Annual Scientific Conference and Annual General Meeting of the European College of Veterinary Public Health

"Science at the service of VPH to gain expertise in controlling Emerging risks in Veterinary Public Health"

Liège, 2\textsuperscript{nd} – 4\textsuperscript{th} October 2017
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Monday 2\textsuperscript{nd} October 2017

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<td>56\textsuperscript{th} CM (salle des Professeurs)</td>
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<td>17:30-20:00</td>
<td>REGISTRATION AND RECEPTION at the Hotel de Ville of Liège</td>
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Opening ceremony

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<tr>
<td>9:00-9:15</td>
<td>Albert Corhay (Rector of ULiège) and Jeroen Dewulf (president of ECVPH)</td>
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KEYNOTES: Scientific advances to gain knowledge in food science related to emerging risks

Chair: Jeroen Dewulf

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<td>9:15 – 9:45</td>
<td>Interaction between micro-organisms and the animal hosts: role of microbial ecosystems</td>
<td></td>
<td>B. Taminiau (University of Liège)</td>
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<tr>
<td>9:45–10:45</td>
<td>New perspective of host resistance mechanisms to parasites and micro-organisms</td>
<td></td>
<td>Johann Detilleux (University of Liège) Carole Moreno-Romieux (INRA Toulouse)</td>
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10:45–11:15 Coffee break and poster viewing

OPEN SESSION – SELECTED RESIDENT’S PRESENTATIONS

Chair: Bojan Blagojevic

10’ presentations

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<td>11.15 - 11.25</td>
<td>Combining network analysis with epidemiological data to support the development of risk-based surveillance strategies of hepatitis E virus in swine population</td>
<td></td>
<td>Morgane Salines</td>
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<tr>
<td>11.25 - 11.35</td>
<td>Staphylococcus aureus nasal carriage in slaughterhouse workers in western Kenya</td>
<td></td>
<td>Elizabeth Anne Jessie Cook</td>
</tr>
<tr>
<td>11.35 - 11.45</td>
<td>Towards harmonisation of animal health legislation: Development of a framework for cross-country comparison</td>
<td></td>
<td>Anaïs Léger</td>
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### 11.45 - 11.55
- **The prevalence of verocytotogenic *E. coli* O157 (VTEC O157) in British cattle populations**
  - Sue C. Tongue

### KEYNOTE Scientific advances to gain knowledge in emerging risks in animal health part 1
**Chair:** Ed Van Klink

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<tbody>
<tr>
<td>12:00 – 12:30</td>
<td>Mitigating the risk of introduction of an epidemic/exotic disease in a country</td>
<td>C. Saegerman (University of Liège)</td>
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<td>12:30 – 13:45</td>
<td>Lunch and poster viewing</td>
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<tr>
<td>13:45 – 15:45</td>
<td>1. Introduction to methods and tools for surveillance evaluation</td>
<td>Petra Müllner / Katharina Stärk</td>
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<td></td>
<td>2. How can we improve public health, food hygiene, and animal welfare in developing country slaughterhouses?</td>
<td>Laura Falzon / Annie Cook</td>
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<td>15:45 – 16:15</td>
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<td>16:15 – 18:00</td>
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**Wednesday 4th October 2017**

### KEYNOTE Scientific advances to gain knowledge in emerging risks in animal health part 2
**Chair:** Len Lipmann

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<tbody>
<tr>
<td>8:45–9:15</td>
<td>Lumpy skin disease: an emerging disease?</td>
<td>Kris De Clercq, (CODA-CERVA)</td>
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<td>9:15 – 9:45</td>
<td>Emerging Risks activities in EFSA – A reflection</td>
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Chair: Lisa Boden

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<td>9:45–10:40</td>
<td>Challenges at the science policy interface:</td>
<td>Ed van Klink (University of Bristol)</td>
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<tr>
<td></td>
<td>• Expectations,</td>
<td>Dominic Mellor (University of Glasgow)</td>
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<td></td>
<td>• Communication, and</td>
<td>Simon More (University College, Dublin)</td>
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<td></td>
<td>• Effectiveness.</td>
<td>Lis Alban (University of Copenhagen)</td>
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<tr>
<td>10:40-11:10</td>
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OPEN SESSION – SELECTED RESIDENT’S PRESENTATIONS

Chair: Gerty Vanantwerpen

10’ presentations

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<tr>
<td>11.10 - 11.20</td>
<td>A new take on Staphylococcal Food Poisoning</td>
<td>Sophia Johler</td>
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<td>11.20 - 11.30</td>
<td>Farmers’ knowledge and expectations of antimicrobial use and resistance are strongly related to usage in Dutch livestock sectors</td>
<td>Tineke Kramer</td>
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<tr>
<td>11.30 - 11.40</td>
<td>Risk factors associated with spatio-temporal clusters of high mortality in Danish swine herds</td>
<td>Ana Carolina Lopes Antunes</td>
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KEYNOTE Scientific advances to gain knowledge in emerging risks part 3

**Chair:** Kurt Houf

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<td>11:30–12:00</td>
<td>Emergence of highly virulent <em>Clostridium difficile</em> PCR-ribotypes in animal and human population</td>
<td>Dr. Patrizia Spigaglia (Istituto Superiore di Sanità, Roma)</td>
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<tr>
<td>12:00–12:30</td>
<td>Management of antimicrobial resistance in animals in Belgium</td>
<td>Dr. Jean-François Heymans, CVO</td>
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<td>- Poster prize</td>
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<td>- Presentation of next year’s venue</td>
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<td>- Closing of the meeting</td>
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<tr>
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<tr>
<td>13:00</td>
<td><em>Lunch and departure</em></td>
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<td>13:00-15:00</td>
<td><em>57th CM</em></td>
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Presidential foreword

Dear Diplomates and Residents,

dear Delegates,

It is my true honor to invite you to the Annual Scientific Conference and Annual General Meeting of the ECVPH meeting in the beautiful city of Liège. Our college is honored to be hosted by the University of Liège who is celebrating this year its 200th anniversary. The council and local organizers have again attempted to propose an appealing Conference Program with a good mixture of science and policy. Moreover, we will provide plenty of time for our residents to allow them to demonstrate the quality and value of their work. As always there will also be plenty of time for networking in a pleasant and inspiring environment.

We are looking forward to welcome you all in Liège.

Jeroen Dewulf
ECVPH President
Scientific Committee

Jeroen Dewulf, Department of Reproduction Obstetrics and Herd Health, Ghent University, Belgium
Marcello Trevisani, School of Agriculture and Veterinary Medicine, University of Bologna, Italy
Ed van Klink, School of Veterinary Science, University of Bristol, United Kingdom
Søren Saxmose Nielsen, Section of Animal Welfare and Disease Control, University of Copenhagen, Denmark
Kurt Houf, Department of Veterinary Public Health and Food Safety, Ghent University, Belgium
Len Lipman, Institute for Risk Assessment Sciences, Utrecht, the Netherlands
Eleni Iosifidou, Department of Hygiene and Technology of Food of Animal Origin, Aristotle University of Thessaloniki, Greece
Lisa Boden, EPIC Centre of Expertise on Animal Disease Outbreaks, University of Glasgow, United Kingdom
Bojan Blagojevic, Department of Veterinary Medicine, University of Novi Sad, Serbia
Gerty Vanantwerpen, Dierengezondheidszorg Vlaanderen, Belgium
Andreas Wunsch, Veterinary Food Safety Expert, FS Training & Consultancy, Austria

Organizing Committee

Prof. Antoine CLINQUART, Food Science Department (University of Liège)
Prof. Georges DAUBE, Food Science Department (University of Liège)
Prof. Véronique DELCENSERIE, Food Science Department (University of Liège)
Prof. Johann DETILLEUX, Animal Production Department (University of Liège)
Dr Nicolas KORSAK, Food Science Department (University of Liège)
Prof. Claude SAEGERMAN, Department of Infectious and Parasitic Diseases (University of Liège)
Prof. Marie-Louise SCIPO Food Science Department (University of Liège)
Prof. Etienne THIRY, Department of Infectious and Parasitic Diseases (University of Liège)
Sponsors

Liège université

QUALITY PARTNER

Liège

Une ville, un esprit.
Abstracts
Keynote lectures

Keynote 1 - Interaction between micro-organisms and the animal hosts: role of microbial ecosystems

Bernard Taminiau a,*, Cristina Rodriguez a, Simone Krings a, Papa Abdulye Fall a, Nicolas Korsak a, and Georges Daube a

a University of Liège, Food Science Department, Fundamental and Applied Research for Animal & Health, Food Microbiology, B43b Boulevard de Colonster 20 b-4000 Liège

b Genalyse Partner SA, rue Hayeneux 62, B-4040 Herstal, Belgium

Host-microbes interactions and coexistence has always play a central role in human and animal life. Microbial induced pathologies and disorders prompted scientists and medical operators towards the development of domains like hygiene, vaccination and antibiotics. Besides, micro-organisms dominate the major biochemical processes on earth and represent a prominent element in industries like agriculture and the food sector. The advances of molecular biology and bio-informatics regarding high-throughput technologies like DNA sequencing has greatly enlarged our vision of the microbial world. Using culture-independent approaches and massive DNA sequencing, host-associated microbiota has been found to be much more diverse than expected, in taxonomy as well as in functions. Several examples of amplicons sequencing and metagenomic studies will be reviewed in order to illustrate their impact on how we can explore microbial diversity to improve our knowledge and management in various domains like food production, livestock health and environmental studies.

Keynote 2 - New perspective of host resistance/tolerance mechanisms to parasites and micro-organisms

Moreno, C. and Detilleux, J.

Moreno, C. INRA, UR 0631 SAGA Station d’Amélioration Génétique des Animaux. Centre de recherche de Toulouse, Auzeville, France.

Detilleux, J. Animal Production Department, University of Liège, Veterinary Faculty, Liège

Several factors explain why emerging infectious disease may decimate populations or become endemic, one being the inherent levels of resistance or tolerance of hosts in the introduced region. If hosts are resistant, transmission of the pathogen will be limited. By contrast, if they are tolerant, transmission will be maintained. This is because tolerance mechanisms protect the host by alleviating the pathology caused by the infection with no effects on the fitness of the pathogens. Tolerance may be further divided into mechanisms that reduce the damage caused by pathogens (direct tolerance) and those that reduce damage caused by the host response triggered by the infection (indirect tolerance). The distinction is important because it is only in the situation where hosts are resistant and indirectly tolerant that the spread of an infectious disease will be limited without loss in performance which is particularly important in commercially raised animals.

Individual levels of resistance and tolerance are estimated by examining (linear and nonlinear) relationships between pathogen levels and host health. Recently, statistical mediation mixed models and health trajectories (coupled or not with ordinary differential equation system) have been proposed to analyze indicators of economic performance over the course of infection and results were formalized under the counterfactual causal theory of causation to obtain credible estimates of direct and indirect levels of tolerance. As an example, in bovine mastitis (a disease characteristic of a cooperative co-evolution between host and microbial populations), tolerance is mainly indirect with milk loss estimated at 1 mg/day per 1000 immune cell/ml over the clinical period. Important individual deviations from the resilient path were observed especially when tissue repair or regeneration occurred and may explain why some cows are more or less indirectly tolerant. Indeed, previous studies in plants, animals and insects have demonstrated that resistance and tolerance to pathogens are controlled by both genetic and environmental factors. Selective breeding is therefore one method to increase the proportion of resistant/tolerant animals in commercial herds.
In recent years, significant putative progresses using genomic methods and tools allowed to increase the efficiency of livestock selection and management, including the use of gene mutations and genomic selection. However, to select for disease resistance traits, some prerequisites are necessary, particularly when the selection is on a gene mutation targeting a single biological mechanism. Firstly, the effect of the selected mutation on the genetic correlations with other traits have to be estimated in order to manage a putative negative effect of the disease resistance selection on production traits and other diseases traits. Secondly, the evolution of the pathogen community under the selection pressure due to an increase in host resistance should be evaluated/controlled in order to prevent a putative adaptation of pathogens. A solution to manage these risks is to apply a moderate selection pressure and to use an integrated strategy. In fact, the genetic selection could be associated with the use of chemical treatment, as well as an adequate fulfillment of nutritional needs and adequate management of pastures to reduce infection risk. Modeling the host/pathogen relation in resource allocation models, will allow to predict the optimal equilibrium to target at the farm level. Then, taking into account the farm management of the breeders in our models, we would like to determine the minimal proportion of resistant animals to introduce at the farm level, in order to control the pathogen population: e.g. sheep flocks infected by gastrointestinal parasite on pasture.

Table 1: some examples of disease resistance in sheep: genetic knowledge & selection strategy

<table>
<thead>
<tr>
<th>Disease resistance</th>
<th>pathogen</th>
<th>Global resistance: Heritability</th>
<th>gene mutation</th>
<th>Negative impact on production/disease</th>
<th>Selection strategy in commercial populations</th>
</tr>
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<tbody>
<tr>
<td>Scrapie resistance</td>
<td>proteins</td>
<td>~0.2 Prnp gene</td>
<td>No but public health problems</td>
<td>Elimination of susceptible alleles</td>
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<tr>
<td>Mastitis resistance</td>
<td>bacteria</td>
<td>~0.1 Soc2 gene</td>
<td>Milk production, lamb survival, animal size</td>
<td>Based on global genetic resistance in France, 20% mastitis decrease in 10 years</td>
<td></td>
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<tr>
<td>Gastrointestinal parasite resistance</td>
<td>nematodes</td>
<td>~0.3</td>
<td>Growth, milk production</td>
<td>Based on global genetic resistance</td>
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Detilleux, J. (2017) A strategy to estimate the rate of recruitment of inflammatory cells during bovine intramammary infection under field management. BMC Veterinary Research 13. DOI: 10.1186/s12917-017-1078-4


Keynote 3 - Mitigating the risk of introduction of an epidemic/exotic disease in a country

Saegerman C.,1 Bianchini J.,1 Cargnel M.,2 Roelandt S., Mathijs E.,2 Vandenbussche F.,2 Van der Stede Y.,2 De Clercq K.,2 Koenen F.2

1 Research Unit in Epidemiology and Risk Analysis applied to veterinary sciences (UREAR-ULg), Center for Fundamental and Applied Research for Animal and Health (FARAH), University of Liège, Belgium
2 Veterinary and Agrochemical Research Center, Brussels, Belgium

Corresponding author: claude.saegerman@ulg.ac.be

During the last decade, a number of epidemic animal diseases occurred in Belgium and its neighbouring countries. Notable examples were avian influenza H7N7 (AI) in the Netherlands and Belgium in 2003 (e.g. van den Berg and Houdart, 2008), the Bluetongue virus (BTV) epidemic in north Western Europe in 2006 (e.g. Saegerman et al. 2008) and Schmallenberg (SBV) disease in 2011 (e.g. Martinelle et al., 2012). The socio-economic consequences of these epidemic diseases were high (Hanon et al., 2009; Humblet et al., 2016). The control of outbreaks of these diseases requires fast and effective actions to prevent the disease from spreading. For AI, BTV, SBV it was clear that the clinical or/and laboratory diagnostic capacity was a limiting factor to notify/confirm these diseases. Therefore, in the future, to avoid that laboratories are overwhelmed with samples coming from a huge epidemic, it is essential to increase their diagnostic capacities. In this keynote, the results of the EPIDIACAP project (risk-based increase of diagnostic capacities for animal epidemic diseases in Belgium) will be presented. The aims of this project were: (i) to prioritise the epidemic/exotic diseases representing a threat with regards to their risk of introduction in Belgium and perform a risk analysis; (ii) to identify gaps in order to optimize the massive diagnostic detection of a new epidemic disease in the country and (iii) to expand the diagnostic capacity of epidemic diseases in the country on the basis of a thoughtful selection of tests to be developed or optimized. The results will allow the Belgian authorities to improve their preparedness in case epidemic/exotic epidemic disease is introduced into the country.

Main references


Keynote 4 - Lumpy Skin Disease: an emerging disease?

Andy Haegeman1, Ilse De Leeuw4, Annebel De Vleeschauwer1, Laurent Mostin2, Willem Van Campe2, Maria Vastag4, Claude Saegerman3, Eeva Tuppurainen4, and Kris De Clercq1

1 Veterinary and Agrochemical Research Centre (CODA-CERVA), Unit for Vesicular and Exotic Diseases, Ukkel, Belgium.
2 CODA-CERVA, Animal Experimental Centre, Machelen, Belgium.
3 Fundamental and Applied Research for Animal and Health (FARAH) Center, University of Liege, Liege, Belgium.
4 Consultant, Veterinary Expertise for Controlling Lumpy skin disease, Sheeppox and Goatpox.

Lumpy skin disease (LSD) is a pox disease of cattle caused by the LSD virus (genus Capripox) and characterized by fever and nodules on the skin, mucosal membranes and internal organs. The disease can cause abortion, a
reduction in milk production, sterility in bulls and damage to hides, which lead to significant loss of income. The disease, which originally affected cattle across Africa, spread to Israel, Egypt and Lebanon in 2012/13 and epizootics began in Turkey in 2013, Azerbaijan and Cyprus in 2014, in Armenia, Greece and the Russian Federation in 2015, and in Albania, Bulgaria, the Former Yugoslav Republic of Macedonia (FYROM), Georgia, Kazakhstan, Kosovo (This designation is without prejudice to positions on status, and is in line with UNSCR 1244 and with the ICI Opinion on the Kosovo Declaration of Independence), Montenegro and Serbia in 2016. In 2017 there were new LSD clinical cases in Albania, FYROM, Greece, Kazakhstan and the Russian Federation.

Mass vaccination appeared to be the only effective way to control this outbreak of a vector-borne disease. But there was widespread hesitation with regard to using a live attenuated vaccine – currently the only type commercially available – because of the scarcity of independent verification of its efficacy and its safety in terms of side effects and contaminating agents, and because of international trade restrictions for live cattle and some cattle products.

Data on the efficacy and safety of vaccination are generally available from field experience only, which makes it difficult to choose the most suitable vaccine. A study at CODA-CERVA in collaboration with the Pirbright Institute (UK) and the FARAH Center (Faculty Veterinary Medicine University of Liege, Belgium) aimed to: i) optimize a LSD virus (LSDV) infection model; and ii) evaluate and compare live and inactivated vaccines against LSD under standardized conditions using the optimized challenge model.

With regard to the first objective, the LSD Neethling virus strain and a field isolate from the 2012/13 LSD outbreak in Israel were compared by assessing the outcome of in vivo challenge. The range of compared variables included: i) clinical signs; ii) virological measures of the level, peak moment and duration of viraemia and virus secretion; and iii) humoral and cellular immunological parameters. Some variables, for example a fever spike at seven to eight days post-infection and seroconversion, were very similar; others such as clinical signs, viraemia and IFNγ release were quite different for the two isolates used. Selection of the most suitable challenge virus for the vaccine evaluation experiments was carried out on the basis of the data gathered.

This optimized challenge model was used to compare several commercially available live attenuated vaccines based on LSD, or sheep pox or goat pox vaccine strains, and recently developed inactivated LSDV vaccines. Each trial used seven vaccinated animals and five unvaccinated control animals. The vaccinated and unvaccinated animals could be clearly distinguished from the different virological, humoral and cellular immunological variables. In the vaccinated groups, different patterns of the variables were observed pre-challenge and post-challenge, which suggested differences in the safety and efficacy of the vaccines tested. Suitable, moderately suitable and unsuitable vaccines for field use in the current emergency were identified on the basis of these data.

Acknowledgements
The studies that yielded these results were funded by: i) the Bill and Melinda Gates Foundation Grant Agreement, Investment ID OPP1126866; ii) the Global Alliance for Livestock Veterinary Medicines (GALVmed), CAO-R34A0856 A1; iii) the Belgian Federal Public Service of Health, Food Chain Safety and Environment, contract RT 15/3 LUMPY SKIN 1; iv) the European Commission and v) CODA-CERVA in Ukkel, Belgium.

Keynote 5 - Emerging Risks Activities at the European Food Safety Authority

Ana Afonso

European Food Safety Authority, Parma, Italy

The European Food Safety Authority (EFSA) was established in 2002 by Regulation 178/2002/EC, the “Food Law”, as part of the measures taken to respond to EU citizens demand for science based policies in the area of food and feed. EFSA’s mission is to provide scientific advice and scientific and technical support for the Community’s legislation and policies in all fields which have a direct or indirect impact on food and feed safety and in this respect take account of animal health and welfare, plant health and the environment. EFSA mission also includes the obligation to provide information on all matters within these fields and communicate on risks. The regulation Article 34 provides the legal basis for EFSA activities in the area of Emerging Risks Identification. It is requested that EFSA establishes monitoring procedures for systematically searching for, collecting, collating and analysing information and data with a view to the identification of emerging risks in the fields within its mission, it also obliges EFSA to forward the evaluation and information collected on emerging risks to the European Parliament, the Commission and the Member States.
EFSA has developed a definition of emerging risks and a relatively simple procedure that translates the regulatory requirement into 3 steps for the identification of emerging risks:

1) Identification of priority emerging issues
2) Information sources and data collection
3) Evaluation to identify emerging risks

The procedure is based on information collected by different methodologies but relies mainly on networks of knowledge. Over the years different methodologies for i) automated collection of information on emerging issues ii) analysis of trends and drivers for emerging risks and iii) prioritization of identified issues, have been developed and used.

The talk will focus on a series of examples relevant to risks for public and animal health analysing benefits and procedural challenges. In particular issues related with emerging risks governance and the applicability of risks assessment principles to the area of emerging risks identification, objectives and expectations of different procedures from early warning to foresight, uncertainty analysis, the concept of information versus knowledge, complex systems modelling approaches and communication of outcomes to different target audiences.

**Keynote 6 - Emergence of highly virulent Clostridium difficile PCR-ribotypes in animal and human population**

**Patrizia Spigaglia**

*Istituto Superiore di Sanità - Rome, Italy*

*Clostridium difficile* is a spore-forming anaerobic bacterium, ubiquitous in the environmental and with a wide host range, recognized as the leading cause of healthcare antibiotic-associated diarrhea in industrialized countries. Over the last decade, an alarming increase in incidence of hospital-associated *C. difficile* infection (CDI) has been observed across the USA, Canada and Europe and it has been associated with the emergence of the highly virulent (HV) strains, recognized as RT 027 by PCR-ribotyping. CDI has also emerged as a cause of diarrhea in the community, in populations previously considered at low risk, such as young people, antibiotic-naive patients or people without healthcare exposure. Besides RT027, a number of emergent HV RTs have recently been identified. In particular, the HV RT078 has been recognized as the major cause of infection in the community. HV strains shared characteristics, such as variations in the sequence and/or the production of the two principal toxins (the enterotoxin TcdA and the cytotoxin TcdB), production of a third toxin (the binary toxin - CDT), increased sporulation and resistance to multiple antibiotics (MDR), which increased their capability to survive, spread and infect the host. Several recent studies efforts towards understanding the acquisition and transmission of *C. difficile* outside the hospital environment. *C. difficile* has been documented in both healthy and diseased animals. Several RTs have been detected in animals and the prevalent is the HV RT 078. Highly related *C. difficile* strains RT 078 have been isolated from humans and animals and may therefore represent a potential zoonotic transmission. Resistance to antibiotics plays a key role in driving epidemiological changes of CDI. In particular, resistance to fluoroquinolones (FQs) has been significantly associated to emergence and spread of HV strains. FQs are highly effective for the treatment of bacterial infections in humans and animals, therefore the wide use of these antibiotics may have contributed to the emergence and diffusion of strains RT 078 in both human and animal population. Common *C. difficile* RTs has been found not only in humans and animals, but also in food, in particular retail meats. These findings have raised concerns about a potential foodborne transmission of *C. difficile* in the community, although an epidemiological link between the consumption of contaminated food and the development of CDI is still to be proven. The data available suggest animals, particularly production animals, as a source of CDI in the community, albeit a transmission route between animal and human has not yet definitively documented. Based on the available evidences CDI prevention and control strategies require a “One Health” approach, emphasizing the need of an inter-disciplinary co-operation among health researchers and practitioners.
Keynote 7 - Policy to address the threat of antimicrobial resistance in Belgium: veterinary measures in the global "ONE HEALTH"

Jean-François Heymans

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The fight against antimicrobial resistance is a priority of the Belgian government, the public administrations and the sectors concerned. The cornerstone of this veterinary fight against antimicrobial resistance is the implementation of a policy aimed at drastically reducing the quantities of antibiotics used in farms, especially "critical" antibiotics.

**From autoregulation to co-regulation...**

Faced with an unfavorable situation concerning antimicrobial resistance in Belgium and after having learned that the actions already in place were insufficient, the business sectors and the authorities in 2011 decided to shift up a gear and create the non-profit organization AMCRA (AntiMicrobial Consumption and Resistance in Animals). The AMCRA is a knowledge centre for the use of veterinary antibiotics and has been active since 1 January 2012.

This non-profit organization has introduced a series of recommendations and tools aimed at reducing the use of antibiotics on a voluntary basis (autoregulation). In addition, the AMCRA has also established strategic objectives to reduce antimicrobial resistance and has introduced operational tools to reach these objectives.

This initiative has allowed for a significant reduction of the use of antibiotics in Belgian farms, which, all things considered, still remains insufficient.

**2016 was a pivotal year**, since two major initiatives were taken to speed up the process (co-regulation):

1. The Federal Ministers of Public Health and Agriculture, who are in charge of the public administrations concerned, have signed an agreement with the representatives of the sectors involved in which they together agree on quantifiable targets to reduce the use of antibiotics in veterinary medicine. Moreover, the parties have defined by this agreement the measures that have to be taken by each of them to reach these goals.

2. A new legislation (royal decree) has entered into effect, which comprises two components concerning the reduction of antimicrobial resistance: On the one hand, limiting the use of critical antibiotics and on the other hand, the mandatory registration of the antibiotics used in farms.

This policy allowed for a significant reduction in the sales of critical veterinary antibiotics in 2016. Although these results are very encouraging, the authorities and the business sectors are well aware that considerable additional efforts will have to be made.
Workshops

WK1 - Introduction to methods and tools for surveillance evaluation

Petra Muellner, Katharina Stärk

Dr. Petra Muellner (Director, Epi-interactive; Dipl. ECVPH) and Prof. Katharina Stärk (Director, SAFOSO; Dipl. ECVPH).

Description of the workshop

This workshop aims to provide an introduction to surveillance evaluation as well as an update on recent developments in terms of frameworks and tools that were recently developed. It will allow participants to discuss the advantages and disadvantages of individual approaches to inform their own work. They will become aware of tools that are currently available and be informed on more in-depth training opportunities. Several recent developments regarding frameworks and tools will be introduced and discussed. This will include a cross-sectorial surveillance evaluation framework (SurF), developed for surveillance managed by the New Zealand Ministry for Primary industries. SurF is a novel cross-sectorial effort that aims to provide a common umbrella for surveillance evaluation in the animal, plant, environment and marine sectors. The evaluation framework was designed to ensure consistency in the evaluation of different biosecurity surveillance systems by providing a robust process that is not sector- or context-specific and hence differs from recently published animal surveillance frameworks that emphasize alignment of attributes with specific surveillance objectives e.g. freedom from disease. Further we will also present and discuss frameworks and further development of tools delivered by the RISKSUR project. Online training material on this tool is available and future courses are expected which will be relevant to both Residents as well as Diplomates active in the field. The workshop will consist of a mix of lectures, discussions and demonstration of the tools and frameworks.

The objectives of this workshops are as follows:

- Provide an overview of different approaches to surveillance evaluation
- To introduce key concepts of surveillance evaluation
- To present and discuss recent developments in the field, particularly tools and frameworks that can assist in evaluation activities

Facilitators

The workshop will be jointly delivered by Dr. Petra Muellner (Director, Epi-interactive; Dipl. ECVPH) and Prof. Katharina Stärk (Director, SAFOSO; Dipl. ECVPH). Petra and Katharina recently assisted the New Zealand Ministry for Primary Industry (MPI) with the development of a novel cross-sectorial surveillance evaluation framework (SurF) that specifically considers the outputs and benefits of surveillance. Both Katharina and Petra are experienced epidemiologists who have worked on surveillance projects in many different countries; from risk-based to molecular-based surveillance. Katharina is further a well-recognized expert in surveillance evaluation and an active contributor to the scientific literature on the costs and benefits of surveillance. She is a past member of the FP7 RISKSUR Consortium, which provided leadership on surveillance evaluation as well as methodological updates through the development of the EVA Tool.
Slaughterhouses have been identified as a hotspot for numerous zoonotic and emerging diseases. Intervening and improving conditions at this level may therefore have an important ripple effect, benefiting not only the slaughterhouse workers but also meat consumers and the public in general. Moreover, animal welfare has so far been given very little importance in developing countries. Yet, with the increased recognition that animal welfare may also influence animal productivity and carcass yield (e.g. fewer condemnations), it is worth considering how this knowledge can be leveraged to improve animal welfare conditions in such contexts.

The objectives of this workshop are:

1. To increase awareness of the situation in some slaughterhouses in developing countries, vis-a-vis current European and international legislation.
2. To benefit from the expertise of the ECVPH residents and diplomats to identify areas for improvement in developing country slaughterhouses, and potential collaborations and solutions.

The 2-hour workshop will be structured as follows:

1. An overview of the current state-of-affairs in Europe and internationally regarding animal welfare and food hygiene in slaughterhouses, vis-a-vis the situation in some developing country slaughterhouses. This session will be used to highlight potential public health, food hygiene, and animal welfare issues in developing country slaughterhouses, while also recognizing the limitations and challenges faced by those who work in such contexts (20-30 minutes).

2. Divide the audience into small working groups, and ask each group to discuss one particular issue (e.g. animal welfare during transport; animal welfare during slaughter; public health during slaughter of animal; public health during carcass skinning and preparation; food hygiene during carcass skinning and preparation; food hygiene during meat transport). Each group will be asked to identify areas that can be improved and/or changed, and what is needed to drive these changes (e.g. improved education; additional resources; understanding cultural differences) (35-45 minutes).

3. Ask the working groups to present their thoughts/ideas to the larger group, and have an overall discussion to identify potential ways forward (35-45 minutes).
Challenge session

Challenges at the science policy interface: expectations, communication, and effectiveness.

1. What does Policy expect from Science?

Ed van Klink
Bristol Veterinary School. University of Bristol / Wageningen Bioveterinary Research, Bacteriology and Epidemiology Department.

The Policy Life Cycle describes processes involved in the drafting, implementation and progress assessment of policies. The cycle starts with Agenda Setting, where an issue or problem that requires attention and needs to be resolved is identified and addressed. In subsequent stages, the issue is first analysed, policies are drafted and implemented, and the resulting effects are monitored. Where relevant, the cycle can be completed by returning to the Agenda Setting stage. Drafting policy is an iterative process: input has to be sought from many different backgrounds, not least from the people who will be affected by the policies. The ultimate result of the process is ideally a well-balanced and well thought through set of measures that effectively addresses the subject of the policy. Technical solutions are combined with desires and requirements from society and from the population affected. In very many cases, especially where animal health and public health is concerned, international agreements and standards should also be taken into account. Policies are therefore almost always the best possible compromise given the existing conditions.

Science can play a part at various levels during the Policy Life Cycle. During the analysis phase, it may be required to enlist the help of scientists to learn more about the ins and outs of a problem. The results of such research will often feed into the policies as they are drafted. Science may also be regarded as an instrument of policy. Often, certainly where it concerns health issues, some of the measures used to, for example, manage the approaches to disease control, might involve setting up a routine surveillance system involving regular sampling and reporting of results. Also in the evaluation of policy, where the effectiveness of the policies needs to be assessed, research can often provide the information on the basis of which these evaluations are carried out. Finally, research can in itself also be a product of policy: it happens sometimes, that towards the implementation phase for a certain problem it is decided that there is a lack of knowledge that needs to be filled in. In those cases research is the implementation measure and after the research has been done, the cycle goes back to agenda setting. This process is sometimes also used to divert attention: when an issue receives a lot of political attention, science is sometimes used to appease the politicians, and it does happen that by the time the results are known the issue is out of the public and political lime light and the cycle is interrupted.

Providing scientific information to the policy process has a lot of challenges. Firstly, especially when a problem requires immediate attention, policy makers often can’t wait for the results of a two year research project. There are ways around this: regularly policy makers will make use of expert opinion as a “second best” option above thorough research. Several governments have standing scientific reference groups for certain issues, such as disease outbreak management. Secondly, in policy it is very difficult to deal with uncertainty. While uncertainty is part and parcel of scientific life, and scientific results without a certain level of uncertainty should be regarded with a healthy dose of scepticism, policy makers prefer clear and unambiguous results that they can explain to politicians in a very easy manner. Thirdly, and associated with the previous point, the way results are presented is all important. High level scientific language may not be the optimal level of communication with the policy maker. A method of explanation needs to be found, that brings the message across without causing confusion. Very important is to make sure that the question to be answered is unequivocally clear. It is worthwhile to dedicate time to the articulation of the question. Also, management of expectations is essential. Finally, communication of the results is a challenge in itself.
2. Challenges at the science policy interface: Communication

Dominic Mellor

Boyd Orr Centre for Population and Ecosystem Health, University of Glasgow, UK
Health Protection Scotland, Glasgow, UK
Director, EPIC Centre of Expertise on Animal Disease Outbreaks

Insofar as primary research can be considered ‘original’ work in an ‘evidence sense’, making such original material ‘operational’ to serve policy almost always requires some degree of translation. To a large extent, this process is more or less embodied in what is currently referred to as Knowledge Exchange (KE), though of course, done properly, KE should also be informing the primary research. Nevertheless, our experiences of working together to deliver operational translations of some of our primary research, as putative solutions to what might be considered policy problems, have highlighted unanticipated issues which have proved very instructive.

As science becomes an ever more sophisticated, its outputs inevitably become more complex and there appears to be a widening gap between its practitioners and its (intended) audience. There is an undoubted need, and appetite, for more education among some of science’s ‘stakeholders’ so that the gap narrows. More pressingly, and perhaps paradoxically, it is essential that we do more to translate our specific complexities into generic simplicities if we are to have impact at grass roots, more often than not through the vehicle of ‘better’ policy.

Based on experiences of working for the EPIC Centre of Expertise on Animal Disease Outbreaks and for Health Protection Scotland, both closely allied to Scottish Government, the role of what have been termed ‘knowledge brokers’ in the process of science policy translation has proved invaluable. Fundamentally, these ‘specialist generalists’ need to be both fluent and credible in the ‘languages’ and processes of science and policy, and other stakeholders. They can contribute to both ‘sides’ of the partnership, but most importantly they serve a trusted and clarifying bridging function between ‘specialist specialists’ helping to forge a coherent team working in unison.

3. Contributing effectively at the science-policy interface: experiences from Ireland

Simon More

UCD Centre for Veterinary Epidemiology and Risk Analysis. School of Veterinary Medicine. University College Dublin, Belfield, Dublin 4, Ireland

Many of us work at the science-policy interface, seeking to contribute knowledge in support of policy decision-making. A key concern is the desire to ensure that our work is as useful as possible in influencing these decision-making processes. In the literature, there has been considerable discussion on this issue, particularly in the contexts of public health and global environmental challenges such as climate change. For example, Watson (2005) suggests key features of a useful scientific assessment, include the transparency of the process and the technical accuracy of the information, but also the need for scientists to present options not recommendations, to be evidence-based not value-driven, and to quantify uncertainties where possible.

In the areas of animal health and welfare, as yet there has been limited discussion on this issue in the published literature. Nonetheless, experiences from the European Food Safety Authority are relevant, given the role of this organisation in risk assessment (‘the science’) in food safety, including animal health and welfare, primarily to assist with decision-making by the European Commission (‘the policy’). EFSA is under considerable third-party scrutiny, and has been criticised, particularly with respect to a perceived lack of independence on the part of some participating experts. In response, and specifically to maximise its effectiveness at the science-policy interface, EFSA is underpinned by five key principles, including scientific excellence, independence, openness, innovation and cooperation.

These EFSA principles may be of assistance at the national level, for those of us who work at the science-policy interface for animal health and welfare. In this presentation, I will consider the applicability of these five principles in helping to maximise our effectiveness at this interface, using Ireland as an example.
4. The Role of the Industry, when providing Science for Policy

Lisa Alban  
Chief Scientist, Danish Agriculture & Food Council. Department for Food Safety and Veterinary Issues, Risk Assessment Group. Adjunct Professor. University of Copenhagen, Denmark

Science is a valuable input for decision-making, but other important aspects are needed before a meaningful and long-lasting policy can identified, come into force and be complied with. Such inputs may be related to cultural belief and traditions but also to economics and feasibility. Feasibility relates to the capability of something being done, effected, or accomplished. In the following it is argued that economics and feasibility need to be addressed, and that this can be done most easily by involving industry, when providing science for policy.

Traditionally, science has been believed to be mainly produced by academia despite that the industry is also an active fabricator. However, knowledge about a given subject for which a policy is needed - e.g. about slaughterhouse hygiene - may be limited within academia. This may result in input being given, which is addressing the challenge in question poorly or the input may be irrelevant or even misleading. Problems may arise when phrasing the risk question (imprecise question), identifying relevant data (no data found), illustration of risk pathways and the associated parameterization (wrong parameters), and identification of solutions (not feasible e.g. due to export requirements or very expensive).

Involvement of industry when providing science for policy is a tradition in some countries, such as Denmark, where for example working groups were established more than a decade ago for handling of Salmonella in poultry, cattle and swine. In these groups, academia, industry and authority discuss, negotiate and find compromises on how to improve food safety. In many cases, the authorities present a political goal aiming at improving food safety or animal health. An example could be that the prevalence of Salmonella on pork leaving the abattoir should be lowered to 1%. Next, the industry will argue for when the goal can be met realistically (e.g. in 5 years), and how individual targets to each slaughter plant may be set may be set at a higher level (e.g. at 2%) while maintaining the national goal of 1%, and for how this may be reached (e.g. hot water decontamination of high-risk pigs). The industry will use arguments related to economics and feasibility and claim that they are the best to identify cost-effective risk-mitigating actions. The role of academia is here to discuss and challenge the input from the industry to ensure that the ambitions are maintained through qualified initiatives and that the necessary documentation is provided. The experience from Denmark is that although the approach is time-consuming and demanding, the output is implementation of long-lasting, cost-effective policies that are complied with and where the target is met – Salmonella in pork is at 1% now.

Such an active collaboration between academia, industry and authorities requires trust and confidence and it may easily be criticized for lack of independence. But it may be argued that if conflict of interest is being interpreted to a wide extent, then only few persons skilled in a given subject can be seen as independent, and the science produced may be irrelevant for the policy for which it was needed. We therefore need to identify ways to collaborate with the industry, while maintaining the trustworthiness and objectivity of the work undertaken. Transparency is here of importance. FAO is using the latter, when allowing industry experts to participate in research work.
Poster abstracts

P1: Methods of boar taint detection

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The castration of boars has an extremely long tradition. Its primary aim, in addition to elimination of boar taint, is to bring a calming effect on the animals which leads to a significant reduction of aggressive behaviour in boars. Methods of boar castration can be divided into traditional and alternative methods. Boar taint is the typical unpleasant smell that passes into the flavour of pork meat and which is caused by the presence of two substances in particular – androstenone and skatole. The aim of the project is a comprehensive evaluation of the effect of the method of castration on the quality of pork meat and evaluation of the influence of the technology of breeding, nutrition, slaughter and processing on limiting components of boar taint, including the development of software for the sensory evaluation of the target descriptors of pork meat and the training of commodity experts. Currently, there is no fast, reliable, online method available which is able to identify boar taint at the slaughterhouse immediately after slaughter. Classical methods in which fat tissue is warmed and trained evaluators then identify boar taint are still largely used for its assessment. However, the human perception of androstenone and skatole is highly individual. While as much as 99 % of the population is capable of identifying skatole, around 40 % is not capable of identifying androstenone. There are extremely precise methods in analytical chemistry that are capable to detect androstenone and skatole at extremely low concentrations, though the applicability of this instrumentation in practice at slaughterhouses and meat-processing plants is extremely limited and extremely costly in financial terms. Large differences are also evident in the interpretation of the results obtained by precise instrumental methods and methods of direct sensory evaluation.

Acknowledgement
This work has been drawn up within the framework of the realisation of project QJ1510233 – CasPigMeat funded by the Ministry of Agriculture of the Czech Republic.
P2: Tracing and inhibiting growth of *Staphylococcus aureus* in a barbecue cheese production after product recall

Sophia Johler, Katrin Zurfluh, Roger Stephan

*University of Zurich, Switzerland*

**Background**
Staphylococcal food poisoning is one of the most prevalent causes of foodborne intoxication worldwide. It is caused by ingestion of enterotoxins formed by *Staphylococcus aureus* during growth in food. Following a recall of barbecue cheese due to the detection of staphylococcal enterotoxins in Switzerland, we analyzed the production process of the respective dairy.

**Objective**
In this study, we aimed to trace *S. aureus* along the cheese production process and develop a sustainable strategy to inhibit growth of *S. aureus* and decrease the risk of food poisoning.

**Materials and Methods**
We traced *S. aureus* in a step-wise blinded process analysis on 4 production days using spa typing, DNA microarray profiling, and PFGE analysis. We selected a new starter culture and used a model cheese production including a challenge test assay to assess its antagonistic effect on *S. aureus* growth, as well as sensory and technological implications.

**Results**
We detected *S. aureus* in 30% of the collected samples taken from the barbecue cheese production. We traced 2 enterotoxigenic *S. aureus* strains colonizing the nasal cavity and the forearms of the cheesemakers to the final product. In the challenge test assay, we showed that the new starter culture inhibited growth of *S. aureus* while meeting the sensory and technological requirements of barbecue cheese production.

**Discussion and Conclusion**
We conclude that while the pasteurization process of the raw milk used for barbecue cheese production was successful, there is still the risk of intoxication due to *S. aureus* contamination by colonized cheesemakers. We were able to show that the new *S. vitulinus* starter culture inhibited growth of *S. aureus*, while meeting the sensory and technological requirements of barbecue cheese production.

**Perspectives**
The dairy has by now successfully implemented the new starter culture in the production process of the barbecue cheese and resumed regular production.
P3: New dominant spa type t2741 in livestock-associated MRSA (CC398-MRSA-V) in Finnish fattening pigs at slaughter

Sophia Johler¹, Annamari Heikinheimo², Laura Karvonen², Jérome Julmi¹, Maria Fredriksson-Ahomaa², Roger Stephan¹

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Background
The emergence of livestock-associated MRSA has become a growing public health concern worldwide. Studies elucidating the population structure, as well as resistance phenotypes and virulence gene profiles of livestock-associated MRSA strains are needed to improve risk assessment and to develop effective control measures.

Objective
The objective of this study therefore was to determine i) clonal complexes and spa types, as well as ii) resistance phenotypes and iii) virulence and resistance gene profiles of livestock-associated MRSA isolated from Finnish fattening pigs at slaughter.

Materials and Methods
Fifty MRSA isolates collected from Finnish fattening pigs at slaughter were characterized by spa typing and DNA microarray profiling. In addition, antimicrobial susceptibility testing was performed using the Kirby Bauer disk diffusion method.

Results
MRSA isolates were assigned to clonal complexes CC1 (n = 4) and CC398 (n = 46). One dominant spa type (t2741) was present in 33 out of 50 investigated isolates, originating form 15 out of 18 farms. Although each herd exhibited isolates assigned to one clonal complex only, five herds harbored MRSA isolates of either two or three different spa types. All tested MRSA isolates were phenotypically resistant to penicillin, oxacillin, cefoxitin, and tetracycline. With the exception of the isolates assigned to t108, all isolates exhibited resistance to clindamycin.

Discussion and Conclusion
A new dominant LA-MRSA clone (CC398/t2741, SCCmec type V) was identified among fattening pigs in Finland. This is the first study identifying t2741 as a common spa type among LA-MRSA in pigs.

Perspectives
Close monitoring of virulence and resistance profiles of LA-MRSA in livestock and human carriers in close contact to livestock production is crucial to recognize emerging hypervirulent clones and to develop efficient control strategies.
P4: Phenotypic and genotypic characteristics of a presumptive new *Bacillus* species within the *Bacillus cereus* sensu lato group

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Background
The *Bacillus (B.) cereus sensu lato* group comprises not only *B. cereus sensu strictu*, but, amongst others, *B. cytotoxicus*, an extremely rare *Bacillus* group species. The thermotolerant organism *B. cytotoxicus* is characterized by the cytotoxin K variant cytK1 that has been associated with high toxicity.

Objective
In this study, we aimed for an in-depth characterization of ten cytK1 positive isolates not consistent with the current species description of *B. cytotoxicus*.

Materials and Methods
The isolates were characterized using whole genome sequencing, Fourier Transform Infrared mass spectroscopic fingerprinting, *panC* and *spoIIIAB* typing as well as sporulation and growth limit assays, and whole genome sequencing. Enterotoxin formation was assessed using a cytotoxicity assay and western blotting, and sphingomyelinase production was determined using both slot blots and a commercial kit system. Exoprotein profiles were generated using silver staining.

Results
The ten strains exhibited characteristics distinct from all other known *B. cereus sensu latu* species. These strains exhibited only limited growth at temperatures of 25-30°C, while growing rapidly at 54°C. Interestingly, these strains had all been isolated from mashed potatoes. Based on western blotting and data from a Vero cell cytotoxicity assay, these strains produced no or only low levels of Nhe. Whole genome sequencing revealed that some strains were closely related to *B. cytotoxicus*, while others formed a distant and clearly distinct new cluster.

Discussion and Conclusion
Our data suggests that the *Bacillus cereus* group is far more diverse than previously expected and may harbour several thermotolerant species.

Perspectives
The current differentiation of *Bacillus cereus* group species is largely based on the presence of plasmids carrying specific virulence factors. However, these mobile genetic elements can easily be lost or acquired. In the light of our findings and several other recently published species descriptions, this plasmid based classification system seems obsolete.
P5: A new take on Staphylococcal Food Poisoning

Sophia Johler, Henna-Maria Sihto, Taurai Tasara, Roger Stephan

University of Zurich, Switzerland

Background
Ingestion of staphylococcal enterotoxins leads to staphylococcal food poisoning, the most prevalent food-borne intoxication worldwide.

Objective
In this study, we aimed to i) identify the genomic background and the most common sources of staphylococcal food poisoning, ii) examine enterotoxin expression and regulation under food-related stress conditions, and iii) investigate outbreaks

Materials and Methods
To obtain data on the genomic level, strains were characterized by whole genome sequencing, DNA microarray profiling, and different typing techniques. To investigate enterotoxin expression and regulation under stress conditions, expression was quantified under several food-related stress conditions in multiple wild type and isogenic regulatory knockout strains using transcriptional fusions, a quantitative Real-Time approach and an ELISA assay. In addition, several outbreak investigations were conducted.

Results
Several new enterotoxin gene variants and a novel pathogenicity island were detected. Outbreak strains characterized closely resembled strains isolated from colonized or infected humans and were distinct from isolates of animal origin. We were able to show that NaCl and glucose stress reduce SED expression, whereas lactic acid stress had no significant effect on SED expression. In contrast, nitrite stress induced SED expression in some strains. However, SEB expression was reduced by NaCl, glucose, and in some strains also nitrite stress.

Discussion and Conclusion
Our results showed that food handlers colonized by or infected with S. aureus were the most common source of staphylococcal food poisoning outbreak strains. Using the findings of outbreak and product related studies, we were able to show that newly-described staphylococcal enterotoxins can cause outbreaks of staphylococcal food poisoning.
In addition, our findings suggest that the production of staphylococcal enterotoxins cannot be reliably predicted based exclusively on viable cell counts.

Perspectives
Legislative guidelines need to be adjusted accordingly in order to assure consumer safety.
P6: Assessing cattle cleanliness at the slaughterhouse in Finland

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Cattle entering slaughterhouse should be clean, since dirtiness affects adversely slaughter hygiene and animal welfare. In addition, official controls should be performed consistently. However, assessment of dirtiness is subjective.

The objective of this study was to assess how official veterinarians, senior inspectors in the competent authority (Evira) responsible for guidance, provincial veterinary officers in Regional State Administrative Agencies responsible for animal welfare in their district, and food business operators assess cattle cleanliness.

In the autumn 2015, a questionnaire containing 38 photographs from cattle cleanliness guidelines from six European countries was formulated. The recipients were asked to rate the photographs on a 3-level scale (clean or slightly dirty, dirty, very dirty). In addition, they were asked to estimate, whether dirtiness affects welfare of the animal.

Altogether 38 responses were received to the questionnaire. The respondents rated similarly five photographs (13%), of which three were clean or slightly dirty and two very dirty. In rest of the cases, at least one respondent rated the animal differently. The raters were unanimous in seven out of 38 cases (18%) on whether the photograph presented an animal welfare problem or not. The provincial veterinary officers assessed animals in 8/38 (21%) photographs dirtier than the other assessors and assessed in 4/38 (11%) cases welfare affected when others did not. The official veterinarians, senior inspectors of Evira and FBO staff ratings did not differ.

The variation in the data shows the subjectivity of cleanliness assessment. This can be diminished to a degree with clear instructions and training. Based on the study, Evira published a guidance for the official veterinarians on the assessment of cattle cleanliness in the slaughterhouses and also had two training sessions for the official veterinarians. The guidance and questionnaire are also used in training new veterinarians to assess cattle cleanliness.
P7: Combining network analysis with epidemiological data to support the development of risk-based surveillance strategies of hepatitis E virus in swine population

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Background
Animal movements between farms influence pathogen spread in the pig production sector. Hepatitis E virus (HEV) is an emerging and worrying foodborne zoonotic agent that is highly prevalent in pig farms.

Objective
This study aims at coupling network analysis of pig trade in France with epidemiological data to evaluate the risk induced by animal movements regarding HEV spread at two different scales: first by analysing the relationships between herd-level network characteristics and HEV seroprevalence; then by assessing the risk for French departments to be exposed to HEV because of their between-department movements.

Materials and Methods & Results
First, pig movement network and results of a nation-wide seroprevalence study were modelled and analysed. Then, the link between network centrality measures of farms and their HEV seroprevalence level was explored using a generalized linear model. Farms’ in-degree and ingoing closeness were found statistically associated with high HEV within-herd seroprevalence (p<0.05). Finally, the risk for each French department to be exposed to HEV through in-going movements was calculated by combining the distribution of HEV seroprevalence in source departments with the number of movements coming from those source departments. Mapping the risk of exposure at department level highlighted differences between geographical patterns of HEV prevalence and risk exposure due to incoming movements. Therefore, surveillance should not only focus on highly prevalent areas but also on those having at-risk movements from infected areas.

Discussion, Conclusion & Perspectives
Pairing network analysis with epidemiological data has evidenced that HEV management and surveillance options in pig production sector should account for animal movements. More generally, the methods we have proposed prove that movement-based parameters can support risk-based selection of farms for surveillance programmes or the implementation of differentiated surveillance strategies depending on the area movement characteristics. Hence, risk-based epidemiological approaches benefiting from network analysis should be fostered.
P8: Rethinking inspection in slaughterhouses: opportunities and challenges of a shared risk management system in poultry slaughterhouses

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Background
Health surveillance systems are increasingly managed in a cooperative way, involving several stakeholders sharing tasks. In France, poultry slaughterhouse staff – specially trained – is allowed to participate in the tasks of official auxiliaries under the supervision and the responsibility of Official Veterinary Services (OVS) and on the basis of a risk analysis. To organise well the interaction between stakeholders in this multi-stakeholder risk management, the current control system is based on alerts from Food Business Operators (FBOs) to OVS.

Objective
A field study was conducted in order to describe the alert ways used on the ground, to identify the impact of this method on the work organisation as well as the opportunities it may offer.

Materials and Methods
Thirty poultry slaughterhouses were surveyed through semi-directive interviews led with both the official veterinarian/auxiliary and/or the quality manager/assistant, separately. The interviews were recorded and computationally transcribed; data were qualitatively analysed.

Results
A wide range of modus operandi - both for control task division and communication tools - was observed on the field depending on the slaughterhouse organisation, the alert severity or the quality of the relationships between the stakeholders. In all cases, internal procedures were implemented and allow alerts to be raised. This surveillance system was considered efficient if the work organisation was clearly described: organisation of positions, definition of missions and roles, implementation of specific procedures on information exchange and training programs. Limiting the administrative burden and building trusting relationships still remained pivotal challenges.

Discussion, Conclusion & Perspectives
In conclusion, this innovative system appears relevant thanks to adapted alert criteria, the system preparation and formalisation, and the cooperation between the stakeholders. It also offers an opportunity for OVS to reaffirm their central position in risk-based meat inspection.
P9: Farmers’ knowledge and expectations of antimicrobial use and resistance are strongly related to usage in Dutch livestock sectors

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Comprehensive strategies to improve on-farm antimicrobial use (AMU) are needed to contain antimicrobial resistance (AMR). Little is known about farmers’ motivating and enabling factors, and about how those influence AMU. In a cross-sectional online survey, Dutch dairy, veal and pig farmers (n=457) reported their on-farm AMU as “Defined Daily Dose Animal” per year (DDDAF) and completed a detailed questionnaire on their view, knowledge and behaviour towards AMU and AMR. Exploratory factor analysis (EFA) on the questionnaire items identified four psychological factors. Linear regression was done to explore the relationship between the obtained factors and on-farm AMU across the three animal sectors. Dairy farmers showed the highest factor scores for ‘knowledge’ and the lowest for ‘perceived risk’. ‘Knowledge’ scores were significantly and inversely related to AMU. Borderline significant associations with AMU were found for ‘perceived risk’ and ‘undesired attitude to regulations’ (negative and positive relationships respectively). There were no apparent differences for these relationships between the three livestock sectors. This study shows that behavioural interventions in farmers such as educational campaigns or increased support by veterinarians could empower farmers with more prudent and rational practices, eventually reducing AMU in food animals.
P10: Animal prevalence of livestock-associated methicillin-resistant *Staphylococcus aureus* in five Danish mink (*Neovison vison*) farms

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**Background**
Livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA) was for the first time isolated from Danish mink in 2013. Subsequent testing of all mink submitted for clinical diagnosis in Denmark, found 34 % (20/58) mink positive for LA-MRSA. In addition, 40 % (20/50) of screened healthy Danish mink farms were found positive. LA-MRSA in mink is believed to originate from contaminated slaughter-offal in the mink feed.

**Objective**
The objective of the present study was to identify the animal-prevalence of LA-MRSA in five Danish mink farms.

**Materials and Methods**
We collected 1,500 mink carcasses from five Danish mink farms. Farmers were asked to collect 100 mink for each of the three consecutive months following the whelping period (May-July 2017). From each carcass, the right forepaw and a pharyngeal-swab was collected for investigation of MRSA by enrichment, followed by screening on selective agar.

**Results**
By July 1st 2017, 20 mink (5 adult, 15 mink kits) from one farm, were all tested negative. Results from the remaining mink will be presented at the conference.

**Discussion and Conclusion**
In the preliminary results of this study, all mink tested negative. This finding may be explained by an overall low animal-prevalence in the farm. Another explanation could be the high proportion of young mink kits (15/20) tested. All mink kits were <5 weeks of age and had therefore not yet started feeding, which may reduce the likelihood of MRSA carriage.

**Perspectives**
The anatomical location of LA-MRSA on mink (pharynx and paws) poses a human health hazard to farmers, who handle the animals and are at risk of bites and scratches from infected sites. To what extent LA-MRSA has dispersed in the environment of LA-MRSA positive mink farms remains for investigation.
P11: Surveilling Surveillance for Emerging Zoonoses. From case onset to global awareness: assessing factors delaying knowledge transfer in emerging zoonotic diseases.

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Background
Disease notification to the World Health Organisation (WHO) is a fundamental aspect of disease control with prompt reporting reflecting a countries’ preparedness for infectious disease outbreaks. The Severe Acute Respiratory Syndrome (SARS) outbreak in 2003 was heavily criticised for delayed disclosure of information leading to many avoidable cases of the disease.

Objective
There have been few studies looking at barriers to efficient reporting of an outbreak. We aim to quantify factors which influence the reporting behaviour of two zoonotic diseases.

Materials and Methods
The WHO’s Global Alert and Response notification system was examined for cases of avian influenza A(H7N9) and Middle East respiratory syndrome coronavirus (MERS-CoV) from the 1st September 2012 to 31st August 2014. Multiple regression compared the patient’s age, gender and province on hospitalisation and reporting rates. Changes to the reporting behaviour as the epidemic progressed was assessed by adding the previous number of cases into the model.

Results
452 and 435 cases of H7N9 and MERS-CoV, respectively, were reported. H7N9 cases hospitalised in Hong Kong (p=0.004) and MERS-CoV patients older than 19 years (p<0.001) were reported significantly quicker in the multivariable analysis. Gender was not significant. The WHO delayed publishing notifications from specific provinces in both outbreaks. The presence of previous, local cases decreased both the hospitalisation and reporting time for both diseases.

Discussion and Conclusion
Despite lessons being learnt from the SARS epidemic, this data implies that there are still differences in a province’s ability to coordinate a large disease epidemic. The universal increase in reporting speed as more cases were diagnosed is encouraging, suggesting that disease control efforts are succesfully enhanced once the onset of an epidemic is recognised.

Perspectives
More standardised reporting methods would minimise delays in information transfer and help to tackle the ever present threats to global health security.
P12: Spatial distribution and risk factors of clinical leptospirosis in cattle based on Micro Agglutination Test results, a survey in France (2015-2016)

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Background
The concern of bovine leptospirosis relies on many infections reported in farmers and associated economic losses. Leptospirosis occurrence is underestimated in cattle because clinical forms (abortion, fever, reduced milk production) can be confused with other reproductive disorder causes like brucellosis or infectious bovine rhinotracheitis.

Objective
The objective of the study was to guide veterinary practitioners and to support \textit{Leptospira} suspicion by determining risk factors of (sub)clinical leptospirosis in France.

Materials and Methods
We used the Micro agglutination tests (MAT) performed at the veterinary reference laboratory for \textit{Leptospira} diagnosis (Laboratoire des Leptospires) from 2015 to 2016. The infected herds were defined according to the MAT titers and number of tested individuals and, were mapped using ArcGIS®. Farmers from 58 case and 59 control farms were randomly selected and interviewed by phone survey to collect 47 zootechnical and environmental variables. Boosted regression trees and two logistic regression models assessed the relationship between the infectious status and (1) feed variables or (2) possible interactions with various animal species.

Results
Two areas with a higher number of occurrences and not related with the highest herd density areas, have been identified in the West and the Centre-East. Absence of drinking facilities (OR=6.8; CI\textsubscript{95%}=[2.9 - 15.8]), feeding with silage (OR=0.3 CI\textsubscript{95%}=[0.1 - 0.7]) and use of straw yards (OR=10.8; CI\textsubscript{95%}=[1.8 - 62.7]) were significantly associated with bovine leptospirosis.

Discussion and Conclusions
At-risk areas were consistent with the distribution of occurrences obtained in the previous years and the veterinary practitioners working in these areas should be aware of the epidemiological situation. Absence of drinking facilities promotes access to water potentially contaminated by \textit{Leptospira} through infected wildlife and straw yards may lead to increased proximity between congeners and potential \textit{Leptospira} transmission. These criteria should be used to guide veterinary practitioners and to support \textit{Leptospira} suspicion.
P13: Risk factors associated with spatio-temporal clusters of high mortality in Danish swine herds

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Background
Recently, several studies have explored the potential of using different data streams for syndromic surveillance. Mortality data are recorded to fulfill the European Commission requirements, which ensures a continuous data flow for a surveillance system. The value of using these data, generated on a regular basis and covering the entire swine population, remains unexplored for swine disease surveillance in Denmark.

Objective
The aim of this study was to identify spatio-temporal clusters of high mortality in Danish swine herds and associated risk factors.

Materials and Methods
A total of 5,010 farms were included in the analysis from December 2013 to October 2015, corresponding to 1,896 weaner herds, 1,490 sow herds and 3,839 finisher herds. A retrospective space-time scan statistic was used to identify local spatio-temporal clusters of mortality for each age group: weaners (up to 30 kg), sows and finishers. Logistic regression models were used to assess the potential factors associated with finisher and weaner herds being included inside vs outside the clusters.

Results
Several multiple-herd clusters (i.e. clusters with at least two herds) were found. The herd size affected whether weaner herds were inside the clusters, and factors such farm type, SPF status and presence of atrophic rhinitis had an impact on finisher herds being inside vs. outside clusters in the univariable analysis.

Discussion and Conclusion
The clusters could suggest the presence of infectious diseases within the cluster area. The impact of farm type is linked to the fact that larger farms specialize in only one age group, with high biosecurity and more specialized personnel, and subsequently a lower mortality.

Perspectives
Mortality data have a potential use in disease surveillance. However, detected clusters might not be due to disease, but the result of changes such as herd management practices.
P14: Towards dog rabies elimination in West and Central Africa

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Background
Dog transmitted rabies still causes the death of more than 25,000 people yearly in Africa. The Global Alliance for Rabies Control has set the ambitious goal to eliminate human rabies cases by 2030. How can this be achieved in Africa with weak health systems and low levels of funding?

Objective
Develop a rigorous scientific approach of dog rabies elimination in West- and Central Africa.

Materials and Methods
Essential components of a science of rabies elimination are: \textit{i}) Social determinants and public engagement: Effective interventions against dog rabies rely on enabling conditions to organize and operate vaccination teams. \textit{ii}) Integrated surveillance seeks to establish a closer intersectoral communication between public health and veterinary diagnostic laboratories and tests novel low-cost diagnostic tests. \textit{iii}) Equity effectiveness of interventions addresses the determinants successful interventions. This requires a close interdisciplinary collaboration between natural, social and cultural sciences for which we have developed a new mixed method. \textit{iv}) Transmission dynamics and intervention financing assesses the role of heterogeneity of the dog populations and cross-sector economics.

Results
We provide first estimates of the burden of rabies in Chad, Mali and Côte d’Ivoire and Liberia. We demonstrate that dog rabies transmission can be interrupted by dog mass vaccination in an African city. We validated successfully a lateral flow rabies diagnostic test and demonstrate the determinants of vaccination effectiveness in Bamako, Mali. We estimated the cost of rabies elimination for Chad at 28 million Euro over a period of 10 years.

Discussion and Conclusion
Dog rabies elimination in West and Central Africa is feasible and cost-effective in principle.

Perspectives
Effective action depends essentially on political will of African Union and its regional economic organisation, regional coordination using geographical barriers and social acceptance. Novel financial instruments like development impact bonds may play a key role for the roll out.
P15: Food Chain Information usefulness in pig meat inspection

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Background
The main purposes of the Food Chain Information (FCI) are to provide relevant data on public health, animal health and animal welfare and to assist the Official Veterinarian in choosing the appropriate inspection procedures. In the EU, the post-mortem meat inspection of pigs shifted towards a visual inspection in 2014 and FCI support is particularly relevant for this risk-based approach.

Objective
To evaluate the relevance of data included in FCI in pig meat inspection.

Materials and Methods
FCI reports obtained between October 2016 and January 2017 at four abattoirs in the north of Portugal were analysed. The completeness and quality of the information were assessed in the items health status, medication, diseases, tests and results of previous ante- and post-mortem exams. Results of current ante- and post-mortem exams were also assessed.

Results
A total of 276 reports comprising 33929 pigs were analysed. Of these, 56.5% declared the health status, 89.9% and 30.4% gave explicit information on medication, and tests, respectively. Regarding diseases and results of previous ante and post mortem exams, 0.4% had an explicit response. The standard reply “nothing to declare” was frequent on the items disease (72.5%), tests (65.2%) and previous results (75.4%). The most common causes of total condemnation in post-mortem inspection were pneumonia and osteomyelitis, registered in 5.6% and 13.5% of the batches respectively. However, none of the respective FCI declarations had reported disease or specific medication.

Discussion and Conclusion
On topics of the FCI that should support risk-based inspection, imprecise or irrelevant information was delivered by the producers. To maintain the objective of relying on FCI to modernize meat inspection, forms should be altered to be easier to fill in and to improve inclusion of relevant data.

Perspectives
The motivation of producers to provide a valuable FCI should be addressed and training considered.
P16: Development of a novel duplex PCR for detection of virulence-associated genes characteristic of enterohemorrhagic/enteroaggregative E. coli O104:H4

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Background
In summer 2011, an outbreak by a novel epidemic strain E. coli O104:H4 (EAHEC), affected a total of 3842 patients with hemorrhagic enterocolitis mostly in northern Germany. The outbreak was caused by combination of typical Shiga-Toxin-producing E. coli (stx2a) and enteroaggregative E. coli (aggA, aggR, setA, pic and aap) loci, including production of extended-spectrum β-lactamases e.g. blaCTX-M-15 and blaTEM-1 (Bielaszewska et al., 2011).

Objective
The aggregative pattern of adherence (AA) exhibited by enteroaggregative E. coli is a plasmid-associated property which correlates with aggregative adherence fimbria I (AAF/I). The genes aggA [a major fimbrial subunit gene], aggC [outer membrane usher], and aggD [periplasmic fimbrial chaperone] are involved in biogenesis of AAF/I. The aim of this study was to develop a reliable duplex PCR method by using two pairs of specific primers to detect the aggA and the aggC gene confirms the presence of the pAA-plasmid.

Materials and Methods
Primers were designed using multiple alignments of aggC sequences of E. coli O104:H4 str. 2011C-3493 plasmid pAA-EA11 and E. coli HUSEC2011 plasmid pHUSEC2011-2. The primers for detection of the aggA gene were used according to Boisen et al., 2008. A collection of 13 E. coli (O3:H2, O6, O10:H4, O10:H4, O26:H11, O86:H2, O86:H47, O104:H4, O111:H2, O157:H7 and O177:H+) strains which were characterized for their virulence markers was used for evaluation of the plasmid-mediated aggA and aggC gene-specific PCR.

Results
The PCR method with two pairs of primers for amplifying the aggA, the aggC target genes to detect the pAA-plasmid in EAEC O104:H4-isolates of artificially contaminated spreadable raw sausage (“Teewurst”) has been set up successfully.

Discussion and Conclusion
Our duplex endpoint PCR assay is suitable for rapid detection of pAA-plasmid of EAEC/EAHEC with high sensitivity and specificity.
P17: The sero-epidemiology of Rift Valley Fever in people in the Lake Victoria Basin of western Kenya

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Background
Rift Valley fever virus (RVFV) is a zoonotic arbovirus affecting livestock and people. This study was conducted in western Kenya where RVFV outbreaks have not previously been reported.

Objective
The aims were to document the seroprevalence and risk factors for RVFV antibodies in a community-based sample from western Kenya and compare this with slaughterhouse workers in the same region who are considered a high-risk group for RVFV exposure.

Materials and Methods
The study was conducted in western Kenya between July 2010 and November 2012. Individuals were recruited from randomly selected homesteads and a census of slaughterhouses. Structured questionnaire tools were used to collect information on demographic data, health, and risk factors for zoonotic disease exposure. Indirect ELISA on serum samples determined seropositivity to RVFV. Risk factor analysis for RVFV seropositivity was conducted using multi-level logistic regression.

Results
A total of 1861 individuals were sampled in 384 homesteads. The seroprevalence of RVFV in the community was 0.8% (95% CI 0.5–1.3). The variables significantly associated with RVFV seropositivity in the community were increasing age (OR 1.2; 95% CI 1.1–1.4, p<0.001), and slaughtering cattle at the homestead (OR 3.3; 95% CI 1.0–10.5, p=0.047). A total of 553 slaughterhouse workers were sampled in 84 ruminant slaughterhouses. The seroprevalence of RVFV in slaughterhouse workers was 2.5% (95% CI 1.5–4.2). Being the slaughterman, the person who cuts the animal’s throat (OR 3.5; 95% CI 1.0–12.1, p=0.047), was significantly associated with RVFV seropositivity.

Discussion and Conclusion
This study investigated and compared the epidemiology of RVFV between community members and slaughterhouse workers in western Kenya. The data demonstrate that slaughtering animals is a risk factor for RVFV seropositivity and that slaughterhouse workers are a high-risk group for RVFV seropositivity in this environment. These risk factors have been previously reported in other studies providing further evidence for RVFV circulation in western Kenya.
P18: *Staphylococcus aureus* nasal carriage in slaughterhouse workers in western Kenya

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**Background**
Methicillin-resistant *Staphylococcus aureus* (MRSA) has been reported in slaughterhouse workers in Europe and the USA.

**Objective**
The objectives of the study were to determine the prevalence of *S. aureus* and multidrug resistant *S. aureus* (MDRSA) colonization in slaughterhouse workers in western Kenya.

**Materials and Methods**
A nasal swab was collected from 738 workers in 142 slaughterhouses in western Kenya. Swabs were cultured on Mannitol Salt agar. *S. aureus* isolates were identified as Gram positive cocci and catalase and coagulase positive. Antimicrobial sensitivity was determined using the disc diffusion method. Risk factor analysis for *S. aureus* carriage was conducted using multi-level logistic regression.

**Results**
The nasal carriage of *S. aureus* in slaughterhouses workers was 18.8% (95% CI 16.0-21.8%, n=138). Female workers were more likely to be carriers OR 3.3 (95% CI 1.9-8.0). Additional risk factors for nasal carriage were pig ownership OR 1.5 (95% CI 1.0-2.3) and being HIV positive OR 2.3 (95% CI 1.3-3.8). Working at a slaughterhouse where workers wore aprons was protective against carriage OR 0.6 (95% CI 0.4-0.9). Thirty-three (24.3%, 95% CI 17.6-31.6%) isolates demonstrated resistance to three or more antimicrobials and were classified as MDRSA. Nasal carriage of MDRSA was 4.6% (95% CI 3.2-6.2%).

**Discussion and Conclusion**
This report demonstrates the prevalence of *S. aureus* in an occupational setting in western Kenya. Almost one quarter of isolates were classified as multi-drug resistant. The study highlights the potential for zoonotic transmission of *S. aureus* particularly to vulnerable individuals. Work is ongoing to determine the carriage of Methicillin-resistant *S. aureus* (MRSA) in slaughterhouse workers.
P19: Antimicrobial Resistance: The interface between human and poultry at slaughter

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Background
The transmission of antimicrobial resistance between animals and humans represents an issue of growing concern regarding Veterinary Public Health. Transmission routes of antimicrobial resistance can be via animal contact, environmental sources or food-borne. Direct contact to broiler was identified as a risk factor for the transmission of ESBL/AmpC genes between broilers and farmers (Huijbers et al., 2014). Based on these results it can be expected that also slaughterhouse worker have an increased occupational exposure risk.

Objective
Part of the German contribution to the FP7 EFFORT project is the assessment of occupational exposure of humans to antimicrobial resistant bacteria in poultry slaughterhouses.

Materials and Methods
The assessment of the exposure risk to antimicrobial resistant bacteria between human and poultry took place in two German poultry slaughterhouses. The environmental samples, such as glove samples, samples of airborne particles and carcasses, were collected at the slaughter line, cooled and afterwards prepared using the method described by Pacholewicz et al., 2013. Additionally a questionnaire was carried out asking for food consumption, medical treatment etc.

Results
To assess the acute exposure at the day of sampling, airborne particles (n=12) within the working area are collected in predefined spots along the slaughter line. Additional carcasses (n=150) and gloves (n=118) worn by the slaughterhouse workers are sampled. To assess the influence the long-term exposure of the workers, fecal samples (n=87) were collected.

Discussion and Conclusion
Based on the laboratory results the different exposure levels of resistant bacteria between groups of workers e.g. in the so-called “black area” and the “white area” within one slaughterhouse, same as between slaughterhouses will be assessed. Also the long-term effect on the human gut flora through exposure at work via contact with live poultry or carcasses will be analysed.
P20: Towards harmonisation of animal health legislation: Development of a framework for cross-country comparison

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Background
In all countries, legislation provides the basis for assuring animal health and to define public health, food safety, surveillance and trade requirements. Relevant texts include legislation at national, union and international level as well as private standards set by the industry. Regarding the substantial number of possible documents and their relevance for international trade, comparison appears to be relevant to establish the current level of protection among trade partners.

Objective
This joint resident project aims to develop a useful framework for comparing legislation in animal health.

Materials and Methods
The development of the framework was guided by the topic covered in the relevant OIE Animal Health Standard and in European legislation using African Swine Fever as an example. The combination of elements covered in these two sources was expected to cover all main points necessary and likely to appear in similar standards about animal health. A systematic analysis of the two sources allowed developing a list of attributes to be included in a framework to assure complete coverage.

Results
A total of 71 relevant elements were identified and in a first step, separated in eight categories: general description, reporting strategy, organisation of the country, communication to the public, surveillance system, control measures in case of suspicion and confirmation, and importation strategy. Within these categories, each item was then phrased as a question. This is list of question is intended to be used when reviewing a document to capture all information relevant for a comparison between texts with the same objective but from a different source.

Discussion and Conclusion
Comparative analysis of legislation and standards proofed to be a challenging and time-consuming exercise that requires a systematic and organised process. This framework provides a structured approach for legislation comparison in animal health. It also provides a basis for further descriptive analysis.

Perspectives
The method was applied to two case studies: African swine fever and veterinary drug residues in foodstuff.
P21: Food heroes – improving resource efficiency through designing innovative solutions to reduce food waste

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Background
The One Health concept includes also aspects of animal health and welfare. Around 40 million one-day-old male chicks in Germany and around 300 million in the EU were culled yearly in laying hen industry production as they are not efficiently for meat production (Weissmann et al., 2013). Promoting of dual purpose chicken breeds could decrease the extent of chick culling.

Objective
In the frame of the Interreg North-West Europe project “Food heroes” the aim of this study was to investigate the capability of dual purpose chicken as an alternative to chick culling by means of evaluating consumer’s awareness for this and willingness to buy dual purpose chicken meat.

Materials and Methods
Face-to-face interviews with consumers were conducted to evaluate the consumers’ willingness to pay for meat of dual purpose chicken. Furthermore sensory tests were performed to compare meat from conventional and dual purpose chickens.

Results
For conventional chicken, 37% of the participants would pay per ½ kg 4.20 € and in the same portion they would pay 3.85 and 5.25 € or more. In the dual-purpose chicken, most of the consumers would pay in the same rate 10.45 or 9.50 €. A smaller but outstanding amount of participants would pay 11.40 and 12.30 € price.

There was no significant difference in the sensory analyses among the conventional and dual-purpose chicken for overall acceptance by the participants.

Discussion and Conclusion
The overall acceptance of both types of meat does not differ significantly according to the participants. However most of the participants showed their willingness to pay a premium price for dual purpose chicken. It can be contributed to the fact that they got to know the practice of chicken culling, rather than the outstanding attributes of the dual-purpose meat.

Perspectives
Further research is needed to evaluate opportunities and feasibility of successful market introduction of dual-puurose chicken meat products.
P22: Molecular detection of *Brucella* spp. in raw milk cheese from endemic regions sold in Germany

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**Background**
Globalization, international trade and the ever-growing flow of goods and people allow worldwide spreading of zoonotic diseases. The risk of introducing eradicated pathogens into the European Union (EU) is omnipresent as considerable amounts of products of animal origin are continuously imported legally and illegally from endemic countries and may reach consumers at retail level.

**Objective**
Foodborne pathogens already eradicated in the EU are of particular interest for public health. The major goal of our study was to elucidate a potential source of human brucellosis in Germany which is officially free from ovine/caprine and bovine brucellosis.

**Materials and Methods**
We evaluated the presence of *Brucella* spp. using both molecular assays and Farrell’s selective culture medium. The genus-specific PCRs targeting *IS711* and *bcsp31* were applied for screening and confirmation, respectively. Two hundred samples of imported raw milk cheese sold by retailers, including loose, non-labelled as well as pre-packed, labelled cheese were investigated.

**Results**
*Brucella* DNA was prevalent in 20.5% (n=41) of the investigated cheese samples; 90% of them were produced from raw milk. Logistic regression indicated a significant association between molecular detection of *Brucella* and raw milk cheeses (*p*=0.0359) as well as cheeses originating from Bulgaria, France, Greece and Turkey. However, viable brucellae could not be isolated from samples tested positive by PCR.

**Discussion and Conclusion**
The presence of *Brucella* in raw milk cheese reveals a major violation of legal regulations, since these products are officially excluded from the European inner market. Our results suggest that human brucellosis may still be a foodborne infection in Germany, transmitted by raw milk cheeses illegally imported from endemic countries.

**Perspectives**
Future studies on the quality and quantity of illegally imported food products will be indispensable to identify the sources of rare foodborne illnesses in the EU and to implement adequate public health measures.
Background

*Salmonella* species are considered among the most important foodborne pathogens, causing 80.3 million illnesses each year worldwide (Majowicz et al., 2010). Since this pathogen is commensal to many animals’ digestive system, meat products are significant sources of foodborne salmonellosis (Eblen et al., 2006). Bacteriophages (phages) are bacterial viruses, unable to infect human, animal or plant cells. Being natural enemies of specific bacteria, they are logical candidates for targeted control of foodborne bacterial pathogens like *Salmonella* spp. Several studies have already demonstrated the efficacy of phage application on food as biocontrol method of foodborne pathogens (Higgins et al. 2005; Leverentz et al., 2001; Soni et al., 2010; Sukumaran et al., 2016).

Objective

The objective is to demonstrate the efficacy of a commercial phage cocktail against *Salmonella* (PhageGuard-S) in three different meat products.

Materials and Methods

Chicken skin, chicken breast fillet and pork meat purchased from the local supermarket were cut into 3x6x1 cm samples. Appropriate dilution of *Salmonella enterica* Se13 overnight culture (LB broth, 30°C) was evenly applied by pipetting on the sample surface (1x10⁴ cfu/cm²). The phage treatment (1-2x10⁷ pfu/cm²) was performed by pipetting an appropriate dilution of PhageGuard-S on the contaminated surface. The samples were stored in sterile petri dishes at 4°C for 24h, 48h or 6days. At these timepoints, *Salmonella* cells were retrieved homogenizing the samples with peptone water, stomaching for 180 seconds, and plating an appropriate dilution onto selective XLD agar plates.

Results

Phage application resulted in 1.3 to 1.8 log₁₀ cfu/cm² *Salmonella* cells reduction.

Discussion and Conclusion

PhageGuard-S appeared very effective in reducing *Salmonella* contamination on meat samples. Other methods to achieve comparable results in the meat industry are represented by chemical interventions, e.g. organic acids (Loretz et al., 2010; Ellebracht et al., 2005; Nagel et al., 2013; Sukuruman et al., 2015). The application of chemical treatments followed by phage application showed an additional 1 log₁₀ cfu/cm² reduction (Sukuruman et al., 2015), which might be exploited to reduce the use of chemicals in food processing by replacing them with natural solutions like phage technology.

Perspectives

Phage application can be regarded as a very effective tool for the meat industry to reduce *Salmonella* spp. load, integrating the implementation of GMP, HACCP and every other safety measures required.
P24: Antibiotic resistance in the Swiss food chain and assessment of the related resistance transfer risk: a systematic review

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Background
Antimicrobial resistance (AMR) poses serious threats to public health. The spread of resistant bacteria from food to humans and the exposure of consumers to AMR are only poorly understood leaving important gaps for control strategies.

Objective
This study aimed (i) to assess the prevalence of AMR bacteria in retailed food produced in Switzerland or imported from trading partners and (ii) to estimate the probability of exposure of the Swiss consumer.

Materials and Methods
A systematic literature review of evidence published between 1996 and 2016 was performed. Data from 315 out of 9'473 collected studies were extracted yielding 122'548 food samples and 38'386 bacteria of which 22’836 samples and 8’811 bacteria were positive for AMR.

Results
A median AMR bacteria prevalence of >50% was observed for meat and seafood harboring Campylobacter, Enterococcus, Salmonella, E. coli, Listeria and Vibrio spp. and to a lesser degree for milk products harboring starter culture bacteria. Predominant AMR bacteria prevalence was found in descending order against tetracyclines, penicillins and macrolides. In combination with Swiss food consumption patterns, AMR exposure scores (low=0, high=2) of levels 1 and 2 were calculated for Campylobacter, Salmonella, E. coli, Staphylococcus and Enterococcus in pork, poultry and beef; Vibrio, E. coli and Staphylococcus in seafood; and Enterococcus and starter cultures in fermented or processed dairy products.

Discussion and Conclusion
While transmission of AMR bacteria from raw meat can be controlled by implementing good hygiene and proper cooking, fermented meat and dairy products consumption may lead to a direct AMR transfer to the consumer yielding a different risk profile. Furthermore, observed knowledge gaps particularly for AMR prevalence in dairy, plant, fermented meat and novel food products as well as the role of indicator bacteria and starter culture bacteria in AMR gene transfer need to be used to inform risk-based AMR surveillance in food.

Perspectives
Food seems to be a partially neglected transmission vehicle requiring more attention to design One Health-based mitigation strategies.
P25: The prevalence of verocytotogenic *E. coli* O157 (VTEC O157) in British cattle populations

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Background
Cattle are a recognised reservoir for human clinical VTEC O157 infection. Establishing the current baseline prevalence in cattle is a vital first step in any investigation of the relationship between infection in cattle and human clinical infection cases.

Objective
The objective of the British *E. coli* O157 in Cattle Survey (BECS) was to generate new estimates for the prevalence of VTEC O157 in cattle destined for slaughter in both Scotland and in England & Wales. In doing so, current isolates would be obtained for further investigation.

Materials and Methods
Two cross-sectional surveys of 160 farms in England & Wales and 110 Scottish farms were completed during 2014/2015. The Scottish farms were a random sample of those previously visited in both of two previous surveys (1998/2000 and 2002/2004). For England & Wales the design was a randomised, structured survey that replicated the original Scottish survey. Faecal pat samples were taken to determine VTEC O157 status of the farm, using previous survey protocols; 1g of faeces from each pat was tested for VTEC O157 using IMS; and one isolate per positive faecal sample was tested for Vero toxin 1 and 2, using multiplex PCR. Herd and pat level prevalence estimates for Scotland were calculated using generalised linear mixed models.

Results
Herd and pat level prevalence estimates for *E. coli* O157 did not differ significantly between the two BECS surveys. The majority of isolates were verocytotoxin positive.

Discussion and Conclusion
*E. coli* O157 continues to be common in British beef cattle, reaffirming public health policy that contact with cattle and their environments is a potential infection source.

Perspectives
The isolates were subsequently phage-typed and a subset was whole genome sequenced. Future analyses will include: current strain composition; comparisons with contemporaneous human clinical cases, plus comparison with previous Scottish estimates.
P26: Modeling the spread of African swine fever in the Belgian pig livestock industry: Validation of a simulation model

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Background
African swine fever (ASF) is a notifiable infectious pig disease. New cases of ASF are regularly reported in Eastern Europe. Consequently, there is a non-negligible risk of ASF spread towards Western Europe. In Belgium, swine industry constitutes an important part of the agricultural sector, thus preventing losses due to disease introduction and spread is an important issue.

Objective
In the present study, the DTU-DADS-ASF model, a stochastic model used to simulate the spread of ASF in Denmark, is adapted and applied to the Belgian context. The goal of this study is to validate the use of this model in Belgium and to simulate the spread and the epidemic consequences of a potential introduction of the virus in Belgium.

Materials and Methods
The model inputs were set according to different sources: literature, official authorities and the National Animal database, which was used to extract data related to pig herds and movements. A network analysis of movement data was done to validate the model computations. The impact of some parameters was studied with a sensitivity analysis. Model outputs were simulated using various scenarios, assuming different kind of herd as source of infection. The model and results analysis were done using R software.

Results
Preliminary results show reasonable model predictions for a wide range of input parameters (model robustness). The results show that the ASF spread is limited to only 3 infected herds (median). The within-herd transmission rate (beta) is found to be one of the most influential parameters. For higher betas, the disease is detected more quickly and the epidemic consequences are lower.

Discussion and Conclusion
Such a model provides important information that is useful to decision makers for better contingency planning. The next step is to validate the economic module that simulates the costs related to the epidemic.
P27: Different control strategies for Foot and Mouth Disease in a densely livestock populated region in Germany

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Background
Foot-and-mouth disease (FMD) is one of the animal diseases with the highest economic consequences for cloven-hoofed animals. Although the last outbreak of FMD in Germany was in 1988, there is a constant risk of introduction.

Objective
The objective of the current study was to evaluate, if emergency vaccination of animals may be beneficial and feasible in a region with high livestock density.

Materials and Methods
The modified Davis Animal Disease Simulation model (DTU-DADS; Halasa, 2013) was adapted to the conditions in Lower Saxony, Germany, including transmission parameters. Due to the fact, that movement data were not available on farm-level, the model was adapted to simulate animal movements between communities, rather than farms. Ten different control options (scenarios), including depopulation and different vaccination strategies were compared with respect to the duration of the epidemic, number of affected farms and animals affected, using 200 simulation runs for each scenario.

Results
The shortest epidemic duration was achieved for the depopulation strategy, followed by vaccination to live for cattle and pigs, while the vaccination of cattle only resulted in a longer duration and in higher numbers of animals to be culled. This number of animals to be culled was similar for the depopulation strategy, the vaccination of cattle and pigs within a 3 km zone or within a 10 km zone.

Discussion and Conclusion
Although the depopulation strategy resulted in the shortest epidemic duration, most likely this strategy will not be socially acceptable. Thus, the different vaccination strategies offer potential benefits, especially the vaccination to live administered to cattle and pigs.

Perspectives
If depopulation of animals is not feasible or acceptable, the vaccination to live of cattle and pigs in a 3 km zone showed the most benefits.
P28: Assessing the possible association between veterinary antimicrobial consumption and resistance in indicator *E. coli* isolated from farm animals in Belgium

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Background
Administration of antimicrobials increases the risk of antimicrobial resistance in commensal and pathogenic bacteria. The continuing emergence of pathogenic organisms resistant to antimicrobials is a global concern because it leads to frequent treatment failure and increased severity of disease.

Objective
Exploring the trend possibly associating antimicrobial consumption and resistance was completed in the present study focused on indicator *Escherichia coli* from farm animals in Belgium.

Materials and Methods
Annual data on antibiotic use and resistance for 11 antibiotics from 2011 to 2015 were retrieved from the Belgian veterinary surveillance program of *E. coli* from veal calves, young beef cattle, pigs and broiler chickens. The correlation between the average antibiotic resistance prevalence per antibiotic for these species and the use of the corresponding antibiotic class and the total use were investigated.

Results
Except for ampicillin, the Kendall's model could not assess a significant correlation between antimicrobial consumption and resistance during the study period. It should be noticed that positive correlations were found for most antimicrobials and borderline significant for colistin, sulfamethoxazole, trimethoprim and tetracycline. Logistic regression models showed significant positive associations between specific antimicrobial use and resistance, except for gentamicin and chloramphenicol. When considering total use, there is a significant positive association between resistance and total use, except for colistin and gentamicin.

Discussion and Conclusion
These analyses were performed on small datasets and care must be taken while making inference. A positive association was found for most of the antimicrobials tested in regard to the use of the corresponding antimicrobial class or the total antimicrobial use. However, other factors can be involved in the selection of resistance determinants.

Perspectives
From 2017 onwards, data concerning resistance and consumption will be collected each year in Belgium following the launching of a mandatory notification and documentation system allowing the analysis on non-aggregated data.
P29: Cost effectiveness surveillance alternatives for bovine tuberculosis: Approach towards benchmarking

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Background
Despite eradication and control measures applied across Europe, bovine tuberculosis (bTB) remains a constant threat. For countries officially bTB free, as Belgium, one of the main concerns is to maintain this status and (early-)detect new breakdowns.

Objective
The evaluation of different cost effectiveness surveillance system components and alternatives for early detection and substantiation of freedom from bTB, in other words to determine the positive and negative predictive values.

Materials and Methods
A stochastic iteration model was performed to compute the expected negative and positive reactors (true and false) in the tested cattle population given different testing schemes applied in different surveillance components (purchase testing, slaughterhouse inspection and risk based serological surveys). The cost of diagnosing in addition to the cost error was modeled as function of different input parameters such as test characteristics (sensitivity, specificity, cost), different testing schemes (intradermal skin test, visual meat inspection, serological test), national cattle population and movement data, as well as minimum legal requirements. For each surveillance alternative scenario simulations were carried out (10000 iterations/simulation (@risk 7)).

Results
Preliminary results revealed clear discrepancy between expected and observed values using conventional surveillance approaches, thereby bringing serious doubts on the reliability and cost effectiveness of the current national surveillance system. A task force was initiated, following a scientific committed advice, where several alternatives were explored. The different simulations outputs were presented to the different animal health stakeholders and an optimal surveillance alternative strategy was identified.

Discussion, Conclusion & Perspectives
This study revealed the usefulness of benchmarking while evaluating surveillance system. In addition the combination of a participative approach to surveillance evaluation together with quantitative approach values guided and enabled sound science and evidence based decisions regarding the future tuberculosis surveillance in Belgium as required by the international standards.
P30: Risk of introduction of Lumpy Skin Disease in France by the import of cattle

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Background
The lumpy skin disease (LSD) virus belongs to the genus Capripoxvirus and causes a disease in cattle with economic impacts. In November 2014, the disease was first reported in Europe (in Cyprus); it was then reported in Greece (in August 2015) and has spread through different Balkan countries since 2016. Although indirect vector transmission is predominant in at-risk areas, long-distance transmission usually occurs through movements of infected cattle.

Methods and principal findings
In order to estimate the threat for France, a quantitative import risk analysis (QIRA) model was developed to assess the risk of LSD being introduced in France by imports of cattle. Based on available information and using a stochastic model, the probability of a first outbreak of LSD in France following the import of batches of infected live cattle for breeding was estimated to be between 4 x 10^-5 and 3.3 x 10^-3 (in 95% of cases).

Conclusion and significance
The development of a stochastic QIRA made it possible to quantify the risk of LSD being introduced in France through the import of live cattle. This tool is of prime importance because the LSD situation in the Balkans is continuously changing. Indeed, this model can be updated to process new information on the changing health situation in addition to new data from the TRAde Control and Expert System (TRACES, EU database). This model is easy to adapt to different countries and to other diseases.
P31: Risk of introduction of Lumpy Skin Disease in France by the import of vectors in animal trucks

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Background
The lumpy skin disease (LSD) virus is a dsDNA virus belonging to the Poxviridae family and the Capripoxvirus genus. LSD is a highly contagious transboundary disease in cattle producing major economic losses. In 2014, the disease was first reported in the European Union (in Cyprus); it was then reported in 2015 (in Greece) and has spread through different Balkan countries in 2016. Indirect vector transmission is predominant at small distances, but transmission between distant herds and between countries usually occurs through movements of infected cattle or through vectors found mainly in animal trucks.

Methods and principal findings
In order to estimate the threat for France due to the introduction of vectors found in animal trucks (cattle or horses) from at-risk countries, a quantitative import risk analysis (QIRA) model was developed. Using stochastic QIRA modelling, the yearly risk of LSDV being introduced by insects that travel in trucks transporting animals is between $6 \times 10^{-5}$ and $5.93 \times 10^{-3}$; it is mainly due to the risk related to insects entering farms in France from vehicles transporting cattle from the at-risk area. The risk related to the transport of cattle going to slaughterhouses (between $2 \times 10^{-7}$ and $3.73 \times 10^{-5}$) or the transport of horses (between $5 \times 10^{-10}$ and $3.95 \times 10^{-8}$) is much lower. The disinsectisation of trucks transporting live animals is of prime importance to reduce this risk.

Conclusion and significance
The risk for trucks entering farms is quite similar to the risk related to the import of live animals themselves coming to France from the at-risk area. This tool can be updated and is of prime importance because the LSD situation in the Balkans is continuously changing. This model is easy to adapt to different countries and to other vectors and diseases.
P32: Does flynets on chicken houses reduce the number of *Campylobacter* positive flocks?

Marianne Sandberg

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**Background**
Danish intervention studies with earlier versions of flynet that hinder flies entering broiler houses have revealed a reduction in prevalence of *Campylobacter*-positive flocks by around 33 %. A part of the reduction was likely related to an increased compliance with biosecurity rules that is often seen as a result of enrollment in a study.

**Objective**
To conduct an evaluation of existing barriers for implementation of flynets in Danish broiler houses: 1) lack of evidence about practicalities and safety, 2) *Campylobacter* reducing effect when biosecurity is sub-optimal, and 3) expenses related to flynets and their on-house montage.

**Materials and Methods**
A total of 12 flynet houses (with 4 different prototypes) and 29 houses with no flynets were included in an intervention study during summer 2016. Compliance with biosecurity differed a lot in the included houses located on the 4 farms with flynets and on the 7 other farms. The difference in prevalence of *Campylobacter*-positive flocks from the summer 2014 and 2015 to after implementation of flynets in 2016 was calculated in houses with and without flynets – and a T-test was used to evaluate whether there was any significant difference between them.

**Results, discussion, conclusion & perspectives**
Only the prototype for horizontal ventilated houses made of kevlar and attached to light shade/walls with velcro worked well – but with a price of about € 6600 per house. This amount could be reduced, if producers put own effort in montage. Houses with flynets had a 26 % reduction in prevalence of *Campylobacter*-positive flocks (from 2014 & 2015 to 2016) as opposed to a 10 % reduction in the ones without flynets (P=0.3). With the existing economic incentive in place, this implies that it will take the broiler producer >35 years to pay the cost back - which exceed lifetime of the flynet. More data obtained summer 2017 will be presented at the conference.
P33: The i-4-1-health project; infection prevention and antimicrobial reduction in human and veterinary medicine and the public sector in the border region of the southern provinces of the Netherlands and Flanders

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Background
Antibiotic resistance is declared one of the biggest threats to public health by the WHO. Without additional measures the hypothesis is that in 2050 more people will die of an infection with a resistant pathogen in comparison to cancer.

Objective
The "i-4-1-health" project has as goal to gain insight in the level/type of resistance in healthy civilians, human patients and the pig/poultry sector. Since pathogens do not respect borders, a cross-border approach is needed.

Materials and Methods
A digital quantification tool for the level of infection prevention will be developed for use in human (IRIS Scan) as well as for veterinary medicine (V-IRIS Scan). The IRIS Scan will measure processes such as hand hygiene and correct use of antibiotics. The V-IRIS Scan will measure the level of biosecurity, the level/type of use of antibiotics, farmers' risk adversity and the potential transmission of resistance to YOPI's. Improvement plots will visualize areas where additional action is necessary and will serve as a tool for the coaches that will guide the hospital personnel or the farmer in antimicrobial stewardship. A track and trace system will be set up to visualize the spread of pathogens and resistance (by whole-genome-sequencing) both in the human/public sector as well as in the veterinary sector.

Results
The i-4-1-health project started in spring 2017 and will run for three years. Many knowledge sharing sessions are planned between people working in public health, human medicine and veterinary medicine. For example on November 7th 2017 a conference will be held with the title: "the veterinarian as coach; business model or utopian dream?".

Discussion and Conclusion
More information can be found via www.i41health.eu.

Perspectives
This project will allow to identify antibiotic resistance and infection prevention in humans and animals. Knowledge hereof can help us in the global fight against antimicrobial resistance.
P34: Quantification of some milk and meat local products for the presence of coagulase positive *Staphylococcus aureus*

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Background
The most gastrointestinal outbreaks in Kosovo are a concerning issue, especially during the summer month which is also in association with products which are produced locally without proper hygienic practices and handled improperly though the production chain. Most of these products lack of production guidelines and the consumer are not aware about the way of consumption on whether they are heat treated prior to consumption or could be directly consumed.

Objective
The main objective of this study was to determine the level of coagulase positive *S. aureus*, as one of the agents causing food intoxications in food products which are locally produced. Such food products are produced in small scale in local dairies and butcheries and are widely consumed. The aim of this study was to evaluate the level of coagulase positive *S. aureus* in food products which are produced in systems, which presumably not implement proper hygienic and manufacturing practices as well as evaluate the conditions of storage (temperature), conditions of keeping (open, closed), marketing (packing) as well as declaration.

Materials and Methods
In this study, 212 samples consisting of milk and meat products such as paprika in cream, soft-cheese, gjiza (ricotta-like product), suxhuk shtepiak (homemade ready to eat sausage) and kremviçe (fresh made sausage) were taken out from the local food supermarkets in different cities throughout Kosovo. Storage temperature, conditions of keeping (open, closed), marketing (packing) as well as declaration was recorded. Isolation and identification was performed using ISO 6888-1 followed by coagulase test.

Results
In this study, 6 samples resulted coagulase positive out of 39 paprika in crème samples, 5 samples out of 37 tested gjiza samples, 16 samples out of 39 soft cheese samples, 9 samples out of 40 suxhuk shtepiak samples and 8 samples out of total 57 kremviçe samples, respectively. Despite the fact of prior pasteurization of the analyzed products in this study with exception kremviçe being a fresh meat product, high contamination rates were found with 84 S. aureus contaminated samples, out of which 22 samples being uncountable at the dilution 10⁻⁶. Poor storage and handling conditions as well as lack of declaration were recorded.

Discussion and Conclusion
Such high levels of coagulase positive *S. aureus* exceed the levels 10⁻², respectively 10⁻³set by the national microbiological criteria as for milk products and are an indicator of poor processing hygiene and poses a high risk of becoming a food safety problem. Further, the way of marketing of these products allows contamination during the storage, handling during sale, involving, portioning and packaging. Outbreaks with such products might occur. The local industry has to implement minimal hygienic standards as well as educate the staff for personal hygiene, good hygienic and good manufacturing practices.

Perspectives
Considering the fact that such products are not listed in the regulation for microbiological criteria, it is very important that the microbiological criteria for such products are set and well defined. Better monitoring of processing hygiene, handling, and packaging have to be instituted as to avoid human outbreaks. All the isolates will be subject of determination of antimicrobial resistance as to compare the resistance with a previous national study on antimicrobial resistance.
Background
Over the last few years, a shift from curative towards preventive medicine occurred in the livestock sector leading to an increased importance of biosecurity to better control infectious diseases by preventing their introduction and/or reducing their spread. Biosecurity measures (BSM) concern all the stakeholders but farmers are one of the main responsible actors. Existing studies report a low implementation level and mention constraints. Barriers such as cost, usefulness, importance, workload and lack of knowledge were investigated but the constraints and decision-making processes of the farmers related to a given BSM is yet to be clarified.

Objective
The objectives of this study were to: (i) assess the level of implementation of the BSM, (ii) assess the correlation between the importance attributed to a BSM and its level of effective implementation and (iii) collect the main reasons leading to a non-implementation.

Materials and Methods
A stratified randomised survey was implemented in Belgium from December 2016 up to April 2017 with 100 face-to-face interviews conducted in 100 Belgian farms (50 dairy herds and 50 beef herds). A descriptive analysis was performed and the correlation between importance that farmers give to a BSM and its level of implementation was assessed in Stata14® by means of the Spearman's correlation test.

Results
Findings show a generally low level of implementation of the BSM and a positive correlation exists between the importance that farmers give to a BSM and its actual effective implementation.

Discussion and Conclusion
Implementation level of BSM related to the prevention of diseases introduction by direct contact is low and almost no BSM are taken against indirect transmission of diseases. Efficiency, feasibility and usefulness are frequently mentioned reasons of non-implementation.

Perspectives
The level of influence of other factors in the decision making process should be further investigated and clarified and evidence based studies would be useful to convince the farmers of the need of implementation of the different biosecurity measures.
List of participants
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