presents:
6th EWDA
Student Workshop:

Human drivers of emerging diseases

26th to 29th March 2015
Les Pensieres, Veryier-du-Lac, France
HUMAN DRIVERS

of

EMERGING DISEASES

Proceedings of the 6th EWDA Student Workshop

Veyrier-du-Lac, France, 26th to 29th of March 2015

[THE EUROPEAN WILDLIFE DISEASE ASSOCIATION SEeks to provide a forum for the exchange of information on wildlife diseases and their management. Through the provision of opportunities for networking, collaborative research and training we seek to raise the profile of wildlife disease research and management. www.ewda.org]
COLOPHON

Cover design: Jenny Lithner
Layout design: Catharina Vendl, Mariella Aalto-Araneda
Editing: Jenny Lithner, Lidewij Wiersma, Catharina Vendl
THE EWDA STUDENT WORKSHOP WAS FOUNDED IN 2005 IN FRANCE; THE SECOND EDITION WAS HELD IN 2007 IN GREECE, AFTER WHICH IT HAS BEEN HELD BIENNIA LLY (2009, 2011, 2013) IN FRANCE
WELCOME

On behalf of the Student Chapter of the European Wildlife Disease Association (EWDA) it is an honour and a privilege to welcome you to the 6th EWDA Student Workshop, held from March 26th to 29th, 2015, at the Conference Centre ‘Les Pensières’, Veyrier-du-Lac, France!

More than 70% of the zoonotic emerging infectious diseases are caused by pathogens with a wildlife origin. In addition, wildlife species are important reservoirs for pathogens of domestic animals, with devastating socio-economic impacts. Wildlife disease research therefore represents a cornerstone in our efforts to protect and enhance global health, and illustrates the urgent need for a multidisciplinary One World – One Health approach.

Wildlife health scientists will have an increasing role to play in public health research and decision-making as the holistic approach combining the health of humans, animals and the environment becomes ever more popular. Therefore we, wildlife health students, must understand and embrace the full scope of wildlife research. Broad understanding of pathogens’ impact on individuals and populations, as well as solid scientific skills, are critical for conducting research to improve global health, and for acquiring the ability to communicate and interact constructively with researchers from different fields.

The EWDA Student Chapter was created in 2005 to offer wildlife health students the opportunity to share the knowledge and experience of leading global health scientists, to understand the importance of the One World – One Health approach, to acquire broad knowledge on wildlife diseases and their impact on human and domestic animal health, and to develop into rigorous and critical scientists. The most important tool the EWDA SC offers to achieve this, is the biennially organized international EWDA Student Workshop.

The 6th EWDA Student Workshop is organized for and by students to strengthen the scientific education of students with various backgrounds working on wildlife diseases in its broadest sense. With 39 highly motivated students (19 PhD, 5 Master’s and 6 bachelor’s students and 9 others (residents, graduated vets etc.)) from 18 different countries, and 9 internationally renowned speakers, organized at a historic conference centre on the shores of Lake Annecy, this edition is already a success.

Dear colleague, attending this workshop is an amazing opportunity! The lectures, the small group working sessions and the panel discussions are incredibly educational and of the highest scientific level. Meeting and interacting with fellow wildlife health students allows you to share experiences and extend your network globally. Realize that the participating experts are usually stuck in their ivory towers, hard to reach for students like you, so grab your chance to talk to them and ask them anything you want to know! Moreover, make the most of this opportunity given, and enjoy your stay in France!
COMMITTEES

The EWDA Student Chapter 2014-2015

Organizing committee

Estelle Rousselet - University of Florida, USA
Catharina Vendl - University of Zurich, Switzerland
Jenny Lithner - Swedish University of Agricultural Science, Sweden
Lidewij Wiersma - Erasmus University Rotterdam, the Netherlands

Fundraising assistant

Pierre-Alexandre Jolly - National Veterinary School of Alfort, France

Scientific advisory committee

Dr. Becki Lawson - Zoological Society of London, UK
Dr. Leslie Reperant - Artemis One Health Research Foundation, the Netherlands
Dr. Steven van Beurden - Utrecht University, the Netherlands

THE SCIENTIFIC ADVISORY COMMITTEE REVIEWED THE ABSTRACTS SUBMITTED BY STUDENTS AND ADVISED ON SUITABILITY FOR ORAL OR POSTER PRESENTATION
SPONSORS

Special thanks to our sponsors! This workshop wouldn’t take place without their kind support.

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Wildlife Disease Association

Bronze sponsors

Bela-pharm GmbH

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Instrumetl

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CONFERENCE LOCATION

Situated on the shores of Lake Annecy, Les Pensières Conference Centre occupies buildings that were part of the Talloires Abbey in the 16th century. Established by Doctor Charles Mérieux on the land of his family property in Veyrier-du-Lac, the Centre soon became one of the most recognized conference centres among scientists and researchers. Over the years, Fondation Mérieux has extended the premises to accommodate the ever increasing number of scientific conferences and symposia.

Fondation Mérieux is an independent family foundation created in 1967 with official charitable status. Fondation Mérieux focuses its expertise in clinical biology to further the fight against infectious diseases among vulnerable populations. It works directly with local actors to create and strengthen biology laboratories, and link them together via a network to allow them to develop their local capacities in the long term. The Foundation helps to disseminate and increase awareness of scientific innovations throughout the world by holding training and conferences for the international public health community at Fondation Mérieux Conference Centre, Les Pensières.

Les Pensières Conference Centre is a world-class facility devoted to global public health that was founded by Fondation Mérieux to encourage new ideas and promote exchange among leading scientists. In promoting the spread of scientific innovation and information within the international community, the Centre is helping the Foundation achieve one of its primary objectives. Stimulating cooperation between researchers, clinical staff, health practitioners and business executives, the Centre is passionately dedicated to nurturing new ideas and strengthening ties between the industrialized and developing world in the global fight against infectious diseases.
Announcement of the 64th International Conference of the Wildlife Disease Association

The 2015 Wildlife Disease Association International Conference will be held at the Novotel Twin Waters Resort, at Maroochydore in Queensland, Australia. The conference will run from Sunday the 26th of July to Thursday the 30th of July, 2015.

Maroochydore is located on Queensland’s Sunshine Coast and is known for its relaxed atmosphere, family friendly beaches and proximity to some of Queensland’s best natural attractions. The Novotel Twin Waters Resort is a modern, world class yet low key resort that nestles in 14 hectares of coastal heathland adjacent the Maroochy River. Local attractions include whale watching, the Eumundi markets, Australia Zoo, the Blackall Range and Noosa and Conondale National Parks.

The conference theme is “Wildlife Disease Driving Evolution” with world renowned plenary speakers leading sessions on One Health, Emerging Wildlife Diseases in Australasia, Wildlife Disease and Evolution and Marine Ecosystems Health. With a day of workshops and four days of presentations on cutting edge wildlife health and disease topics this a conference you cannot afford to miss.

So why not consider coming to join us “down under” in 2015 and combine a fantastic and educational scientific program with a relaxing stay on Queensland’s aptly named Sunshine Coast.

WDA - All wildlife disease, all conservation, all One Health, all the time!!
Human Drivers of emerging diseases

Keynote Speakers

Wildlife Disease Ecology Driving Evolution
- Reina Plowright – Centre for Infectious Disease Dynamics, Pennsylvania State University (Plenary)
- Michael Kock – Faculty of Veterinary Science, University of Pretoria
- Robert Paulin – Department of Zoology, University of Otago

Emerging Wildlife Disease in Australasia
- Rick Speare – Tropical Health Solutions (Plenary)
- Hume Field – EcoHealth Alliance
- Tanja Strive – CSIRO Biosecurity

One Health and PREDICT
- William Karesh – EcoHealth Alliance (Plenary)
- Jonna Mazet – Faculty of Veterinary Science, UC Davis
- Peter Daszak – EcoHealth Alliance

Workshops

- Wildlife Health Risk Assessment and Multi-criteria Decision Analysis – Patrick Leighton and Ted Leighton
  – full day workshop
- Kooka medicine and rehabilitation – Australia Zoo Wildlife Hospital Staff, Peter Timms and Damien Higgins
  – full day workshop at Australia Zoo Wildlife Hospital (limited to 30 people)
- Chytridiomycosis – An Martel, Lee Berger, Lee Skerratt, Frank Pasmans – half day workshop (limited to 40 people)
- Oiled wildlife response – Kerri Morgan, Mike Ziccardi – full day workshop
- Wildlife Pathology – Gross lesion recognition – Michael Garner – half day workshop

Tours (Wed 29 July)

Whale Watching, Maroochy River cruise and Aboriginal dream time exploration, Mary Cairncross Reserve guided tour near the Glasshouse Mountains.

Questions
jh@asnevents.net.au

Registrations now OPEN
www.wda2015.org/registration
### PROGRAM OF THE 6th EWDA STUDENT WORKSHOP

**Thursday 26th of March 2015**

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<th>Place</th>
<th>Activity</th>
<th>Presenter</th>
<th>Topic</th>
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<tbody>
<tr>
<td>11:30</td>
<td>L</td>
<td>Registration opens</td>
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<tr>
<td>12:00</td>
<td>R</td>
<td>Lunch</td>
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<tr>
<td>13:00</td>
<td>LH</td>
<td>Student mixer</td>
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<td>15:30</td>
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<td>Tea break</td>
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<tr>
<td>16:00</td>
<td>LH</td>
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<tr>
<td>16:10</td>
<td>LH</td>
<td>Presentation</td>
<td>Dolores Gavier-Widén</td>
<td><em>Fondation Merieux and its history</em></td>
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<tr>
<td>16:25</td>
<td>LH</td>
<td>Presentation</td>
<td>WDA, EWDA, EWDA SC</td>
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<tr>
<td>16:40</td>
<td>LH</td>
<td>Short talk</td>
<td>Katinka de Balogh</td>
<td><em>Introduction of FAO</em></td>
</tr>
<tr>
<td>16:50</td>
<td>LH</td>
<td>Keynote lecture</td>
<td>Katinka de Balogh</td>
<td><em>Emerging diseases and food security: looking into the future</em></td>
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<tr>
<td>17:50</td>
<td>LH</td>
<td>Short break</td>
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<tr>
<td>18:00</td>
<td>LH</td>
<td>Lecture</td>
<td>Christian Gortazar</td>
<td><em>Wildlife management: Anthropogenic factors of spillover, spillback and persistence of disease</em></td>
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<tr>
<td>19:00</td>
<td>R</td>
<td>Dinner</td>
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<td>20:00</td>
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<td>Science Trivia Night</td>
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**Friday 27th of March 2015**

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<th>Topic</th>
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<tr>
<td>08:00</td>
<td>LH</td>
<td>Opening</td>
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<tr>
<td>08:10</td>
<td>LH</td>
<td>Student session</td>
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<tr>
<td>08:50</td>
<td>LH</td>
<td>Lecture</td>
<td>Gabor Czirjak</td>
<td><em>Anthropogenic drivers of wildlife disease emergence: an immunological perspective</em></td>
</tr>
<tr>
<td>09:40</td>
<td>LH</td>
<td>Student talk</td>
<td>Kim Grützmacher</td>
<td><em>Using a Field Laboratory as Preventive Measure to Protect Wild Habituated Great Apes from Anthropozoonotic Respiratory Infection</em></td>
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<tr>
<td>09:55</td>
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<td>Coffee break</td>
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<tr>
<td>10:15</td>
<td>LH</td>
<td>Short talk</td>
<td>Jan Semenza</td>
<td><em>Introduction of ECDC</em></td>
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<tr>
<td>10:25</td>
<td>LH</td>
<td>Keynote lecture</td>
<td>Jan Semenza</td>
<td><em>Drivers of infectious disease threats in Europe and how to deal with them</em></td>
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## Saturday 28th of March 2015

<table>
<thead>
<tr>
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<th>Place</th>
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<tr>
<td>08:10</td>
<td>SR</td>
<td>Small group working session part 1</td>
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<td>10:00</td>
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<tr>
<td>10:20</td>
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<td>12:20</td>
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<tr>
<td>13:50</td>
<td>LH</td>
<td>Student talk</td>
<td>Helen Esser</td>
<td>Host–parasite coextinction: evidence from tick-host communities and implications for disease transmission</td>
</tr>
<tr>
<td>14:05</td>
<td>LH</td>
<td>Lecture</td>
<td>Dolores Gavier-Widén</td>
<td>Early detection and characterization of emerging diseases: the fascinating role of pathology</td>
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<td>14:55</td>
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<tr>
<td>15:00</td>
<td>LH</td>
<td>Student sessions</td>
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<tr>
<td>15:40</td>
<td>LH</td>
<td>Presentation</td>
<td>Christian Gortazar</td>
<td>Scientific presentation session</td>
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<td>16:15</td>
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<td>Tea break</td>
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<td>Student sessions</td>
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<td>LH</td>
<td>Short talk</td>
<td>Gabor Czirjak</td>
<td>Introduction of IZW</td>
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<td>17:40</td>
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<tr>
<td>17:50</td>
<td>LH</td>
<td>Presentation</td>
<td>Christian Gortazar, Leslie Reperant, Lidewij Wiersma</td>
<td>Science as career-introduction</td>
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<tr>
<td>18:40</td>
<td>LH</td>
<td>Panel discussion</td>
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<td>How to start a career in science and government agencies, applications, interviews etc.</td>
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</table>
Time | Place | Activity | Presenter | Topic
---|---|---|---|---
19:20 | | Preparation for student act-out | | 
20:30 | D | Final Banquet incl. Auction | | 

Sunday 29\textsuperscript{th} of March 2015

Timing and topics of student sessions refer to page 48.

**KEYNOTE LECTURES BY**

Katinka de Balogh (THU 16:40), Jan Semenza (FRI 10:15), Ab Osterhaus

(Sun 11:10)
SPECIAL SESSIONS

Student mixer and science trivia night (Thursday March 26th)

The Student mixer is organized prior to the Workshop to get to know the other participants during a relaxing activity. If weather allows, the Student mixer will take place outdoors. The science trivia night will serve as an ice breaker in addition to the student mixer. Students and speakers will spend a relaxed evening building up teams and competing in a science trivia.

Dynamic slide show (Friday March 27th)

To make poster presentations more appealing and exciting, the students will present snappers that will consist of a maximum of two slides to be presented in no more than 2 minutes sharp. The aim of the snapper is to make other participants willing to come, see and discuss the posters during coffee and tea breaks. This is your chance to be original and reveal just enough of your work to get people craving to see more!

Scientific presentation session (Saturday March 28th)

This session will serve as an opportunity to get generalized feedback and advice about presenting science – be it speaking, writing or creating visual displays. There will be time for questions and comments from the audience. The students will be given a chance to apply the tips acquired from this session during the Student act-out on Sunday morning!

Student Sessions

During the student sessions the student participants will get the opportunity to practice their skills in public speaking. Two weeks in advance every student was assigned a paper or a topic related to the workshop topic for presentation. As the time of the talk is limited to 5 min., the students have to focus on the most important aspects of their subject. In many cases the audience will also get some insight into the topic of the students’ research project, as the students’ talks are often related. The talks will be held in a relaxed learning environment.

Small group working sessions (Saturday March 28th)

The objective of the small group working sessions is to strengthen the scientific approach of participating students, using specific tools and methods introduced by the experts. Small groups of students will be led by an invited speaker on a research project that will take about four hours to be completed: from dreaming up a scientific research project to presenting scientific results.

For this purpose, the invited speakers have prepared a project outline and recommended literature to read in advance. The idea is that the topics of the individual groups cover a variety of aspects related to wildlife disease research: from surveillance to disease control, from evaluating study-design to mathematical modelling, from human factors affecting disease emergence to emerging diseases’ effects on wildlife conservation.

Students can choose their topic and expert, so that the speakers will end up only with highly interested and motivated students. A platform for sharing of knowledge is provided, but students are responsible for squeezing all information out of the speakers during their time together!

During the small group working sessions, students will be introduced to the speaker’s field of expertise. A wildlife health related problem will be identified, and the tools to resolve it will be provided to the students by the session leader. Group discussions will go in depth into the theoretical background, and determine the strengths and shortcomings of the theory. A real-life situation will then be presented to the students and it will be up to them to resolve it with the newly acquired skills. The inner workings of the sessions are mostly left up to the session leader.

The outcome of the session will be a 5-minute presentation to be given during the Student act-out the following day. Students are invited to prepare this 5-minute talk to summarize the research discussed and convey what they learnt during their small group session. Theoretical and practical backgrounds will be...
presented to the other students in a concise manner. Students should keep only the essentials for the presentation, as 5 minutes are short. Following the oral communication, there will be some time for questions asked by the audience.

Science as a career session (Saturday March 28th)

This session is initiated to inform students about the motivation and drive of different generations of researchers within the field of wildlife diseases. In short, four wildlife health scientists (a PhD-student, a resident, postdoc and a (retired) professor) will tell why they chose a career in science and how they see their work as part of their life. Time for personal questions will be limited to 10 min. There will be additional time to ask questions during the following panel discussion.

Professional panel discussion 1 + 2 + 3 (Friday March 27th and Saturday March 28th and Sunday 29th March)

This panel will bring together the invited professionals to discuss important messages conveyed during the workshop as well as additional matters of relevance. The main topic during the Friday’s session will be ‘Women in science’. Speakers are invited to talk about their personal experience in regards to the topic. The session on Saturday will focus on ‘How to start a career in science and government agencies; job applications, interviews etc.’. This will be an open sequel of the ‘Science as a career’-session giving the students the opportunity to address their questions to the speakers. The last session on Sunday will offer a platform to summarize the lessons learnt during the four days of lectures. Students and speakers will be invited to comment on the workshop organization and express critique. It also serves as the opportunity to open a last scientific discussion between the students and the professional participants. During the panel discussions, students are invited to ask professional and personal questions to invited speakers in a relaxed atmosphere to learn more about their personal philosophy of science!

Student act-out (Sunday March 29th)

During the Student act-out the students will present a summary of the research discussed during the small group working sessions the day before. The Student act-out should result in an overview of the group work topics, but more importantly in an overview of different areas of wildlife health research. During the talk, students should apply the tips and guidelines discussed in the Scientific Presentation session on Saturday. Students should keep only the essentials for the presentation, as 5 minutes are short. Following the oral communication, there will be some time for questions asked by the audience.
SMALL GROUP WORKING SESSIONS

1. Marc Artois – Abundance index and estimation of prevalence in commensal mammals

Zoonotic diseases and livestock diseases maintained and transmitted by wild animal infections are difficult to control. An objective risk analysis frequently leads to the conclusion that a unique option available for the mitigation of the exposure of humans or livestock, to the pathogen, is the culling of wild animal reservoir.

The lack of epidemiological background to base a decision and the usually poor efficiency of a lethal control is a common lesson of decades of disappointing attempts to manage the infections of wildlife.

Nevertheless, the public demand, namely the need to support farmers in great economic difficulties urges health authorities and veterinary services to do something... The apparently best compromise in efficiency, visibility and limited costs is frequently to encourage animal killing or organize large scale destruction of free living animals.

In this talk, I suggest that objective risk analysis, is not the only possibility to assess the balance between options (eradicate, control, mitigate or do nothing). A subjective risk analysis can show that interests which are in competition are influenced by cultural, historical, sociological and philosophical (ethical) perspectives. By considering the place we, humans, are giving to animals, the argument that culling is the only option to solve the problem can be debated. Since arbitration is necessary between medical, social, economic and ethical issues, health and veterinary authorities shall take in account the ethical dimension and learn to manage difficult epidemiological situations by supporting farmers, and conserving natural resources.

References

2. Katinka de Balogh – The role of education in achieving One Health objectives

Katinka de Balogh is a senior officer in charge of Veterinary Public Health and One Health activities at the FAO. To prepare for her session and to gain additional information please refer to links and references mentioned below.

Links

- About the animal health network section of the FAO: http://www.fao.org/animal-health/en/

References

- De Rosa, M. and de Balogh, K. (2005) Experiences and difficulties encountered during a course on veterinary public health with students of different nationalities. Journal of Veterinary Medical Education 32: 373-376

3. Dolores Gavier-Widén – Design a national wildlife health surveillance program for your country

You are asked by the government of your country to lead a team that will work on designing a national wildlife health surveillance programme. The objective of the program is to detect and monitor emerging infectious diseases in wildlife with especial focus on diseases with a high zoonotic, economic or social impact. The resources that will be made available to the program are limited. You have to choose well!

Here are some key words for your planning:
- general (passive) surveillance, targeted (active) surveillance
- interdisciplinarity
- prioritization of pathogens/diseases and or wildlife hosts
- scientific networks, collaboration
- diagnostic tools, test validation
- national, EU and international organizations and agencies
- field work, sampling
- reporting
- information and communication plan and tools
- new technologies

References

4. Christian Gortázar – Practical wildlife disease issues and the future role of humans in their control

Practical wildlife disease issues and the future role of humans in their control”

In this working session we will analyze 2-4 current wildlife disease issues in terms of (1) the true role of wildlife (as opposed to domestic animals or other actors) in infection maintenance; and (2) options for intervention under different scenarios, e.g. limited funding vs. no limits. After this initial discussion, we will design intervention experiments paying attention to the scientific perspective and also to the health management perspective. The final discussion will deal with the more philosophical question, whether intervention on natural systems is justified, or not.

References


5. Albert Osterhaus – Human viruses emerging from the animal world


The topic of Albert Osterhaus’ small group working session may still be subject to changes.
6. Leslie Reperant – Taming modelling to work out the working wheels of disease dynamics

Important note: Students need to bring their own laptops with XLS installed!

Mathematical modelling provides an amazing tool arsenal for the study of disease dynamics, from evolutionary and epidemiological patterns at the grand population scale to evolutionary and pathogenesis patterns within hosts. It can help you define hypotheses, test assumptions on the working wheels of disease dynamics and design your experiments or field studies. If you can dream it, you can model it, even if you don’t have data yet! But, yes, mathematical modelling may look scary with its front lines of equations and armies of Greek letters. The secret: all these scary looks are decoys. During this small group session, you will realize that the knots and bolts of modelling can be tamed readily, and within a few hours you will be able to develop without fear or pain a mathematical model, workable in Microsoft Excel®.

References

MARC ARTOIS

Education
Veterinarian (since 1976) with a first university degree (PhD) in ecology (impact on rabies on fox population demography or vice versa) and a second degree (PhD) in biology of behaviour (fox behaviour and rabies transmission). Diplomate of the European College of Veterinary Public Health, population medicine.

Research interests and positions held
After 20 years spent at the French reference laboratory on rabies (currently ANSES Nancy), I moved in the year 2000 to the formerly called Veterinary school of Lyon, now called VetAgro Sup, to become a professor.

I’ve spent near 40 years working on behavioural ecology of synanthropic wild animals, such as the European red fox, the wild and feral cats, the feral and stray dogs, the Mallard, the European bank vole and finally the brown rat. My interest is on the communicable pathogens these animals can carry and spread to other populations, including humans and cattle or poultry. I’ve tried to find the most efficient behaviour traits allowing the pathogens to be transmitted, either directly or through an indirect contact (called by David Macdonald or Malcolm Bennett “dangerous liaisons” as a paraphrase of the Laclos’ famous novel).

Besides my fascination for animal behaviour, I see myself as a Veterinary Public Health scientist involved in research allowing the human beings to protect themselves and their domestic animals against some pathogens that the above commensal animals maintain.

During years, I was involved in health surveillance of free living wildlife as well. It is relatively recently, that I realised this activity needs a scientific approach to be adapted to the very specific constraints of monitoring pathogens in wildlife. Trying to overcome challenges posed by data collection and information management, is the way I try to keep my bones off the tiring life of a field ecologist, but maintaining a link to my former professional life...

Lecture given at the 6th EWDA Student Workshop
Friday, 27th March, 12:15, lecture: Ethics, Social Science and Policy: Breaking more than just the species barrier?

Selected publications
Background and Education

Katinka de Balogh is of Dutch and Hungarian origins and grew up in Latin-American. She studied veterinary medicine in Berlin and Munich and obtained her doctorate in tropical parasitology from the Tropical Institute of the University of Munich in 1984. She also specialized in tropical animal production and health (France) and in Veterinary Public Health (VPH) (Netherlands).

Expertise and positions held

After a short career as a zoo veterinarian in the Rotterdam Zoo she moved to Africa where she worked for 9 years as a district veterinary officer in rural Zambia and lecturer at the veterinary faculties of Lusaka (Zambia) and Maputo (Mozambique). After positions at the World Health Organization (WHO) and at the Utrecht veterinary faculty in the Netherland, she moved in 2002 to Rome (Italy) to take up a position at the Headquarters of the Food and Agriculture Organization of the United Nations (FAO). After working on pro-poor livestock policy and in crisis management presently she leads the global Veterinary Public Health activities of FAO and she is focal point for One Health.

Lectures given at the 6th EWDA Student Workshop

Thu, 26th March
- 16:40, short talk: Introduction of FAO
- 16:50, keynote lecture: Emerging diseases and food security: looking into the future

Selected publications

- De Rosa, M. and de Balogh, K. (2005) Experiences and difficulties encountered during a course on veterinary public health with students of different nationalities. *Journal of Veterinary Medical Education* 32: 373-376
GABOR CZIRJAK

Education

In 2004 Gábor Czirják received his veterinary degree ‘Doctor of Veterinary Medicine (DVM)’ and in 2007 his Masters degree in Animal pathology and public health from the University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca in Romania. He conducted his PhD thesis in Veterinary Medicine & Ecology, Biodiversity and Evolution at the University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca in Romania and at the University Paul Sabatier in Toulouse, France.

Current position held

- Research scientist, head of wildlife immunology group at the Leibniz Institute for Zoo and Wildlife Research (IZW) in Berlin, Germany since 2010

Research Interest

- Immunology of captive and free-living wildlife species both from evolutionary ecological, disease and conservation points of views; models: bats, carnivores, rodents and birds
- Effect of environmental pollutants on health status of free-living species
- Host – bacteria/fungi interactions

Lectures given at the 6th EWDA Student Workshop

Fri., 27th March, 08:50, lecture:
- Anthropogenic drivers of wildlife disease emergence: an immunological perspective
Sat., 28th March, 17:25, short talk:
- Introduction of the IZW

Selected publications

FRANCOIS DIAZ

Education

Francois Diaz was born in France and received a doctoral degree in pharmacy. He also holds a Master’s degree in international law and law of international organizations.

Position held

He works as chargé de mission at the Headquarters of the World Organisation for Animal Health (OIE) in the Scientific and Technical Department in Paris, France. He has been employed at the OIE since 2005.

Lecture given at the 6th EWDA Student Workshop

Sun., 28th March, 13:50, lecture:
- OIE activities related to wildlife and biodiversity
DOLORES GAVIER-WIDÉN

Education

- Associated Professor (docent in Pathology), Faculty of Veterinary Medicine and Animal Science, Swedish University of Agricultural Sciences (SLU), 2005.
- Doctor of Philosophy (Pathology), University of California at Davis, 1992.
- Master of Science (Pathology), University of California at Davis, 1986.
- DVM, Veterinary Faculty, Buenos Aires University, February 1982.

Research interests and positions held

Current position: Deputy Head of Department, National Veterinary Institute (SVA), Department of Pathology and Wildlife Diseases, Uppsala, Sweden.

- Veterinary Laboratory Agency, Veterinary Research Officer (Pathologist) 1996-1999.

Research interests include infectious diseases of wildlife, pathology and pathogenesis, emerging infections, neuropathology. Tuberculosis, tularemia, prion diseases, viral encephalitis, calicivirus infection of leporids, avian influenza.

Lectures given at the 6th EWDA Student Workshop

Thu., 26th March, 16:25, presentation:
- Introduction of the WDA, EWDA, EWDA SC

Sat., 28th March, 14:05, lecture:
- Early detection and characterization of emerging diseases: the fascinating role of pathology

Selected publications

CHRISTIAN GORTAZAR

Education

Christian Gortazar (San Sebastián, 1967) got a Degree in Veterinary Sciences at Universidad de Zaragoza, in 1990, and a PhD (on the role of diseases in red fox population dynamics) at the same University in 1997.

Research interests and positions held

Since 1999, he is Professor at IREC, a multidisciplinary research institute dealing with conservation and management of wildlife and their habitats (www.SaBio-IREC.com). His lecturing on wildlife diseases is part of IRECs MSc and PhD programs, where he has mentored 15 successful international PhD students. He has acted as principal researcher in numerous grants and contracts on wildlife epidemiology and disease control. Research interests include viral, bacterial and parasitic diseases of wildlife, with emphasis on the epidemiology and control of relevant diseases shared with livestock and humans, such as tuberculosis.

Christian Gortazar is the Past-Chairman of the European Section, Wildlife Disease Association (2012-2014).


Lectures given at the 6th EWDA Student Workshop

Thu., 26th March, 18:00, lecture:
- Wildlife management: Anthropogenic factors of spillover, spillback and persistence of disease

Sat., 28th March, 15:40, presentation:
- Scientific presentation session

Sun., 29th March, 09:50, short talk:
- Introduction/research focus of IREC

Selected publications

AB OSTERHAUS

Education
MSc: Utrecht University, Veterinary faculty, 1973 (cum laude)
PhD: Utrecht University, Veterinary faculty, 1978

Research interests and positions held
As professor of Virology in Rotterdam and Utrecht, The Netherlands, and in Hannover, Germany, **Ab Osterhaus** has a long track record as scientific researcher and PI of numerous major scientific projects.

At Erasmus MC he ran the >40 persons virology diagnostic lab and the >100 persons virology research lab. His research program followed a novel integrated “viroscience” concept, bringing together world leading scientists in molecular virology, immunology, epidemiology, pathogenesis, and intervention studies on human and animal virus infections.

After having handed over the chairmanship of the Erasmus MC Viroscience lab in 2014, he is currently establishing new One Health Institutes in Utrecht and Hannover.

Major performances include the discovery of more than 50 new viruses of humans and animals (e.g. human metapneumovirus, coronaviruses, influenza viruses), elucidation of the pathogenesis of major human and animal virus infections, and development of novel intervention strategies. This has enabled health authorities like WHO, to effectively combat disease outbreaks like SARS and avian influenza. The spin-off, Viroclinics Biosciences BV, is another societally relevant success, allowing effective testing and refining of diagnostic tools and other intervention strategies.

Awards, prizes, guest lecture invitations, (co-)organisanship of international meetings and editorships of scientific journals further highlight his international recognition. He has acted as PhD mentor for more than 60 students, holds several key patents and is the author of more than 1000 papers in peer-reviewed journals, together cited more than 50,000 times, and his H index is more than 90. Most of all, Ab Osterhaus firmly believes scientists have a role to play in translating their knowledge for the benefit and protection of society.

**Lectures given at the 6th EWDA Student Workshop**
Fri., 27th March, 18:00, short talk:
- Background of Ebola

Sun., 29th March, 11:10, keynote lecture:
- Human drivers on viral evolution and emergence, what to expect in the future? (Are we prepared for what we may cause?)

**Selected publications**
(from >1000 co-authorships, H index > 92)
LESLIE REPERANT WORKS AS A RESEARCH SCIENTIST AND
GRANT ACQUISITION COORDINATOR AT THE ARTEMIS ONE
HEALTH RESEARCH FOUNDATION IN UTRECHT. SHE IS THE
CREATOR OF THE EWDA STUDENT WORKSHOP, WHICH SHE
L.REPERANT@ERASMUS.NL

LESLIE REPERANT

Education

Leslie Reperant graduated in veterinary medicine from the National Veterinary School of Lyon, France in 2005 and obtained her PhD at Princeton University, Department of Ecology and Evolutionary Biology, USA in 2010.

Positions held

After one year of post-doctoral research at Princeton, she moved to the Department of Viroscience in Rotterdam, the Netherlands to carry out a two-year Marie Curie International Incoming Fellowship. Since November 2014, she is working as a research scientist and grant acquisition coordinator at the Artemis One Health Research Foundation in Utrecht, the Netherlands.

Research interests

She is interested in the ecology of emerging and zoonotic pathogens and in particular in their ability to cross species barriers. During her Marie-Curie Fellowship, she studied the epidemiological and evolutionary dynamics of influenza viruses of different host origin in light of their pathogenesis within individual hosts, by use of mathematical modelling and experimental approaches. She is currently expanding similar modelling and experimental approaches to the study of the ecology and evolution of other viruses, such as morbilliviruses and lyssaviruses, within a One Health context.

Lecture given at the 6th EWDA Student Workshop

Fri., 27th March, 17:00, lecture:
- Human host and pathogen evolution: predictably unpredictable?

Selected publications

JAN C. SEMENZA

Education

Jan Semenza was initially trained in molecular cell biology at the Medical research Council in Cambridge, UK, where he isolated an intracellular receptor for the sorting of heat-shock proteins, now recognized as an essential component of eukaryotic cells. He extended his training into public health with an MPH from UC Berkeley.

Positions held

He directs the work on environmental and social determinants of infectious diseases at the European Centre for Disease Prevention and Control (ECDC) in Stockholm. He was an Epidemic Intelligence Service Officer at the U.S. Centers for Disease Control and Prevention (CDC). He also worked with the World Health Organization (WHO) and conducted public health projects in Uzbekistan, Sudan, Egypt, Denmark, Brazil, and Haiti.

Professor Semenza was a faculty member at UC Berkeley, UC Irvine, Oregon Health and Science University, and at Portland State University where he taught in the Oregon Master’s Program of Public Health.

Research interests

His interest in reducing climate risks for society at large, extents back almost 20 years; in July 1995, a record-breaking heat wave killed more than 700 people in Chicago. He led the CDC response to this environmental disaster and elucidated the underlying environmental, societal, and behavioural causes of this tragic event. The findings of this study were immediately incorporated into an action plan for the city of Chicago with detailed measures to prevent future heat-related deaths. The heat wave emergency response plan for Chicago became a blueprint for other climate change adaptation policies in other metropolitan areas. He was subsequently awarded a Certificate of Commendation by the City of Chicago for this investigation. He is currently working on environmental and climatic drivers of vector-borne and water-borne disease transmission in Europe. His research has been published in high-impact journals such as Cell, New England J of Medicine, Lancet ID, Science, Nature Climate Change and in several books.

Lecture given at the 6th EWDA Student Workshop

Fri., 27th March
  - 10:15, short talk: Introduction of ECDC
  - 10:25, keynote lecture: Drivers of infectious disease threats in Europe and how to deal with them

Selected publications

**STUDENT ABSTRACTS**

**STUDY OF THE RELATIONSHIP BETWEEN T- GONDII INFECTION AND FEED SOURCE IN SEA GULL CHICKS FROM THE MEDITERRANEAN BREEDING AREAS**

**POSTER PRESENTATION**

**Blanch-Lázaro, Berta**; Cabezón, Oscar1,2; Cerdà-Cuéllar, Marta2; Morera, Virginia3; García-Bocanegra, Ignacio4; González-Solis, Jacob3; Puig-Ribas, Mariat; Dubey, Jitender PS; Almería, Sonia6,2,*

1 Servei d’Ecopatologia de Fauna Salvatge, Departament de Medicina i Cirurgia Animals, Facultat de Veterinària, Universitat Autònoma de Barcelona, Bellaterra, Spain.
2 Centre de Recerca en Sanitat Animal (CRESA). IRTA, Campus de la Universitat Autònoma de Barcelona, 08193 Bellaterra, Barcelona, Spain.
3 Institut de Recerca de la Biodiversitat (IRBio) and Departament de Biologia Animal, Universitat de Barcelona, Spain.
4 Departamento de Sanidad Animal, Facultad de Veterinaria, UCO, Córdoba, Spain.
5 Animal Parasitic Diseases Laboratory, Animal and Natural Resources Institute, Agriculture Research Service, United States Department of Agriculture, Beltsville, MD, USA.
6 Departament de Sanitat i d’Anatomia Animals, Facultat de Veterinària, Universitat Autònoma de Barcelona, 08193 Bellaterra, Spain.

**Background:** *Toxoplasma gondii* is a zoonotic intracellular protozoan parasite of worldwide distribution. Felids are the definitive hosts and warm-blooded species, including birds, can be intermediate hosts. *T. gondii* has been recently considered as a waterborne parasite. Birds are suspected to act as dispersive agents of *Toxoplasma* into isolated territories without felines. Scavenging species regularly feeding on refuse dumps and sewage water, such as some seagulls, are good candidates to become infected by *Toxoplasma*. The objectives of the present study were (1) to assess the role of seagulls as intermediate hosts and reservoirs of *T. gondii*; (2) to explore factors related to the presence of antibodies against this protozoa parasite in seagulls, particularly in relation to their feeding habits (marine, freshwater, terrestrial, refuse) and access to human waste.

**Method:** Serum from yellow-legged gull chicks (*Larus michahellis*; n=479) from Spain (Ebro Delta, Medes Islands, Dragonera Island, and Columbretes Islands, Ons Island) was collected from 2009 to 2011. In 2011, we also sampled 47 Audouin’s gull (*Larus audouinii*) chicks from Alboran Island. All colonies were close to inhabited territories with the exception of Alboran and Columbretes. All breeding colonies, except the one at Ebro Delta, were located in feline-free islands. To assess the origin of food (marine, freshwater, terrestrial environments, and refuse sites) of chicks we analyzed stable isotopes (carbon (C), nitrogen (N), and sulphur (S)) from feathers and reconstructed their diet using a triple-isotope, four-endpoint mixing model. Sera were examined by the modified agglutination test (MAT) to detect antibodies against *T. gondii*. Titres of 1:25 or higher were considered positive.

**Results:** The seroprevalence in yellow-legged gulls (22.8%) was significantly higher than in Audouin’s gull chicks (2.2%) (P<0.001). Seroprevalence in 2009 (43.3%) was significantly greater than in 2010 (12.5%) and 2011 (11.6%) (P<0.001). Seroprevalence was higher in chicks older than 21 days of age (P<0.001). Freshwater origin (36.5%) as main food source and marine origin (50%) as secondary source of food showed statistically higher risk of infection (P<0.001).

**Discussion:** Seroprevalence of *T. gondii* showed significant differences among sampling years suggesting fluctuating rates of transmission. Seroprevalence of antibodies against *T. gondii* was significantly higher in chicks >21 days of age. Therefore, the presence of antibodies in these colonies indicates horizontal transmission through their feeding. In the aquatic ecosystems, filter-feeding invertebrates or fishes are suggested to be a route of transmission of *T. gondii* to warm-blooded animals linked to aquatic ecosystems. Higher seroprevalences related to freshwater and marine sources of food indicate the aquatic environment as one of the main routes of transport and accumulation of *T. gondii* oocysts in the Mediterranean basin.

**Conclusions:** The assessment of *T. gondii* infection in seagulls confirms the susceptibility to *T. gondii* infection and assesses this bird species as intermediate hosts. Therefore, our results suggest that gulls can act as carriers of the parasite in their migrations, having the capability to introduce pathogens in remote islands as naive territories and expose to other susceptible hosts. In this sense, our results identify the yellow-legged and Audouin’s gulls as a good sentinel species to monitor the presence of *T. gondii*. 
TOXOPLASMA GONDII – TRANSMISSION DYNAMICS IN THE CANADIAN ARCTIC
POSTER PRESENTATION

Bouchard, Émilie1; Elmore, Stacey A1; Alisauskas, Ray T2; Samelius, Gustaf3,4; Al-Adhami, Batoul5; Gajadhar, Alvin A5; Jenkins, Emily J1

1University of Saskatchewan, Department of Veterinary Microbiology, Saskatoon, Canada; 2Environment Canada, Prairie and Northern Wildlife Research Centre, Saskatoon, Canada; 3Swedish University of Agricultural Sciences, Department of Ecology, Grimsö Wildlife Research Station, Riddarhyttan, Sweden; 4Snow Leopard Trust, Seattle, USA; 5Canadian Food Inspection Agency, Centre for Foodborne and Animal Parasitology, Saskatoon, Canada

Background: Toxoplasma gondii is a single-celled parasite infecting a wide range of birds and mammals worldwide. It usually causes no symptoms but can cause neurological, ocular, and reproductive problems, especially if the immune system is compromised or if a mammal becomes infected while pregnant. Seroprevalence in some Inuit communities is much higher than in other parts of North America. Inuit are thought to be exposed through handling and consumption of Arctic wildlife. As T. gondii can only produce oocysts in the intestines of felids, and wild and domestic felids are rare in the tundra regions of the Arctic, there are other transmission mechanisms occurring. Previous work has demonstrated that migratory birds are a potential source of introduction of toxoplasmosis, and that foxes are likely infected through carnivory. The main objective of this research is to determine major routes of transmission of T. gondii in a terrestrial Arctic ecosystem at Karrak Lake in the Queen Maud Gulf Bird Sanctuary, Nunavut.

Methods: We hypothesize that T. gondii is also maintained via vertical transmission (i.e. geese to eggs, female foxes to the pups). To test this hypothesis, we will collect and test blood samples from live-trapped adult and juvenile Arctic foxes, and tissues and eggs from harvested geese. Samples are analyzed in laboratories by molecular (PCR) and serological methods (ELISA, IFA) developed and refined previously.

Results: Laboratory work is ongoing for blood samples collected from captured foxes at Karrak Lake in 2014. Results will be presented.

Discussion: Numerous studies have demonstrated that T. gondii is capable of vertical transmission in a variety of hosts, including humans, but few have examined the possibility that strict vertical transmission is maintained over several generations in natural host populations. High prevalence of Toxoplasma in certain hosts that are geographically isolated from definitive felid hosts, such as the arctic fox populations are intriguing scenarios to speculate whether vertical transmission is important or not. It may also help to determine its origin and the extent of genetic diversity and the relative roles of sexual recombination (oocyste) vs clonal propagation (asexual reproduction).

Conclusions: This research will provide important information about how Arctic peoples become exposed and the health effects of toxoplasmosis in threatened wildlife. Moreover, we need more information on the significance of food-borne routes of transmission of T. gondii in the North in order to implement culturally appropriate and effective local prevention measures.
PLAGUE (YERSINIA PESTIS) PERSISTENCE ON PRAIRIE ON PRAIRIE DOG COLONIES IN UTAH AND THE GREAT PLAINS
POSTER PRESENTATION

Bron, Gebbiena M.; Osorio, Jorge, E.; Rocke, Tonie, E.

1University of Wisconsin, Madison, WI, USA; 2University of Wisconsin, Madison, WI, USA; 3USGS National Wildlife Health Center, Madison, WI, USA

Background: Plague, caused by the bacterium Yersinia pestis, is a potentially fatal disease for humans and animals and is primarily transmitted by fleas. In the western United States, plague is enzootic and frequently decimates prairie dog colonies during epizootics. Accidental spillovers to domestic animals and humans also occur. Prairie dogs (Cynomys spp.) are social burrowing animals and keystone species of the grassland ecosystem. They have been considered a Y. pestis amplifying host, but how the plague bacterium is maintained between epizootics is not clear and host-vector-pathogen interactions are poorly understood. In 2013, field efficacy trials for a new plague management tool, the prairie dog oral sylvatic plague vaccine (SPV), started on 29 blind placebo-controlled paired study sites in seven US states with known plague histories. We have taken advantage of this unique framework to study plague disease ecology, in particular the flea-host relationship (biological diversity and host sharing).

Method: We selected 12 SPV paired study sites; 6 on black-tailed prairie dog (C. ludovicianus; BTPD) colonies (2 in South Dakota, 4 in Montana) and 6 on Utah prairie dog (C. parvidens; UTPD) colonies (2 low-elevation and 4 high-elevation) to determine rodent (other than prairie dog), flea diversity and plague prevalence. During the summers of 2013 and 2014, small mammals were live-trapped, sampled and fleas collected on each pair for 3-5 consecutive nights.

Results: Nearly 1700 individuals were caught and 2900 fleas were collected. Small mammals and fleas were identified to species. A subset of fleas will be tested for presence of Y. pestis DNA by PCR. The North American deermouse (Peromyscus maniculatus) and small rodent flea Aetheca wagneri were most abundant. The grasshopper mouse (Onychomys leucogaster) had the largest flea diversity, including the prairie dog flea, Oropsylla hirsuta.

Conclusions: This study will further assess the impact of SPV on non-target small rodents. The data presented herein can begin to inform the development and implementation of management tools to limit the spread of plague epizootics, reducing consequent domestic animal and human exposures.

This work is supported by the Morris Animal Foundation D14ZO-031 and D14ZO-412.
HOST-PARASITE COEXTINCTION: EVIDENCE FROM TICK-HOST COMMUNITIES AND IMPLICATIONS FOR DISEASE TRANSMISSION
ORAL PRESENTATION

Esser, Helen1,2; Jansen, Patrick1,2; Herre, Allen2; Bongers, Frans1; Prins, Herbert1

1Wageningen University, Wageningen, the Netherlands; 2Smithsonian Tropical Research Institute, Panama City, Panama

Background: Extinction cascades form one of the most insidious, but often-ignored drivers of biodiversity loss. By eliminating organisms that are essential to the survival of others, the initial loss of keystone or host species can catalyse secondary extinctions throughout ecological communities. Parasites are expected to be particularly prone to local co-extinction because they need minimum thresholds of host abundance in order to maintain viable populations. This is especially likely for parasites such as ticks, which show strong host specificity and have complex life cycles involving multiple host species. However, despite the relevance to the transmission of tick-borne pathogens, direct empirical tests of these hypotheses are lacking.

Methods: We used drag sampling and camera trapping to survey the diversity and abundance of tick and vertebrate host communities across 12 previously connected forest fragments in the Panama Canal. These fragments ranged 1000-fold in size, had similar vegetation cover, and were equally old and well-protected from illegal hunting.

Results: Host diversity and abundance declined strongly with fragmentation, as predicted by theory of island biogeography. With loss of wildlife, tick communities impoverished as well, resulting in strong declines in both abundance and diversity. Specialist tick species only occurred in fragments where their specific host species were present. Further, less diverse tick communities were dominated by species that are host generalists.

Discussion: Our results indicate that loss of wildlife has cascading effects on tick communities through local host-parasite co-extinction. Only those tick species that are able to feed from a wide variety of hosts are able to survive in degraded environments. In species-poor communities, these generalist ticks may feed proportionally more from small mammals such as rodents and opossums, which are often disease reservoir hosts. Hence, dominance of generalist tick species resulting from wildlife diversity loss could facilitate interspecies pathogen transmission. At the same time however, reduced tick abundance may mitigate disease risk. The net effect of these two contrasting forces remains to be elucidated.

Conclusions: The results of this study suggest that local extirpation of wildlife may cause co-extinction of host-specific tick species with remaining communities dominated by species that could facilitate interspecific pathogen transmission.
RESULTS OF THE ENTOMOLOGICAL AND BIRDS SURVEILLANCE FOR FLAVIVIRUSES IN LOMBARDY (NORTH-ITALY) DURING 2014
POSTER PRESENTATION

Prosperi, Alice; Faccin, Francesca; Chiari, Mario; Lelli, Davide; Moreno Martin Ana Maria; Marco Farioli; Lavazza Antonio.
1 Istituto Zooprofilattico Sperimentale della Lombardia e dell’Emilia Romagna “Bruno Ubertini”, Brescia, Italy
2 Public Veterinary Service, Lombardy Region, Milano, Italy

Background: The surveillance was mainly directed to detect West Nile Disease (WNDV) and Usutu viruses (USUV). WNDV is a worldwide-diffused Flavivirus (family Flaviviridae) firstly reported in Italy in 1998 (Tuscany) and then become endemic in Northern regions. It has an enzootic cycle within mosquitoes and both migratory and residential wild birds, and it could cause variable clinical signs, from fever to neuroinvasive disease, in humans and horses. USUV is another flavivirus well distributed in Europe since 2001 that could cause meningoencephalitis in immunocompromised patients. The close antigenic correlation between WNDV and USUV may be a problem in the interpretation of diagnostic results. The aim of this study is to present the results of the first year of surveillance in Lombardy Region (North Italy), established in order to early identify Flaviviruses circulation.

Methods: The monitoring was done by virological investigation in both mosquitoes (caught using CO2-CDC trap) and wild birds (Pica pica, Corvus corone cornix, Garrulus glandarius). The different species of mosquitoes were identified at the stereomicroscopy. Culex spp were grouped in pools of 100 individuals each and then examined. At necropsy, the birds’ organs sampled for analysis included brain, spleen, heart and kidneys. All this samples were tested in real-time RT-PCR, targeting the WNV 3’-noncoding region, which can detect also USUV, differentiated and then sequenced.

Results: Real-time RT-PCR analysis was performed on 647 pools of mosquitoes. Of these, 26 and 15 resulted positive for WND and USUV respectively. Out of 1400 wild birds examined, 13 resulted WND positive. In the same period 13 WNV clinical cases in humans were diagnosed in the same areas. The time and spatial distribution of positive cases in mosquitoes and birds were variable, but they always occurred before human cases.

Discussion: The diagnostic activity of this surveillance program has proven effective for both individuation of Flaviviruses circulation and discrimination between WNDV and USUV. In fact, the results obtained were also confirmed by the National Reference Centre for Animal Exotic Disease of Teramo.

Conclusions: The 2014 surveillance program supported by the Lombardy Public Veterinary Service represents an integrated surveillance for the early identification of Flaviviruses circulation. Having such a rapid health alarm system is of extreme value as it enables regional infrastructures for optimal management of acute human cases and adoption of prevention strategies.
CHARACTERIZATION OF A NOVEL GAMMAHERPESVIRUS IN PYRENEAN CHAMOIS (RUPICAPRA PYRENAICA PYRENAICA)
POSTER PRESENTATION

Fernández-Aguilar X¹, Esperón F², Cabezón O¹, Velarde R¹, Mentaberre G¹, Delicado V¹, Muñoz MJ², Serrano E¹, López Olvera J.R¹.

¹Servei d’Ecopatologia de Fauna Salvatge, Facultat de Veterinària, Universitat Autònoma de Barcelona, 08193 Bellaterra, Barcelona, Spain. ²Centro de Investigación en Sanidad Animal (CISA-INIA), Carretera Algete a El Casar s/n, 28140 Valdeolmos, Madrid, Spain.

Background: Gammaherpesvirus is an emerging group of viruses of human health and veterinary interest. In natural hosts, the viruses rapidly establish latent infections without significant clinical signs. Acute and fatal disease may be developed in susceptible non natural hosts, particularly in viruses from the Malignant Catarrhal Fever group.

As part of etiologic investigations on respiratory disease in Pyrenean chamois (Rupicapra pyrenaica pyrenaica) we have identified a novel gammaherpesvirus in lung tissue. The aim of this study is to molecularly describe this virus and assess its potential pathological role.

Methods: From 2012 to 2014, lung samples from 81 Pyrenean chamois from the National Game Reserve of Freser-Setcases (Pyrenees, NE Spain) were tested by a pan-herpesviral PCR. Five positive samples were sequenced throughout the glycoprotein B up to the DNA polymerase gene using specifically designed primers (3500 bp). Body condition, age and sex were analysed for individual risk factors.

Results: Thirty-seven samples (45.7%) were positive to the PCR. The sequences obtained revealed a new gammaherpesvirus clustered to the Rupicapra rupicapra gammaherpesvirus-1 (RrHV-1) into the group of malignant catarrhal fever (MCF) viruses. No significant differences were found in prevalence between sampling periods, sex or age class, and no lesion pattern was observed in association with the herpesvirus infection. The chamois infected with the RrHV-1 were distributed throughout the NGR-FS and no cluster distribution was observed.

Discussion: The high prevalence of virus found in lung tissue without exhibiting any clinical sign suggests that the infection probably remained at latency stage in most of the chamois sampled. It is probable that dynamics of RrHV-1 infection in chamois resembles to its close MCF viruses, and chamois most probably become infected at perinatal period or at the first six months of life. Considering that RrHV-1 belongs to the MCF group, the spillover from chamois to sympatric ungulates can eventually occur and susceptible incidental host species may develop MCF syndrome.

Conclusions: In this study we have identified a novel gammaherpesvirus RrHV-1 from the MCF group. Epidemiological and phylogenetic results suggest that Pyrenean chamois is the natural host. Prudent interpretations of the results should be made and assume that RrHV-1 may act as a potential pathogen for Pyrenean chamois at specific conditions.
THE IMPACT OF HETEROGENEITY IN ENVIRONMENTS AND SOCIALITY ON MICROORGANISM DISTRIBUTION IN WILD PRIMATE POPULATIONS

POSTER PRESENTATION

Gogarten, Jan F.1,2,3*

1McGill University, Department of Biology, McGill University, Montreal, Canada; 2Epidemiology of Highly Pathogenic Microorganisms, Robert Koch Institute, Berlin, Germany; 3Department of Primatology, Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany. *This work represents the culmination of a series of projects making up my doctoral dissertation, with a large number of collaborators; key contributors to various aspects of these projects include: Colin A. Chapman, Jonathan Davies1, Aerin L. Jacob1, Roman M. Wittig3, Sébastien Calvignac-Spencer2 and Fabian H. Leendertz2.

Background: Theory suggests there may be some optimum group size for any environment, at which groups are expected to stay near. Yet increasing evidence suggests environments are not homogeneous or stable, even on small spatial or temporal scales, suggesting group sizes should vary across time and space. This is especially important in light of changing climates and anthropogenic disturbance. Thus, many aspects of social organization may be changing on a faster time scale than previously appreciated. Heterogeneity in group sizes and sociality should impact the distribution of mutualistic and pathogenic microorganisms within and between groups. These changes are expected to have cascading impacts on health and ultimately survival of individuals living in different contexts.

Methods: I investigated group size stability for five primate species over 15 years in Kibale National Park, Uganda. To understand mechanisms behind group size changes observed for red colobus (Procolobus rufomitratus), versus the stability observed for other primates, I present data on forest structure between 1990 and 2013, consider changes in predator population, and explore evidence for disease dynamics. To understand how these changes impact individuals living in these changing groups, I present longitudinal data from a group of red colobus followed continuously for 6 years as it increased from 57 to 98 members. To understand how changing social structure might impact the distribution of microorganisms and disease, I examine retroviral and bacterial communities in a group of sooty mangabeys (Cercocebus atys) in Taï Forest, Cote d'Ivoire using non-invasive assays and genetic approaches.

Results: Surveys indicate group sizes did not change for most species, with the exception of red colobus, where group sizes increased. The cumulative size of red colobus food trees increased, suggesting changing food availability was an important factor, while predation and disease seemed to play lesser roles. Longitudinal data suggest increasing group sizes resulted in altered activity budgets; individuals spent less time feeding and socializing, and more traveling, whiling increasing diet diversity. Surprisingly, increasing group size did not show a relationship with female fecundity. Preliminary results suggest social network structure impacts the distribution and evolution of microorganisms in sooty mangabey groups.

Discussion: Overall, results suggest that the Kibale primate community is in a non-equilibrium state. Behavioral changes appear to allow animals to compensate for the greater competition apparent at larger group sizes. Evidence from mangabeys suggests these changes may ultimately impact pathogen evolution and transmission dynamics, providing evidence for a strong link between sociality and health.
Using a Field Laboratory as Preventive Measure to Protect Wild Habituated Great Apes from Anthrozoonic Respiratory Infection: Oral Presentation

Grützmacher, Kim; Leendertz, Fabian
Robert Koch Institute, Berlin, Germany

Background: Respiratory disease, due to infection with common human pathogens, such as human metapneumovirus (HMPV) and human respiratory syncytial virus (HRSV), have been shown to cause high morbidity and considerable mortality in wild great apes habituated to humans for research or tourism. In recent years, many great ape habituation projects have implemented hygiene rules such as overall limited numbers of people with controlled health status entering great ape habitat, the wearing of surgical masks or respirators, minimum viewing distance of seven metres, among others. Establishing field laboratories at great ape habituation sites for on-site and real time testing of pathogens can be used for outbreak investigations as well as a management tool.

Methods: A field laboratory was set up in a western lowland gorilla (Gorilla gorilla gorilla) field site in the Central African Republic. The laboratory equipment allowed for DNA/RNA extraction from throat swabs, feces or tissue, cDNA syntheses, conventional PCR and gel electrophoreses. 10 of 18 gorilla fecal samples and 20 of 81 human throat swabs were tested in the field laboratory. All samples, including separate sets of those already tested in the field, were re-tested at Robert Koch Institute (RKI) under controlled laboratory conditions for validation.

Results: In four of the 18 gorilla fecal samples and four of the 81 human throat swabs RSV was detected and genetically identical between gorilla and human samples. Additionally, a rhinovirus and HMPV was detected in two different human throat swabs. 97% (29/30) of the results from the field could be confirmed at the RKI. 83% (5/6) of humans in whom a respiratory virus was detected, had shown respiratory symptoms.

Discussion: Being able to reproduce 97% of the results from the field supports the efficacy of a field laboratory. The fact that three common human respiratory viruses were circulating among project employees demonstrate the necessity for effective preventive measures. Excluding symptomatic people from approaching great apes is one of the most effective prevention tools, as it reduces the occurrence of human respiratory pathogens at the human great ape interface. However, detection of HMPV in an asymptomatic human shows, that evaluating the health status of humans solely by absence of respiratory symptoms is not sufficient to rule out virus shedding.

Conclusions: Even though operating a field laboratory is highly cost and labour intensive, it should be considered as an effective option to prevent infecting wild habituated great apes with common human respiratory pathogens.
Background: Diseases can greatly impact species populations by causing temporary or permanent declines in abundance. Carnivores, amongst those canids and felids, are especially threatened by infectious diseases. One reason for this might be that infections spill over from domestic animals to wildlife. Determining the immunocompetence of threatened populations is of importance because it is a critical aspect of disease resistance and will thus help identifying those vulnerable to novel pathogens.

Methods: Between 2002 and 2013 275 cheetahs, 38 leopards, ten lions, ten caracals, eight black-backed jackals and eight brown hyenas were immobilized and sampled on Namibian farmland and in Namibian National Parks. We tested the bacterial killing capacity of serum against Escherichia coli, a functional test of the innate immune response. We adapted previously published protocols to fit our research species. Using our adapted protocol it is now possible to conduct comparative studies on many different species. The results of this study were also compared to previously published results of different taxa.

Results: Species differed significantly in their bacterial killing capacity, with feline species having much stronger bacterial killing capacity than canid species. Bacterial killing capacity was related to phylogenetic distances of the species, rather than social system, body mass or foraging behaviour. Bacterial killing capacity of all felids was exceptionally high compared to canids and all other taxa.

Discussion: A higher transmission risk of pathogens is likely to be reflected in the immune responses because pathogen infection imposes a strong selective pressure on their hosts. Although social species, like the lion, have a higher exposure probability to pathogens this was not reflected in their bacterial killing capacity. A higher intake of carrion or a larger body mass was neither reflected in the bacterial killing capacity. Instead we found that the immune responses could be explained by the phylogenetic relatedness of the species. As the bacterial killing capacity only tests innate immunity, it is possible that adaptive immunity better reflects transmission risk, whereas innate immunity is related to phylogeny, as it is the evolutionary “older” part of the immune system.

Conclusions: The results of this study show a strong innate immune response by feline species compared to all other species and does suggests that they are well equipped to handle infections that spill over from domestic animals.
SANITARY ASPECTS OF GAMEBIRD PRODUCTION AND RELEASE IN SPAIN: THE RED-LEGGED PARTRIDGE AND AVIAN NEWCASTLE DISEASE VIRUS (NDV)
POSTER PRESENTATION

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Background: In the recent past the number of captures of red legged partridge (Alectoris rufa), the most important small game specie in central and southern Spain and a staple prey for endangered predators, is undergoing a continuous decline despite the increasing amount of releases. The release of farm-reared partridges is a criticised management tool for several reasons. The most important arguments against partridge releases are the sanitary risk for natural population and poor survival of released partridges. Newcastle Disease (NDV) due to pathogenic strains of aPMV-1 is a worldwide distributed viral disease that causes serious losses and is strictly controlled in poultry. Much less is known in gamebirds, that are generally closely related and species and are raised under similar conditions. In this study we aim to evaluate the exposure of red-legged partridges from different origins to aPMV-1.

Methods: For this purpose, 551 red legged partridge sera collected from 2005 to 2014 were analysed. Including samples from 385 farmed partridges, 73 partridges harvested in hunting estates where partridges are released regularly and 93 samples from partridges hunted or captured in “release-free” hunting estates. The sampling covers most of national territory of Spain. A commercial competition ELISA kit was used to test the sera. Suitable ELISA positive samples were tested by hemaglutination inhibition against aPMV-1.

Results: High prevalence of antibodies against NDV were found in farmed partridges (14,8 %) and the ones from the estates with releases (21,9 %). These seroprevalences were significantly higher (X² test, p<0,05) than those in partridges from “release-free” states (4,3 %).

Discussion: High prevalence of antibodies against NDV in the farmed and release estates partridges could be explained by an increased exposure to and transmission of NDV due to the intensive management and aggregation. The role of NDV in the survival rate of released partridges is not yet clear but it may be an additional factor in a multifactorial context.

Conclusions: With this study we demonstrate a higher exposure to aPMV-1 in red legged partridges bred intensively and after release into hunting states. Exposure could be enhanced by aggregation and intensive management in captivity. NDV infection could have an effect on the survival rate of released partridges. Work funded by the Spanish Ministry for research and competitiveness (AGL2008 – 02504) and the regional government of Castilla - La Mancha (POIC2014-001-P).
IDENTIFICATION AND CHARACTERIZATION OF FRINGILLA COELEBS PAPILLOMAVIRUS IN ITALY

POSTER PRESENTATION

Prosperi, Alice; Gallina, Laura; Casà, Giovanni; Chiari, Mario; Alborali, Giovanni Loris; Scagliarini, Alessandra; Lavazza, Antonio.

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2 Università degli studi di Bologna – Dipartimento di Scienze Mediche Veterinarie

Background: The Fringilla coelebs Papillomavirus (FcPV) belongs to the family of Papillomaviridae, which includes different species capable to infect both man and animals, causing epithelial proliferative lesions, usually self-limiting and often evolving in spontaneous regression. To date, only four species of avian papillomavirus have been isolated: Fringilla coelebs papillomavirus (FcPV), Psittacus erithacus papillomavirus (PePV), Francolinus leucoscepus papillomavirus (FIPV) and the not yet classified Pygoscelis adeliae papillomavirus 1 (PaCV1). Papillomavirus virions are spherical, with a diameter of 55-60 nm, with no envelope and with a constant morphology regardless to the site and the type of injuries. They have a circular dsDNA genome of about 8000 bp, which encodes for six early proteins (E1, E2, E4, E6, E7, E9) and two late ones (L1, L2). The incidence of this disease is usually low (1.3%), but when it comes out in a community it usually infect the main part of the individuals. Clinically the lesions induced by FcPV look like squamous papillomas, mainly located in foot and tarsus-metatarsus. Early reports of lesions referable to papillomavirus in chaffinches and bramblings date back to 1969, but only few data are available on the genome of these viruses and in particular there are no references about the strains circulating in Italy.

Methods: Some chaffinches were conferred to the diagnostic department of IZSLER, with a picture of severe pododermatitis. Samples from these animals were examined using negative staining electron microscopy. The genome was amplified using RCA (Rolling Circle Amplification) and analysed using restriction enzymes; restriction fragments were then cloned and sequenced.

Results: Clinical signs and lesion initially led to a presumptive diagnosis of acariosis, but birds did not recover after specific therapy. By EM observation a high amount of virions morphologically resembling Papillomavirus. By genomic analysis the sequence of the genes E1, E2 and E7 were defined.

Discussion: The EM allowed the identification of the etiological agent. The genes E1, E2 and E7 of the Italian FcPV, showed a high percentage of identity with the only sequence available in the database, corresponding to a strain isolated in USA.

Conclusions: This study represents the first characterization of FcPV circulating in Italy, showing a high homology with the USA one. This is also an example of the still importance of EM as diagnostic tool.
ENDOPARASITES AND IMMUNITY OF NATIVE AND INVASIVE WATERFOWL IN GERMANY
POSTER PRESENTATION

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Background: Invasive species have dramatically expanded their range because of increasing globalization and parasites have been considered to play an important role in the invasion processes. Several hypotheses have been proposed such as the “enemy release”, “novel weapon” or the “immunocompetence advantage”. According to the enemy release hypothesis, invasive animals lose their natural pathogens and parasites during establishment in new habitats, conferring them competitive advantage compared with local species. The novel weapon hypothesis assumes that invasive species carry pathogens which are highly pathogenic to native species. The immunocompetence advantage hypothesis suggests that species which evolved strong immune defences are the prime candidates for successful invasion. Most of these hypotheses have been tested in heterothermic animal species or passerines, despite the successful invasion of Europe by several water birds, such as the Egyptian goose (Alopochen aegyptiaca) or the ruddy duck (Oxyura jamaicensis).

Methods and aims: Our project aims to study water birds in its native and invasive range. From 2015 to 2017 we will measure the endoparasites and immune function of free-living Egyptian geese and mallards (Anas platyrhynchos) both in their native and invaded habitats. Parasites will be determined using morphological identification keys and PCR for genetic identification, while the different branches of the immune system will be assessed by several assays developed for free-living wild birds.

Results: The results of this study will lead to a better understanding of the impact of water bird invasion on native ecosystems with focus on parasitic infections and immunity. Additionally the study will provide data on the differences in immune functions between native and invasive Egyptian goose populations, and will test the different parasite-associated hypothesis of invasive species.

Discussion: Human driven phenomena such as climate change and global movement may intensify and accelerate the process of invasion. As invasive waterfowl populations are rapidly increasing in Europe, the impact on native species, on their habitats and health status are of great research interest both from conservation and public health points of views. Potential displacement of native species by invaders needs to be evaluated in order to develop science-driven conservation measurements and implementation strategies.
TRACKING TOXOPLASMA GONDII IN FRESHWATER ECOSYSTEMS: INTERACTION OF THE PARASITE WITH THE EXOTIC MUSTELID AMERICAN MINK (NEOVISON VISON) IN SPAIN

Cabezón, Oscar; Blanch-Lazaro, Berta; Puig-Ribas, Maria; Alarcia-Alejos, Olga; Gómez, Asunción; Palazón, Santiago; Podra, Madis; Mañas, Sisco; Lavín, Santiago; Dubey, Jitender; Almería, Sonia

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Background: Toxoplasma gondii is a zoonotic protozoan that causes serious illness in humans and infects animals worldwide. Felids are the definitive hosts, excreting oocysts in faeces to the environment. Several authors have suggested the important role of water-borne transmission of the parasite. The objective of the present study was to analyze the seroprevalence of T. gondii in American minks (Neovison vison), a widely distributed invasive species living in freshwater habitats in Spain.

Methods: Serum samples were collected from 526 American minks from Northern Spain from 2011 to 2014. Antibodies to T. gondii were assayed by the modified agglutination test (MAT titres ≥1:25).

Results: Antibodies were found in 409 (77.76%) American minks. No significant differences were found between geographical locations (Catalonia (72.00%), La-Rioja (85.71%) and Castilla-León (77.82%)).

Conclusion: This study shows high and widespread natural exposure of American minks to T. gondii in freshwater habitats in Spain. Water-borne transmission of oocysts may be an important mode of transmission for American minks, which could be a sentinel species for T. gondii contamination in aquatic habitats.
**SPREAD OF ESCHERICHIA COLI THROUGH A LEMUS POPULATION**

**POSTER PRESENTATION**

**Springer, Andrea**; Fichtel, Claudia; Mellmann, Alexander; Kappeler, Peter M. 

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**Background:** Increased exposure to infectious disease is assumed to be one of the major costs of group-living. Epidemiological models allow predicting the potential impact of infectious diseases on host populations and the effectiveness of control measures, but they may produce dramatically different predictions depending on whether contact heterogeneities arising from social behaviour are taken into account, especially with regard to threshold population sizes for disease invasion and transmission and mortality rates. It can be difficult, however, to assess whether the contact patterns that have been measured in wildlife are actually meaningful for pathogen transmission.

**Methods:** In order to shed light on this question, we used *Escherichia coli* as a model organism for faecal-orally transmitted pathogens in a wild population of primates, Verreaux’s sifakas (*Propithecus verreauxi*), in their natural habitat in Madagascar and investigated whether its’ transmission would be influenced by host social structure and ranging behavior. We used a molecular epidemiological approach, multi-locus sequence typing (MLST), to investigate genetic similarities between *E. coli* bacteria from different individuals and groups to infer transmission pathways. We then used network analysis to test the influence of different predictor variables, including group membership, intergroup encounter rates and a measure of space-use sharing (Utilization Distribution Overlap Index, UDOI), on the probability of *E.coli* type sharing. Additionally, all isolates were tested for multidrug-resistance due to the presence of extended-spectrum beta-lactamases (ESBL).

**Results:** From 39 individuals belonging to ten social groups, a total of 29 different MLSTs were isolated. Sharing of *E.coli* MLSTs was significantly correlated with belonging to the same social group. Intergroup encounter rate and UDOI were equally potent explanatory factors for *E.coli* type sharing between social groups. None of the isolates produced ESBL.

**Discussion:** *E.coli* appears to be transmitted via social relationships in this population of lemurs and may serve as a model organism for other faecal-orally transmitted infectious agents in this species. However, it cannot be distinguished whether transmission requires direct contact between the individuals or whether shared space-use is sufficient. As sifakas scent-mark and overmark by means of rubbing their perianal region on trees, this constitutes a likely route of intergroup transmission. Spill-over of *E.coli* from humans and domestic animals to this population seems to be low, as no multidrug resistance due to ESBL was found.

**Conclusion:** Our results demonstrate that social relationships play an important role for the spread of faecal-orally transmitted infectious agents in this species of lemurs. More generally, we show that integrative field studies on the health status of wild primate populations are feasible and that they can potentially shed light on central questions linking sociality, ecology and conservation.
**GENOTYPING OF COXIELLA BURNETII FROM DOMESTIC RUMINANTS AND HUMAN IN HUNGARY**

**POSTER PRESENTATION**

Sulyok, Kinga M1; Kreizinger, Zsuzsa1; Dán, Ádám1; Hornstra, Heidie M1; Pearson, Talima R3; Keim, Paul S3; Balla, Eszter4; Gyuranecz, Miklós1

1Institute for Veterinary Medical Research, Centre for Agricultural Research, Hungarian Academy of Sciences, Budapest, Hungary; 2Veterinary Diagnostic Directorate, National Food Chain Safety Office, Budapest, Hungary; 3Center for Microbial Genetics and Genomics, Northern Arizona University, Arizona, USA; 4National Center for Epidemiology, Budapest, Hungary

**Background:** *Coxiella burnetii*, the causative agent of Q fever, is a zoonotic intracellular bacterium with worldwide distribution. Domestic ruminants are the main reservoirs of the agent with usually subclinical manifestation of the disease, but may suffer from reproductive disorders, and abortion and stillbirth can occur. In humans, Q fever is typically an acute febrile illness with non-specific clinical signs, such as atypical pneumonia and hepatitis. The aim of the study is to describe the genetic diversity of *C. burnetii* in Hungary and the genetic investigation of a Q fever outbreak that occurred in Hungary during the spring of 2013.

**Methods:** A total of 14 samples: (cattle, n=6, sheep, n=7 and human, n=1) collected from across Hungary were studied by 10-loci multispacer sequence typing (MST) and 6-loci multiple-locus variable-number of tandem repeat (TR) analysis (MLVA).

**Results:** Four MST genotypes were identified: the previously described ST20 from cattle, the known ST28 and the novel ST37 from sheep, and ST18 from sheep and human samples originating from the epidemic exclusively. All MST genotypes yielded different MLVA genotypes, with two and three different MLVA types within the ST18 and ST20 samples, respectively. Three novel MLVA types were defined in the ovine materials correlated with ST18, ST28 and ST37 and one novel was described from human blood correlated with ST18. The MLVA pattern of the sheep and human samples of the epidemic differed only in one TR. The phylogenetic analysis showed clustering based on host species, suggesting host-specific evolutionary adaptations.

**Discussion:** The present study provides information about the genotypic diversity of *C. burnetii* occurring in Hungary. From the examined 14 *C. burnetii* samples originating from cattle, sheep and human four MST types (containing one novel profile) and seven MLVA types (including four novel profiles) have been identified. The obtained genotypes clustered based on host species, suggesting host-specific evolutionary adaptations. Although limited number of samples was analysed, this study revealed high genetic diversity among *C. burnetii* in Hungary.

**Conclusion:** Understanding the background genetic diversity is essential in identifying and controlling outbreaks. Our results provide data for the European surveillance and epidemic investigations and add information about the status of Q fever in the Central European region.
PREVALENCE AND DIVERSITY OF ADENOVIRUSES IN FREE-LIVING LIZARDS OF THE IBERIAN PENINSULA AND OF VARIOUS CAPTIVE REPTILIAN AND AMPHIBIAN CARCASSES

POSTER PRESENTATION

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Background: Adenoviruses are medium-sized, non-enveloped viruses with a double-stranded DNA genome. In spite of the fact that they are ubiquitous pathogens of all major vertebrate classes, the individual types poses narrow host spectra. Genus Atadenovirus is one of the five accepted genera within family Adenoviridae known for its mixed host origin, yet they are considered to have co-evolved with squamate reptiles. In this study we screened samples of various origins i.e. those of free-living and of captive hosts.

Methods: Samples of captive animals had been obtained from local pet stores and private pet owners whereas we acquired a vast number of cloacal swabs of various endemic, free-living Iberian lizard species as well. DNA was isolated from internal organs, i.e. liver, lung, kidney and the intestine. Swabbing took place during a faunistic examination. We utilized a nested PCR method with consensus primers to perform the screening for the presence of adenoviruses, targeting a fragment of approx. 300 bp from the DNA-dependent DNA polymerase gene. PCR amplified fragments were sequenced, the sequences were aligned, then submitted to phylogenetic tree reconstruction based on the maximum likelihood method.

Results: 13 out of the 253 swabs turned out to be positive, which implies an average prevalence of 5.1% in total. A novel, hitherto unknown adenovirus was derived from two specimens of Iberian green lizard (Lacerta schreiberi). Two variants of another novel adenovirus were obtained from altogether 11 specimens of Iberian wall lizard (Iberolacerta cyreni). These variants were only 92% identical at amino acid level. As for the carcasses, 9 out of the 38 reptilian (23.6%), and two out of 24 amphibian (8.3%) samples proved to be positive. Out of the amphibian carcasses two were found to be positive, both from poison dart frogs (Phyllobates vittatus and Dendrobates auratus, respectively). The former one is identical to the poison dart frog adenovirus that had been derived by our research team (unpublished). The latter one, however, is a new variant. As for the reptilian carcasses, we detected two novel adenoviruses; one from a veiled chameleon (Chamaeleo calyptratus) and one from a heavily autolysed Chinese water dragon (Physignathus cocincinus), respectively. Seven out of the eight bearded dragon corpses proved to be infected by three different genotypes of agamid adenovirus 1, which is a well-known infectious agent of agamid species worldwide. According to the phylogenetic calculations, all of the new viruses belong to genus Atadenovirus.

Discussion: Besides revealing four completely new adenoviruses and variants of previously detected ones, this is the first time that a study on the prevalence and diversity of free-living reptiles has been carried out. It is already well-known that adenoviruses are rather common infectious agents of squamates, however, all such observations are limited exclusively to dead individuals. Moreover, the fact, that these viruses have been derived from endemic and vulnerable species of the Iberian Peninsula, may have significance from a conservation perspective as well.

Conclusion: Our study confirms the common presence of adenoviruses in squamates, even in healthy individuals that may not display any remarkable clinical signs. The high prevalence, however, noticed in case of carcasses of captive origin suggests that the human drive (i.e. individuals of various but closely related species often kept in mutual enclosures, stress factors that arise in captivity) play a crucial role in adenovirus evolution and pathogenicity. This is supported by the multiple genotypes present in almost every bearded dragon in Hungary as well as worldwide. As far as the poison dart frogs are concerned, adenovirus infection was detected exclusively if multiple species were placed in the same enclosure at pet stores. Such a practice was usually followed by mass mortality of these frogs. We cannot say for sure, whether the adenovirus infection is the right candidate to blame, nevertheless, awareness is the first step to prevent such events, even in a natural habitat, to occur.

(Support: Hungarian Scientific Research Fund OTKA NN107632)
BACKGROUND: Waterfowl (Anseriformes) and shorebirds (Charadriiformes) represent the main natural reservoirs for Avian Influenza Virus (AIV). Understanding AIV persistence and transmission dynamics is crucial for ongoing surveillance on predicting emerging pathogenic strains and improving prevention of outbreaks. The aim of this work was to monitor the evolution of AIV in its natural environment in regard to the ecology of its reservoir hosts.

METHODS: During a 30 month period (March 2012- September 2014) the relation between AIV and wild bird population movements was studied in a small inland wetland (209 Ha) of the Basque Country (Spain) where different AIV subtypes and high AIV prevalences had previously been recorded. Sampling was performed monthly by collecting fresh bird faeces and AIV detection was carried out by rRT-PCR. Likewise, avian censuses and meteorological data were gathered.

RESULTS: A total of 2725 samples were analysed and AIV was detected in 0.26%. The highest prevalence occurred along the breeding season (0.47%) and autumn migration (0.43%). All positive samples contained low pathogenic strains. Detected prevalence was significantly lower (p<0.0001) when compared to a similar study carried out at the same place between 2007-2009. In the former, prevalence reached a total 6.6%, with also high outcomes during breeding season (28.26%) and autumn migration (21.74%).

DISCUSSION: The concentration of positive results throughout the aforementioned periods may be related to two scenarios in wild bird ecology; firstly, a high water bird aggregation densities and therefore a greater virus titre input to the environment during migration and secondly, fledging chicks appearance with a less efficient immune system. Yet, observed prevalence decrease when compared to the previous study, could be related to both influenza’s natural dynamic cycles and other inherent epidemiological factors. In this regard, ongoing research concerning the molecular host species identification in positive samples along with the study of the host migratory traits will certainly help on a better understanding of the complex epidemiology of AIVs.

CONCLUSION: Although it is difficult to elucidate why AIV’s prevalence is subjected to such variation, this large scale work may contribute to a better understanding of the complex epidemiology of this pathogen in the ecosystem. Nevertheless, the need of continuous surveillance of AIV in the wild is still deemed necessary.

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EFFECTS OF HUMAN-INDUCED HABITAT CHANGES ON EMERGING PARASITE INFECTIONS IN LEMURS
POSTER PRESENTATION

de Winter, Iris1, Heitkönig, Ignas1, van Hooft, Pim1, Ploeger, Harm2, Wright, Patricia3

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Background: Besides habitat loss and hunting, new threats for primate survival are emerging – including diseases and parasite infections. Madagascar’s natural forests are home to a group of the most threatened primate species in the world; lemurs. With increasing forest destruction, people and wildlife get to live closer together and parasites may spread more rapidly with potentially large impacts on population viability and public health. Our main question is how human-induced habitat changes influence the occurrence of parasite infections. We also aim to understand the link between parasite infections and lemur health, to develop effective conservation guidelines.

Methods: Methods included the non-invasive collection of health parameters and faecal samples that were screened for parasitic eggs and larvae.

Results: Three genuine parasitic whip- and pinworms (Callistoura, Trichuris and Lemuricola spp.) and two protozoa species (Giardia and Cryptosporidium) were found. Parasite infections were relatively low in lemurs occurring in moderately disturbed areas compared to populations that live in very disturbed or pristine habitats. We found no parasite transmission between lemurs and livestock.

Discussion: In moderately disturbed areas with a higher canopy openness, parasite survival is lower through higher desiccation rates. In addition, the presence of introduced fruit trees appeared to result in considerably higher body condition scores and immune status in lemurs.

Conclusions: We emphasize the importance of monitoring the relation between human-induced habitat changes and parasite infections, the current and future distribution and transmissibility of parasites within lemur populations and of incorporating these insights into conservation efforts. The protection of intermediately disturbed forests does not only benefit lemurs, but also proves to be crucial for both their – and other forest-dependent species’ – survival.
INTERFERON-ß RESPONSE AGAINST LYSSAVIRUS IN EUROPEAN BAT SPECIES
POSTER PRESENTATION

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**Background:** Lyssaviruses are the causative agents of rabies, a fatal zoonotic disease of nerve system. European bats harbour two specific types of Lyssaviruses, European Bat Lyssavirus (EBLV-1 and -2). Although cases of rabies caused by EBLV-1 or -2 are described, there are no reports about epidemics in bats. Due to the long co-evolution between bats and EBLV’s, innate immune pathways might contribute to this disease resistance in European bats.

Interferons (IFNs) play a major role in such defences against viral infection. There are glycoproteins released by host cells in response to pathogens and mediate a complex response which interferes with the viral replication.

**Methods:** Myotis myotis IFN-ß was cloned and sequenced. Recombinant IFN-ß expressed from M. myotis cell lines were used to investigate their signalling pathway and to further characterize IFN-ß induced genes. Furthermore, their antiviral activities against different lyssaviruses (EBLV-1, EBLV-2 and RABV) were analysed. Finally, established M. myotis cell lines which display different susceptibility to Lyssaviruses were used to evaluate the involvement of IFN-ß in lyssavirus resistance.

**Results:** IFN-ß is highly conserved among bat species, and shares high sequence and structural similarity with other mammalian IFN-ß. PolyI:C as simulant for viral infection induced a strong IFN-ß expression in M. myotis cell lines and to further characterise IFN-ß induced genes. Furthermore, their antiviral activities against different lyssaviruses (EBLV-1, EBLV-2 and RABV) were analysed. Finally, established M. myotis cell lines which display different susceptibility to Lyssaviruses were used to evaluate the involvement of IFN-ß in lyssavirus resistance.

**Discussion:** M. myotis IFN-ß is as very effective in blocking lyssavirus replication as other mammalian IFN’s. The ability of MmBr cells to produce IFN-ß after infection might be one mechanism that bats can survive after lyssavirus infection without clinical symptoms.

**Conclusion:** After infection of lyssavirus the M. myotis cells can express IFN-ß and induce IFN stimulated genes in vitro, but with different levels in different cell lines. The involvement of other IFN’s in an effective immune defence against viral infection in regards to the special transmission pathway in bat communities will be further investigated.
### STUDENT SESSIONS: TOPICS AND TIMETABLE

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<td>Janes et al. 2012_Emerging infectious diseases_the role of social science</td>
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<td>11:45</td>
<td>Leonora Szirovicza</td>
<td>Short introduction of chytridiomycosis in frogs based on Skerratt et al. 2007_Spread of Chytridiomycosis has caused the rapid global decline and extinction of frogs</td>
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<td>Martin Heilmann</td>
<td>Wildlife-livestock disease interface in Africa based on 'Kock 2005_What is this infamous Wildlife-Livestock Disease interface-A review for the current situation in Africa'</td>
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<td>Jan Gogarten</td>
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<td>16:20</td>
<td>Venla Johansson</td>
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<td>Olalla Torrontegui</td>
<td>The current situation of Avian Influenza in wild birds in Europe and its human drivers</td>
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<td>Tuva Vamborg</td>
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<td>Alice Prosperi</td>
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<td>Francesca Marie Contadini</td>
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<td>Francesca Faccin</td>
<td>Hahn 2000_AIDS as a zoonosis_Scientific and Public health implications</td>
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<td>Pierre-Alexandre Jolly</td>
<td>Short introduction of Hendra virus infections in Flying foxes, horses and people and its human drivers based on 'Plowright 2011_Urban habitation, ecological connectivity and epidemic dampening; The emergence of Hendra virus from flying foxes'</td>
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<td>Valérie Baede</td>
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<td>Elias Salem</td>
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<td>Jordi Martinez Guijosa</td>
<td>Holmes 2013_What can we predict about viral evolution and emergence</td>
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<td>Speaker</td>
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<td>Émilie Bouchard</td>
<td>Toxoplasma gondii: Human-wildlife interface and pathogenesis in people</td>
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<td>Jan Lakemeyer</td>
<td>Human impacts on marine mammal health in German waters</td>
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<td>Gebbiena M. Bron</td>
<td>The plague is still alive - an overview of current yersinia pestis endemics worldwide</td>
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<td>Hunting and its public health implications in Spain</td>
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<td>Diana Patricia Mora</td>
<td>A short overview of the collaboration of WHO/FAO/OIE shown by means of an example</td>
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<td>Kinga Mária Sulyok</td>
<td>A short overview of the current Q fever-situation within the human-lifestock-wildlife interface in Europe</td>
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<td>17:05</td>
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<td>Yaqing Zhu</td>
<td>Bats as reservoirs of emerging disease pathogens based on 'Smith 2013_Bats and their virome; an important source of emerging viruses capable of infecting humans'</td>
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<td>Ilona Judhianto</td>
<td>Human drivers of zoonoses in Indonesia</td>
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<td>Anastasios Xeidakis</td>
<td>Cortazar 2011_Establishing a European network for wildlife health surveillance</td>
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<td>Jeyhun Aliyev</td>
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<td>Jose Francisco Lima Barbero</td>
<td>A short overview of the SARS epidemic - its origin and human drivers</td>
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<td>Stuart Patterson</td>
<td>Culling programs for badgers for TB prevention in the UK - useful or not?</td>
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<td>13:15</td>
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<td>Berta Blanch Lázaro</td>
<td>Wolfe 2005_Bushmeat hunting, deforestation and prediction of zoonotic disease emergence</td>
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<td>Iris de Winter</td>
<td>Human drivers of zoonoses in Madagascar</td>
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<td>13:30</td>
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<td>María Puig Ribas</td>
<td>Thompson 2013_Parasite zoonoses and wildlife; One Health, spillover and human activity</td>
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A

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