiotic Resistance in Switzerland. November 2020. FOPH publication number: 2020-OEG-64.

Main authors: Dagmar Heim, Andreas Kronenberg, Gudrun Overesch, Caterine Plüss-Suard, Saskia Zimmermann-Steffens

## 5.4 Press Releases and Broadcasting

- «Swiss Scientists Have Recreated the Coronavirus in a Lab», A synthetic virus could help develop drugs, vaccines, and diagnostic tests but could also be used as a bioweapon; OneZero (https://onezero.medium.com/swiss-scientists-have-recreated-the-coronavirus-in-a-lab-d12816bfdbe3)
- «Berner Forscher leisten Pionierarbeit im Kampf gegen das Coronavirus», Jörg Jores und Volker Thiel klonen das Coronavirus – als erstes Team weltweit. Ihre Arbeit verrichten sie in einem Hochsicherheitslabor in Mittelhäusern; Der Bund; March 5, 2020
- «Einen Impfstoff gibt es bereits», Berner Corona-Forscher Volker Thiel und Jörg Jores von der Uni Bern erforschen das Coronavirus seit vier Wochen. Sie glauben, dass solche Epidemien in Zukunft zunehmen werden, Bieler Tagblatt, March 6, 2020
- Dieses Hochsicherheits-Labor forscht an Covid-19», Weltweit suchen Forscher nach Medikamenten zur Bekämpfung des Coronavirus. Eine zentrale Rolle spielt dabei das Labor des Instituts für Virologie ausserhalb von Bern.; 20Minuten; March 6, 2020
- «Der Medizinalstandort Bern gewinnt in der Krise an Profil», Berner Forscherinnen und Forscher gehören in diesen Tagen zu den gefragtesten Corona-Experten Europas. Die Universität könnte davon profitieren; Berner Zeitung; April 17, 2020
- «Synthetic SARS-CoV-2 goes viral»; by Tessa Cleaver; BioTechScope - High impact Science that translates; https://biotechscope.com/synthetic-sars-cov-2-goes-viral/; May 6, 2020
- «Scientists Clone SARS-CoV-2 Genome with Quick Yeast-Based Method» by Ruth Williams; TheScientist; https://www.the-scientist.com/news-opinion/scientists-clone-sars-cov-2-genome-with-quick-yeast-based-method-67515 ; May 6, 2020
- «A platform for RNA virus cloning» by Linda Koch, Nature Reviews Genetics - Research Highlights | https://doi.org/10.1038/s41576-020-0246-8 |
- «Tierärzte verdienen jeden zweiten Franken mit Antibiotika» by Angelika Hardegger; Neuen Zürcher Zeitung (NZZ); August 4, 2020.
- «Antibiotika: Tiermast birgt grosse Risiken für Menschen» by Daniel Mennig; saldo 19/2020; www.saldo.ch/artikel/artikeldetail/antibiotika-tiermast-birgt-grosse-risiken-fuer-menschen/; November 18, 2020

- «Des chercheurs bernois créent une « usine » à nouveau coronavirus» by Marie-Christine Petit-Pierre; Heidi News; March 4, 2020
- «En Suisse, le Covid-19 s'invite au cœur de la recherche scientifique» by Laure Wagner; Swissinfo; May 7, 2020
- «Le coronavirus cloné à Berne», live interview for the RTS broadcast «CQFD» by Fabien Labroussaa; https://pages.rts.ch/la-1ere/programmes/cqfd/06-05-2020; May 6, 2020
- «Le coronavirus cloné par des chercheurs bernois», by Etienne Meyer-Vacherand; Le Temps; May 8, 2020
- « Les virus, les comprendre pour mieux les étudier » by Clément Etter, In vivo magazine (CHUV); Dossier 22; https://www.invivomagazine.com/fr/focus/dossier/article/599/les virus-les-comprendre-pour-mieux-les-apprivoiser.

# 6 Graduations and Visting Scientists

## 6.1 American College of Veterinary Microbiology (ACVM)

*Diplomate: Lutz Schönecker*

*Area of specialization*: Bacteriology & Mycology

*Supervisors*: Sonja Kittl and Stefanie Gobeli Brawand

## 6.2 European College of Veterinary Microbiology (ECVM)

In 2020 the IVB became an approved ECVM training center with an approved training programme.

*De facto Diplomate:* Jörg Jores

*De facto Diplomate:* Gudrun Overesch

## 6.3 PhD Degrees

- N/A

## 6.4 Dr. vet. med. Degrees

*Name of student*: Alinta Kraft

*Title of Thesis*: The prevalence of *Dichelobacter nodosus* in clinically footrot-free sheep flocks: a comparative field study on elimination strategies

*Supervisors*: Peter Kuhnert and Adrian Steiner

*Abstract*: Background: Ovine footrot caused by *Dichelobacter nodosus* (*D nodosus*) is an infectious disease affecting sheep worldwide. Switzerland plans a nationwide footrot eradication program, based on PCR-testing of interdigital swab samples. The aim of this study was to test for the presence of *D nodosus* in clinically footrot-free sheep flocks which had been subjected to different treatment strategies, to assess whether they were feasible for the eradication process, especially focussing on antimicrobial flock treatments. Clinical scoring and PCR-results were compared. Ten farms had used hoof bathing and hoof trimming without causing bleeding, ten had used individual treatments and flock vaccines to gain the free status and ten had become free through whole-flock systemic macrolide treatment. For every farm, three risk-based collected pool samples were analysed for the occurrence of virulent and benign *D nodosus* by PCR detection of *aprV2/aprB2*.

Results: Six flocks from any treatment group tested positive for *aprB2* in all pools. Clinical signs were absent at the time of sampling, but some flocks had experienced non-progressive interdigital inflammation previously. Two flocks tested *aprV2*-positive in the high-risk pool. One of them underwent a progressive footrot outbreak shortly after sampling. Individual retesting indicated, that virulent *D nodosus* most likely was reintroduced by a recently

purchased ram. In the second flock, a ram was tested positive and treated before clinical signs occurred.
Conclusions: All treatment strategies eliminated the causative agent and were found to be suitable for implementation in the PCR-based eradication process. PCR-testing proved to be more sensitive than visual scoring, as it also detected clinically healthy carriers. It will be of benefit as a diagnostic tool in elimination and surveillance programs.

### 6.5 Master Degrees

*Name of student*: Rubén Sánchez Barbarroja

*Title of thesis*: Functional characterization of candidate toxin-antitoxin systems in mycoplasmas using synthetic genomic tools

*Supervisors*: Fabien Labroussaa and Joerg Jores

*Name of student*: Jennifer Eleonora Keller

*Title of thesis*: Methicillin-resistant *Macrococcus* spp. in animals in Switzerland: occurrence, antimicrobial profiles and novel species.

*Supervisors*: Vincent Perreten and Sybille Schwendener

*Name of student*: Stefanie Stegmüller

*Title of thesis*: Longitudinal study on ESBL/pAmpC -producing and colistin-resistant *Escherichia coli* in pigs

*Supervisor*: Gudrun Overesch

*Name of student*: Corinne Gerber

*Title of thesis*: Antimicrobial susceptibility of bacterial pathogens isolated from dogs, cats and horses in Switzerland

*Supervisor*: Gudrun Overesch

## 6.6 Visiting Scientists

Yanet López Dorta. Molecular epidemiology of multidrug-resistant bacteria from food-producing animals from Cuba using Whole Genome Sequence (WGS). National Centre for Animal and Plant Health (CENSA), San José de las Lajas, Mayabeque, Cuba. Supervisor: Vincent Perreten

# 7 Scientific Meetings Organized, Keynotes given and Grants Awarded

## 7.1 Scientific Meetings Organized by IVB Staff

- N/A

## 7.2 Keynote/Invited Lectures Given by IVB Staff

- Jörg Jores, 10th September 2020, Institute of Animal Breeding and Genetics, University of Veterinary Medicine Hannover, Hannover, Germany, Title: Application of Synthetic Genomics to Mycoplasmas and Viruses to Decipher Virulence Traits and to Develop Rational Vaccines
- Peter Kuhnert, 10th September 2020, Institute of Animal Breeding and Genetics, University of Veterinary Medicine Hannover, Hannover, Germany, Title: Bakterielle Klauenkrankheiten bei Schaf und Rind
- Brilhante M, GCB Students' Symposium, University of Bern, Bern, Switzerland, 30 January 2020. Title: Clinical contamination with high-risk clones of carbapenemase-producing *Klebsiella pneumoniae* causing infection in pets in Switzerland.

## 7.3 Competitive Grants Awarded

- N/A

## 7.4 Other funding

- N/A

# 8 Organization Chart (Organigram)