

3rd Joint AITVM-STVM Conference

From 21st to 24th
MAY 2024



Association of Institutions for
Tropical Veterinary Medicine



Society of Tropical Veterinary Medicine



Le **CORUM**
Conference Center
Montpellier
FRANCE



La Région
Occitanie
Pyrénées - Méditerranée



INRAE

**TROPICAL VETERINARY MEDICINE
IN CHALLENGING TIMES**

BOOK OF ABSTRACTS



© G. LAVESSIERE, Cirad & Alpha Visa Congrès



WELCOME

Dear Colleagues,

On behalf of the Organizing Committee, it is our pleasure to invite you to participate in the **3rd Joint Conference of the AITVM-STVM*** entitled:

**‘TROPICAL VETERINARY MEDICINE IN CHALLENGING TIMES:
how should academic and research programs adapt?’**

This conference locally hosted by the French Agricultural Research Centre for International Development (CIRAD) will be held from **Tuesday 21 to Friday 24 May 2024** at the CORUM International Congress Centre in **Montpellier**, France.

The advancement of the field of tropical veterinary medicine to sustainably support agricultural development is what unites both AITVM-STVM organizations. During the conference, you will be able to exchange and share your experiences and research results in all aspects of tropical veterinary medicine through keynote lectures, oral and poster presentations. It will be a unique opportunity to promote young researchers and network within the international research community in veterinary sciences, particularly linking Southern and Northern countries’ academic and research actors.

Both AITVM and STVM have organized successful meetings for decades and joined forces by organizing their first joint conference in Berlin in 2016, followed by a second meeting in 2018 in Buenos Aires. After a COVID-19 related gap, during which a virtual joint event was held in 2022, we are now pleased to be able to meet in person again in 2024. We are therefore eagerly looking forward to four days of exciting presentations and discussions including the famous AITVM-STVM social event in the charming and vibrant city of Montpellier, close to the Mediterranean Sea.

We hope that you will join us during this special conference!

Yours sincerely,

Mohd Hair BEJO, AITVM president

Ard NIJHOF, STVM president

Michel De GARINE-WICHATITSKY, CIRAD Scientific organizer

Nathalie VACHIER, CIRAD Scientific organizer

* AITVM: Association of Institutions for Tropical Veterinary Medicine

* STVM: Society for Tropical Veterinary Medicine



COMMITTEES

Local Organizing Committee

- CIRAD (France)
- Catherine CÊTRE-SOSSAH
- Patricia GIL
- Samia GUENDOZ
- Philippe HOLZMULLER
- Ferran JORI
- Betty MEDOUGA

Organizing Committee

- Michel De GARINE-WICHATITSKY - CIRAD (France)
- Mohd Hair BEJO - Universiti Putra Malaysia (Malaysia), AITVM president
- Betty MEDOUGA - CIRAD (France)
- Ard NIJHOF - Freie Universität Berlin (Germany), STVM president
- Nathalie VACHIERY - CIRAD, head of ASTRE (France)

Scientific Committee

- Aurélie BINOT - CIRAD (France)
- Jérémy BOUYER - CIRAD (France)
- Michel DE GARINE - CIRAD (France)
- Alexis DELABOUGLISE - CIRAD (France)
- Karla GEORGES - University of West Indies (Trinidad and Tobago)
- Mohd Hair BEJO - AITVM board, Universiti Putra Malaysia (Malaysia)
- Latiffah HASSAN - AITVM board, Universiti Putra Malaysia (Malaysia)
- Christine MARITZ-OLIVIER - STVM board, University of Pretoria (South Africa)
- Tshepo MATJILA - AITVM board, University of Pretoria (South Africa)
- Damien MEYER - CIRAD (France)
- Ard NIJHOF - STVM board, Freie Universität Berlin (Germany)
- Martine PEETERS - IRD (France)
- Valérie RODRIGUES - CIRAD (France)
- Renata SERVAN DE ALMEIDA - CIRAD (France)
- Ala TABOR - STVM board, University of Queensland (Australia)
- Séverine THYS - CIRAD (France)
- Nathalie VACHIERY - CIRAD (France)

Administrative secretariat

Registration, accommodation - Sponsorship

Alpha Visa Congrès / AITVM-STVM 2024

624 rue des Grèzes

34070 Montpellier - France

Tel: +33 4 67 03 03 00

E-mail: aitvm-stvm@alphavisa.com

Web: www.alphavisa.com/aitvm-stvm/2024

ORGANIZERS



• AITVM

Association of Institutions for Tropical Veterinary Medicine

info@aitvm.org

<http://www.aitvm.org/>



• STVM

Society for Tropical Veterinary Medicine

<http://www.socropvetmed.org/>



• CIRAD

Center for international cooperation in agronomic research for development

<https://www.cirad.fr/en/>

ACKNOWLEDGMENT

The Organizers would like to thank **public partners and sponsors/exhibitors** for their support of the 3rd Joint AITVM-STVM Conference 2024:

Public partners



Sponsors/exhibitors



KEYNOTE SPEAKERS

SESSION 1 - One (Tropical Animal) Health/integrated Approaches and Perspectives

**Dr Chadia WANNOUS**

One Health Global Coordinator
World Organization for Animal Health (WOAH)
Paris (France)

c.wannous@woah.org

<https://www.worldresiliencesummit.org/roundtables/dr-chadia-wannous->

Dr. Wannous is the One Health Senior Specialist and Global Coordinator for the World Organisation for Animal Health (WOAH) focusing on prevention of health threats at the human-animal-environment interface through One Health initiatives, including on zoonotic and vector borne diseases, AMR, and integrating the environment in the One Health approach.

Before joining WOAH, Dr. Wannous worked in the UN System for more than a decade on health emergencies prevention, preparedness, and response, including serving as the Senior Policy Advisor to the UN Special Envoy on Ebola response in West Africa and to the UN System Influenza Coordination.

Dr. Wannous coordinated the Toward a Safer World Network for Pandemic Preparedness and the health components of the Sendai Framework for Disaster Risk Reduction and led its Science and Technology Partnership.

Dr. Wannous is a public health professional with a PhD in International Health and Development.

SESSION 2 - Animal Health and Production

**Professor Ala TABOR**

Professorial Research Fellow
Animal BioTICKnology Lab
Centre for Animal Science
Queensland Alliance for Agriculture & Food Innovation
The University of Queensland
Brisbane, Queensland (Australia)

a.tabor@uq.edu.au - @AlaLTUQ

<https://qaafi.uq.edu.au/profile/492/ala-tabor> - <https://www.facebook.com/ala.tabor.1>

Professor Ala Tabor joined the University of Queensland in October 2010, after 18 years of conducting research with the Queensland State Government. She is a research-focused academic with a strong background in industry engagement associated with animal health and agricultural biotechnologies using genomics tools with over 110 publications including four patented animal vaccines. Ala has been researching bovine venereal diseases for more than 20 years. Currently, she is screening a new Australian trichomonas vaccine and her team is developing novel 'single sample' molecular diagnostic methods for bovine trichomonosis and genital campylobacteriosis in collaboration with industry. She has also patented vaccines for the Australian paralysis tick and the cattle tick *Rhipicephalus microplus* species complex.

SESSION 4 - Veterinary Parasitology

**Professor Philippe JACQUIET**

ENVT
Laboratory of parasitology
Toulouse (France)

philippe.jacquet@envt.fr

https://guiderecherche.univ-toulouse.fr/4DCGI/Entite_C_3310_10068

SESSION 7 - Teaching and continuing Education in Tropical Veterinary Medicine

**Professor Olivier SPARAGANO**

BSc, MSc, PhD, PGCertAP, FHE, FSTVM, FRES, FRSB
Dean of Agricultural Sciences and Practice
Royal Agricultural University
Gloucestershire (UK)

Olivier.Sparagano@rau.ac.uk

<https://www.rau.ac.uk/about-rau/our-staff/professor-olivier-sparagano>

Professor Sparagano received his BSc and MSc from the University of Paris VII, France, his MRes from the University Blaise Pascal, France, and his PhD from the Institut Pasteur and the University Lyon I, France. Before joining RAU as the Dean for Agricultural Sciences and Practice he was working at City University of Hong Kong (as Professor of Veterinary Parasitology and Head of the Department of Infectious Diseases and Public Health). He was the Associate Pro Vice-Chancellor for Research and Professor of Animal Health and Biotechnology at Coventry University, UK. Prior to this appointment, he was the Associate Dean for Research in the Faculty of Health and Life Sciences at Northumbria University, UK. Olivier is a Chartered Biologist, a Fellow of the Society for Tropical Veterinary Medicine (of which was the President three times), a Fellow of the Higher Education Academy, a Fellow of the Royal Entomological Society, a Fellow of the Royal Society of Biology and an Associate Member of the Royal Society for Chemistry. He has published over 190 peer-reviewed papers and over 370 conference abstracts. He is currently on the Top 2% most cited scientist list established by Stanford University in 2021, 2022 and 2023.

AWARDEES

**2024 CIRAD Student Awardee****Francis Sena NUVEY, PhD**

Centre Suisse de Recherches Scientifiques
Abidjan, Côte d'Ivoire

Francis is a senior epidemiologist with expertise in transdisciplinary One Health approaches in research, emergency preparedness and response to public health events, and health policy evaluation. He has over ten years' experience in field epidemiology, clinical nursing as well as the design, implementation and evaluation of empirical scientific research. Francis is leading research projects that focus on strengthening health and food systems to address priority health issues affecting human, animal, and ecosystem health. In the implementation of his projects, Francis works collaboratively with policy makers, practitioners, and scientists in the Swiss Tropical and Public Health Institute, Switzerland and the Centre Suisse de Recherches Scientifiques en Côte d'Ivoire. Francis is currently a postdoctoral scientist at the Friedrich-Loeffler-Institut, Institute of International Animal Health/One Health.

**STVM Norval-Young Award****Sekgota Marcus MAKGABO, PhD**

University of Pretoria
Pretoria, South Africa

S. Marcus recently completed his PhD studies at the Department of Veterinary Tropical Diseases, University of Pretoria, South Africa. His research is mainly focused on the tick-borne hemoparasitic diseases, specifically anaplasmosis in South Africa, employing comparative genomics and molecular methods. He identified complex *Anaplasma marginale* infections, driven by co-infection and superinfection with distinct *A. marginale* strains, in cattle at a wildlife-livestock interface. He further identified four known and 13 novel *Anaplasma* 16S rRNA sequences circulating in wildlife samples using high sequencing throughput technology with potential for transmission to livestock and human, which may serve as a source of cross-reaction in the current detection assays. He is further working on techniques for the isolation of *Anaplasma* DNA directly from a carrier animals/host and on projects focusing on zoonotic infections transmitted from wildlife reservoir species to humans and/or domestic animals at the human/livestock/wildlife interface in rural South Africa. S. Marcus is currently a Microbiology and Biomedical Sciences lecturer at the University of South Africa (UNISA), South Africa.

TABLE OF CONTENTS

[click to go to page](#)

PROGRAM

■ Program at a glance	9
■ Tuesday 21 May	10
■ Wednesday 22 May	11
■ Thursday 23 May	13
■ Friday 24 May	14

ABSTRACTS TUESDAY 21 MAY

PLENARY SESSION - Keynote & Oral presentations

■ SESSION 1: One (Tropical Animal) Health / Integrated Approaches and Perspectives	17
Keynote 1: Dr Chadia WANNOUS	18
Oral presentations	19

ABSTRACTS WEDNESDAY 22 MAY

PLENARY SESSIONS - Keynotes & Oral presentations

■ SESSION 2: Animal Health and Production	30
Keynote 2: Professor Ala TABOR	31
Oral presentations	32
■ SESSION 3: Transboundary Animal Diseases	37
Oral presentations	38
■ SESSION 4: Veterinary Parasitology	45
Keynote 3: Professor Philippe JACQUIET	46
Oral presentations	47

ABSTRACTS THURSDAY 23 MAY

PLENARY SESSION - Oral presentations

■ SESSION 5: Vector-Borne Diseases	55
Oral presentations	56

ABSTRACTS FRIDAY 24 MAY

PLENARY SESSIONS - Keynote & Oral presentations

■ SESSION 7: Teaching and continuing Education in Tropical Veterinary Medicine	70
Keynote 4: Professor Olivier SPARAGANO	71
■ SESSION 8: Drug Resistance	72
Oral presentations	73

click to go to page

ABSTRACTS POSTERS

S1 - One (Tropical Animal) Health / Integrated Approaches and Perspectives	81
S2 - Animal Health and Production	89
S3 - Transboundary Animal Diseases	94
S4 - Veterinary Parasitology	102
S5 - Vector-Borne Diseases	106
S7 - Teaching and continuing Education in Tropical Veterinary Medicine	115
S8 - Drug Resistance	116
List of posters	117
List of participants	120
List of sponsors/exhibitors	125





PLANNING AT A GLANCE

**'TROPICAL VETERINARY MEDICINE IN CHALLENGING TIMES:
how should academic and research programs adapt?'**

TUESDAY 21 MAY		WEDNESDAY 22 MAY		THURSDAY 23 MAY		FRIDAY 24 MAY	
11:30	CONFERENCE REGISTRATION	09:00	SESSION 2 Animal Health and Production	08:30	SESSION 5 Vector-Borne Diseases	09:00	SESSION 7 Teaching and education in Tropical Vet Medicine
13:00	CONFERENCE OPENING	11:00	Coffee break - Exhibition - Posters	10:15	Coffee break - Exhibition - Posters	09:30	Speed talk session and posters
13:45	SESSION 1 One Health / Integrated Approaches and Perspectives	11:30	SESSION 3 Transboundary Animal Diseases	10:45	SESSION 5 (continued) Vector-Borne Diseases	10:00	SESSION 8 Drug Resistance
15:00	Coffee break - Exhibition - Posters	12:30	Lunch & Coffee Visit of exhibition - Posters	12:15	SESSION 6 Women for One Health	10:45	Coffee break - Exhibition - Posters
15:30	SESSION 1 (continued) One Health / Integrated Approaches and Perspectives	13:30	SESSION 3 (continued) Transboundary Animal Diseases	13:30	CULTURAL VISIT	11:15	SESSION 8 (continued) Drug Resistance
17:00	POSTER SESSION	14:15	SESSION 4 Veterinary Parasitology	15:00		12:00	CLOSING CEREMONY Prize Awards
18:00		15:45	Coffee break - Exhibition - Posters	15:15		12:45	
19:45	WELCOME RECEPTION	16:15	SESSION 4 (continued) Veterinary Parasitology	18:30			
		17:30		19:30	SOCIAL EVENT La Gazette Café - Montpellier		

Area Antigone 2 - Level 2
Room Antigone 3 - Level 2

TUESDAY 21 MAY

11:30-13:00 **Conference registration**

Area Antigone 2 - Level 2

PLENARY SESSIONS

13:00-13:45 **Conference opening**

Room Antigone 3 - Level 2

- Mohd Hair BEJO - AITVM president
- Ard NIJHOF - STVM president
-  Elisabeth CLAVERIE De SAINT-MARTIN - CIRAD Chief Executive Officer
Nathalie VACHIERY & Michel De GARINE-WICHATITSKY - CIRAD local organizers

13:45-15:00 **SESSION 1**

Room Antigone 3 - Level 2

One (Tropical Animal) Health / Integrated Approaches and Perspectives

Chairs: Alexis DELABOUGLISE (CIRAD, Montpellier, France) & Séverine THYS (CIRAD, Montpellier, France)

- 13:45-14:15 •  Keynote 1 - One Health approach - The role of veterinary services and animal health sector
Dr Chadia WANNOUS - World organization for animal health (WOAH), Paris, France
- Selected short oral presentations**
- 14:15-14:30 • S1-01 (CIRAD student Award) - Farmers' wellbeing significantly impacted by poor animal health in the Ghanaian livestock system - Francis Sena NUVEY - Afrique One - REACH, Centre Suisse de Recherches Scientifiques, Abidjan, Côte d'Ivoire
- 14:30-14:45 • S1-02 - Analysing dog movements in Southeast Asia and their epidemiological implications: a socio-ecological approach
Thibaut LANGLOIS - ASTRE, Univ. Montpellier, CIRAD, INRAE, Montpellier, France
- 14:45-15:00 • S1-03 - Participatory workshops in Guinée Forestière to co-construct a pilot community-based surveillance system for the early detection of zoonotic diseases - Maxime TESCH - ASTRE, CIRAD, Montpellier, France

15:00-15:30 **Coffee break - Visit of exhibition - Posters**

Area Antigone 2 - Level 2

PLENARY SESSION

15:30-17:00 **SESSION 1 - Continued**

Room Antigone 3 - Level 2

One (Tropical Animal) Health / Integrated Approaches and Perspectives

Chairs: Michel De GARINE-WICHATITSKY (CIRAD, Montpellier, France) & Olivier SPARAGANO (Royal Agricultural University, Gloucestershire, UK)

Selected short oral presentations

- 15:30-15:45 • S1-04 - Rapid response for zoonotic emergencies in Guinea: a study of barriers and opportunities
Saa André TOLNO - ASTRE, CIRAD, Montpellier, France
- 15:45-16:00 • S1-05 - Using ALERT serious board game to engage in One Health surveillance system: a pilot study of added-value in learning and engaging stakeholders
Mathias TALLA MBA - ASTRE, CIRAD, Montpellier, France
- 16:00-16:15 • S1-06 - A new contribution to epidemiological surveillance: presentation of the MOOD epidemic intelligence platform
Sarah HOUBEN - Avia-GIS, Zoersel, Belgium
- 16:15-16:30 • S1-07 - Engaging farmers in the outbreak control of Rift Valley Fever in Rwanda and neighboring countries: a narrative review - Karen CEBALLOS - Institute of Tropical Medicine, Antwerp, Belgium
- 16:30-16:45 • S1-08 - Modelling health information flows in event-based surveillance
Elena ARSEVSKA - ASTRE, CIRAD, Montpellier, France
- 16:45-17:00 • S1-09 - Regional response to a natural disaster of volcanic origin: the experience of the Caribbean
Jennifer PRADEL - ASTRE, Univ. Montpellier, CIRAD INRAE, Montpellier, France

17:00-18:00 **POSTER SESSION**

Area Antigone 2 - Level 2

18:00-19:45 **Welcome reception**

Area Antigone 2 - Level 2

WEDNESDAY 22 MAY

08:00-09:00 **Conference registration**

Area Antigone 2 - Level 2

PLENARY SESSION

09:00-11:00

SESSION 2

Room Antigone 3 - Level 2

Animal Health and Production

Chairs: **Mohd Hair BEJO** (Universiti Putra Malaysia, Serdang, Malaysia) &
Ala TABOR (University of Queensland, Brisbane, Queensland, Australia)

09:00-09:30

- **Keynote 2 - Novel developments in the management of bovine venereal diseases**
Professor Ala TABOR - University of Queensland, Brisbane, Queensland, Australia

Selected short oral presentations

09:30-09:45

- **S2-01 - Characterization of reproductive tract microbiome and immune biomarkers for Bovine Genital Campylobacteriosis in vaccinated and unvaccinated heifers**
Mst Sogra Banu JULI - Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, Queensland, Australia

09:45-10:00

- **S2-02 - Detecting venereal pathogens in cattle using long read sequencing and adaptive sampling**
Hannah SIDDLE - Queensland Alliance for Agriculture and Food Innovation, University of Queensland, Brisbane, Queensland, Australia

10:00-10:15

- **S2-03 - Community animal health workers (CAHWs) can provide quality animal health services to livestock keepers living in remote rural areas of the Global South**
Alexia RONDEAU - Vétérinaires Sans Frontières International, Cenon, France

10:15-10:30

- **S2-04 - Unlocking potential: Investigation into non-specific effects of veterinary vaccines for enhanced animal health and production**
Sintayehu AREGA - Department of Public and Community Health, Jaramogi Oginga Odinga University of Science and Technology, Bondo, Siaya, Kenya

10:30-10:45

- **S2-05 - Supporting vaccine development for tropical animal health through the refinement of animal models**
Alec EVANS - Clinglobal, Tamarin, Mauritius

10:45-11:00

- **S2-06 - Genomic variation in *Cyprinus cyprinidallo3* and its implications for their evolution**
Nurul FUANDILA - ISEM, University of Montpellier, Montpellier, France

11:00-11:30

Coffee break - Visit of exhibition - Posters

Area Antigone 2 - Level 2

PLENARY SESSION

11:30-12:30

SESSION 3

Room Antigone 3 - Level 2

Transboundary Animal Diseases

Chairs: **Arnaud BATAILLE** (CIRAD, Montpellier, France) & **Ladi Amos CHABIRI** (NVRI, Vom., Jos, Plateau State, Nigeria)

Selected short oral presentations

11:30-11:45

- **S3-01 - A highly performant ELISA for the detection of specific CCHFV antibodies in multiple species, including humans**
Loïc COMTET - Innovative Diagnostics, Grabels, France

11:45-12:00

- **S3-02 - Assessing interactions between domestic and wild pigs and implications for the transmission of African swine fever and other pathogens in rural habitats of Madagascar**
Rianja RAKOTOARIVONY - ASTRE, CIRAD, Antananarivo, Madagascar

12:00-12:15

- **S3-03 - Clinico-pathological study of Peste des petits ruminants' virus on rural indigenous sheep and goats in Plateau State, North Central Nigeria**
Ladi Amos CHABIRI - Diagnostic Services, NVRI, Vom., Jos, Plateau State, Nigeria

12:15-12:30

- **S3-04 - Combining animal mobility field surveys and Expert knowledge to map the risk of the spread of Peste des petits ruminants in three states in Northern Nigeria**
Sandra IJOMA - Veterinary Public health and Preventive Medicine, NVRI, Vom., Jos, Plateau State, Nigeria

12:30-13:30

Lunch & Coffee - Visit of exhibition - Posters

Area Antigone 2 - Level 2

PLENARY SESSIONS

13:30-14:15

SESSION 3 - Continued

Room Antigone 3 - Level 2

Transboundary Animal Diseases

Chairs: **Catherine CÊTRE-SOSSAH** (CIRAD, Montpellier, France) & **Renata SERVAN DE ALMEIDA** (CIRAD, Montpellier, France)

Selected short oral presentations

13:30-13:45

- **S3-05 - Comparative evolutionary analyses of Peste des petits ruminants virus genetic lineages**

Arnaud BATAILLE - ASTRE, CIRAD, Montpellier, France

13:45-14:00

- **S3-06 - Modelling RVF vector population dynamics in a tropical setting in South-Eastern Madagascar**

Laure J.G. CHEVALIER - ASTRE, CIRAD, Montpellier, France

14:00-14:15

- **S3-07 - West Nile virus virulence and transmission in vertebrate hosts and mosquitoes is modulated by different regions of the virus genome**

Sylvie LECOLLINET - ASTRE, CIRAD, Petit Bourg, Guadeloupe

14:15-15:45

SESSION 4

Room Antigone 3 - Level 2

Veterinary Parasitology

Chairs: **Philippe JACQUIET** (ENVT, Toulouse, France) & **Sophie THEVENON** (CIRAD, Montpellier, France)

14:15-14:45

- **Keynote 3 - Multiresistance of *Haemonchus contortus* (Nematoda: Trichostrongylidae) to anthelmintics: a global threat to small ruminant farming**

Professor Philippe JACQUIET - ENVT, Toulouse, France

Selected short oral presentations

14:45-15:00

- **S4-01 - Immunization of cattle with a *Rhipicephalus microplus* chitinase peptide containing predicted B-cell epitopes reduces tick biological fitness**

Juan MOSQUEDA - Faculty of Natural Sciences, Universidad Autonoma de Queretaro, Queretaro, Mexico

15:00-15:45

- **S4-02 - Integrating ROS-tolerant entomopathogenic fungi with a vaccine targeting tick immunity decreases infestations in a semi-field pasture test**

Isabel Kinney Ferreira DE MIRANDA SANTOS - Ribeirão Preto Medical School, Univ. of São Paulo, Ribeirão Preto, SP, Brazil

15:45-16:15

Coffee break - Visit of exhibition - Posters

Area Antigone 2 - Level 2

PLENARY SESSION

16:15-17:30

SESSION 4 - Continued

Room Antigone 3 - Level 2

Veterinary Parasitology

Chairs: **Philippe JACQUIET** (ENVT, Toulouse, France) & **Sophie THEVENON** (CIRAD, Montpellier, France)

Selected short oral presentations

16:15-16:30

- **S4-03 - Long Read Whole Genome Sequencing and Assembly of two *Tritrichomonas foetus* strains isolated from Queensland and Northern Territory in Australia**

Harvey SANTOS - Centre for Animal Science, Queensland Alliance for Agriculture & Food Innovation, The University of Queensland, St Lucia, Queensland, Australia

16:30-16:45

- **S4-04 - Novel genomic technologies for tick control in Australian beef cattle**

Hannah SIDDLE - Queensland Alliance of Agriculture and Food Innovation, Univ. of Queensland, Brisbane, QLD, Australia

16:45-17:00

- **S4-05 - Pre-existing antibodies to antigens affect efficacy of a vaccine for the cattle tick, *Rhipicephalus microplus***

Isabel Kinney Ferreira DE MIRANDA SANTOS - Ribeirão Preto Medical School, Univ. of São Paulo, Ribeirão Preto, SP, Brazil

17:00-17:15

- **S4-06 - Trials and tribulations of cattle tick vaccines – an Australian update**

Alicja (Ala) TABOR - Queensland Alliance of Agriculture & Food Innovation, Univ. of Queensland, Brisbane, QLD, Australia

17:15-17:30

- **S4-07 - Vaccination against cattle ticks in Mexico: Current status and Perspectives**

Consuelo ALMAZÁN - Immunology and Vaccines Laboratory, College of Natural Sciences, Autonomous University of Queretaro, Queretaro, Mexico

THURSDAY 23 MAY

PLENARY SESSION

08:30-10:15

SESSION 5

Room Antigone 3 - Level 2

Vector-Borne Diseases

Chairs: *Peter-Henning CLAUSEN* (Freie Universität Berlin, Berlin, Germany) & *Karla GEORGES* (University of the West Indies, Mt Hope, Trinidad & Tobago)

Selected short oral presentations

- 08:30-08:45 • **S5-01 - A new cell line derived from the tsetse fly *Glossina morsitans morsitans***
Lesley BELL-SAKYI - Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, Liverpool, UK
- 08:45-09:00 • **S5-02 - Application of SHERLOCK detection for epidemiological surveys of Animal African Trypanosomiasis**
Roger ELOIFLIN - UMR INTERTRYP, IRD, Montpellier, France
- 09:00-09:15 • **S5-03 - First epidemiological and molecular report of ticks and tick-borne pathogens in small ruminants across North and North-western Pakistan**
Olivier SPARAGANO - Agricultural Sciences and Practice, Royal Agricultural University Cirencester, Cirencester, UK
- 09:15-09:30 • **S5-04 - SSR-seq loci to study the population genetics of vectors: tsetse flies in three sleeping sickness foci: Boffa (Guinea), Bonon (Côte d'Ivoire) and Maro (Chad)**
Thierry DE MEEUS - Intertryp, IRD, Montpellier, France
- 09:30-09:45 • **S5-05 - Whole blood transcriptome of trypanotolerant and trypanosusceptible cattle during trypanosome infection highlights modulation of genes involved in immuno-metabolism**
Sophie THEVENON - BIOS UMR INTERTRYP, CIRAD, Montpellier, France
- 09:45-10:00 • **S5-06 - Vectorial capacity of *Aedes aegypti* in transmitting Lumpy Skin Disease Virus: Insights from experimental infection studies**
Elizabeth RIANA - Parasitology Unit, Department of Pathology, Faculty of Veterinary Science, Chulalongkorn University, Bangkok, Thailand
- 10:00-10:15 • **S5-07 - Investigation of African Trypanosomiasis in the ruminant population of Trinidad and Tobago**
Karla GEORGES - School of Veterinary Medicine, University of the West Indies, Mt Hope, Trinidad & Tobago

10:15-10:45 **Coffee break - Visit of exhibition - Posters**

Area Antigone 2 - Level 2

PLENARY SESSION

10:45-12:15

SESSION 5 - Continued

Room Antigone 3 - Level 2

Vector-Borne Diseases

Chairs: *Ard NIJHOF* (Freie Universität Berlin, Berlin, Germany) & *Nathalie VACHIER* (CIRAD, Montpellier, France)

Selected short oral presentations

- 10:45-11:00 • **S5-08 (Norval-Young Award) - Rodents as potential reservoir hosts for *Anaplasma* spp. at the human-livestock-wild-life interface of the Mnisi community, South Africa**
S. Marcus MAKGABO - Department of Veterinary Tropical Diseases, University of Pretoria, Pretoria, South Africa
- 11:00-11:15 • **S5-09 - Expanding the detection and surveillance of ticks and tick-borne diseases in the Caribbean region**
Roxanne CHARLES - The University of the West Indies, Port of Spain, Trinidad & Tobago
- 11:15-11:30 • **S5-10 - Development of a pan-species ELISA test for detection Heartwater across mammals**
Valérie RODRIGUES - ASTRE, CIRAD, Petit Bourg, Guadeloupe, France
- 11:30-11:45 • **S5-11 - Epidemiology of livestock-associated ticks and tick-borne pathogens in northern Nigeria**
Richard BIRTLES - Human and Natural Sciences, University of Salford, Salford, Greater Manchester, United Kingdom
- 11:45-12:00 • **S5-12 - Defining the impact of *Theileria* infection on the regulatory landscape of bovine lymphocytes**
Rachel OWEN - The Roslin Institute, University of Edinburgh, Edinburgh, Midlothian, United Kingdom
- 12:00-12:15 • **S5-13 - Secreted *Theileria annulata* effector protein Ta9 binds and potentially activates proto-oncogenic macrophage Hck**
Ard NIJHOF - Freie Universität Berlin, Institute for Parasitology and Tropical Veterinary Medicine, Berlin, Germany

12:15-13:30 **Lunch & Coffee - Visit of exhibition - Posters**

Area Antigone 2 - Level 2

PLENARY SESSION

13:30-15:00

SESSION 6

Room Antigone 3 - Level 2

Women for One Health

Chair: **Séverine THYS** (CIRAD, Montpellier, France)

- Round table

15:15-18:30

Cultural guided visit of Montpellier city

19:30

Social event

La Gazette Café - Montpellier

FRIDAY 24 MAY

PLENARY SESSIONS

09:00-10:00

SESSION 7

Room Antigone 3 - Level 2

Teaching and continuing Education in Tropical Veterinary Medicine

Chairs: **Mohd Hair BEJO** (Universiti Putra Malaysia, Serdang, Malaysia) & **Ard NIJHOF** (Freie Universität Berlin, Berlin, Germany)

09:00-09:30

- **Keynote 4 - One Health and Veterinary Medicine Education: when research meets co-learning**
Professor Olivier SPARAGANO - Royal Agricultural University, Gloucestershire, UK

09:30-10:00

Speed talk posters

- **S1-P02 - Circulation of multi-resistant bacteria in humans and animals in the urban area of Lome in Togo**
Esso-tchella Madera BODOMBOSSOU - ASTRE, CIRAD, Montferrier-sur-Lez, France
- **S1-P07 - Integrating the One Health perspective for the agroecological transition in a living Lab in Cambodia**
Chhuon VANNY - Faculty of Agricultural Economics and Rural Development, Royal University of Agriculture Cambodia, Phnom Penh, Cambodia
- **S2-P04 - Fishery and food safety: potential smoked fish value chain in Kampong Chhnang, Tonle Sap Lake of Cambodia**
Raksmey PHOEURK - Faculty of Agricultural Economics and Rural Development, Royal University of Agriculture, Phnom Penh, Cambodia
- **S2-P05 - Characterization of the evolution of basic haematological and biochemical variables in relation with bovine trypanotolerance during *Trypanosoma congolense* infection**
Gnion Fabrice SOMÉ - UMR INTERTRYP, CIRAD, Montpellier, France
- **S3-P04 - Bioeconomic modelling of area-specific control of foot and mouth disease (FMD) in Thailand**
Thanicha CHANCHAIDECHACHAI - Department of Population Health Sciences, Faculty of Veterinary Medicine, Utrecht University, Utrecht, the Netherlands
- **S4-P01 - Unravelling the epidemiology of ticks and tick-borne infections in Benue state, Nigeria**
Raymon ADA - School of Science, Engineering & Environment, University of Salford, Salford, United Kingdom
- **S4-P04 - Occurrence, prevalence, and distribution of haemoparasites of poultry in Sub-Saharan Africa: a scoping review**
Danisile TEMBE - University of KwaZulu-Natal, Durban, South Africa

10:00-10:45

SESSION 8

Room Antigone 3 - Level 2

Drug Resistance

Chairs: *Tennille AUGUSTE* (University of the West Indies, Champs Fleurs, Trinidad & Tobago) & *Ulf MAGNUSSON* (Swedish University of Agricultural Sciences, Uppsala, Sweden)

Selected short oral presentations

10:00-10:15

- **S8-01** - Characterization of antimicrobial resistance integrated surveillance in CaribVET's network
Tennille AUGUSTE - CaribVET/The University of the West Indies, Champs Fleurs, Trinidad & Tobago

10:15-10:30

- **S8-03** - Medically rational use of antibiotics for reducing resistance and supporting effective animal production in low- and middle-income countries
Ulf MAGNUSSON - Department of Clinical Science, Swedish University of Agricultural Sciences (SLU), Uppsala, Sweden

10:30-10:45

- **S8-04** - Multi-resistance of *Rhipicephalus microplus* to amitraz, alpha-cypermethrin, and ivermectin on livestock in Ecuadorian subtropical farms
Ximena PÉREZ-OTÁÑEZ - Centre for Earth and Climate research., UCL, Ottignies-Louvain-La-Neuve, Belgium

10:45-11:15

Coffee break - Visit of exhibition - Posters

Area Antigone 2 - Level 2

PLENARY SESSIONS

11:15-12:00

SESSION 8 - Continued

Room Antigone 3 - Level 2

Drug Resistance

Chairs: *Tennille AUGUSTE* (University of the West Indies, Champs Fleurs, Trinidad & Tobago) & *Ulf MAGNUSSON* (Swedish University of Agricultural Sciences, Uppsala, Sweden)

Selected short oral presentations

11:15-11:30

- **S8-05** - On the current resistance situation of Triclabendazole against *Fasciola hepatica* in German sheep flocks
Stephan STEUBER - Veterinary Medicines, Federal Office of Consumer Protection and Food Safety (BVL), Berlin, Germany

11:30-11:45

- **S8-06** - Phenotypic and genotypic characterization of pyrethroid resistant stable fly (*Stomoxys calcitrans*) populations on German dairy farms
Peter-Henning CLAUSEN - Institute for Parasitology and Tropical Veterinary Medicine, Freie Universität Berlin, Berlin, Germany

11:45-12:00

- **S8-07** - Unravelling the socioeconomic factors linked to antibiotic use in poultry farms: a qualitative study in the Analamanga region, Madagascar
Sophie MOLIA - ASTRE, CIRAD, Montpellier, France

12:00-12:45

Closing Ceremony

Room Antigone 3 - Level 2

Prize Awards

- **Norval-Young Award:** 2022 Virtual Event Best Presenter awarded to Sekgota Marcus MAKGABO, PhD
- **2024 CIRAD Student Award** awarded to Francis Sena NUVEY, PhD
- **Dik Zwart Award:** Best Oral presentation by a young scientist during the 2024 Conference
- **Dik Zwart Award:** Best Poster presentation by a young scientist during the 2024 Conference



ABSTRACTS TUESDAY 21 MAY





ONE HEALTH

SESSION 1

**One (Tropical Animal) Health /
Integrated Approaches and Perspectives**



One Health approach - The role of veterinary services and animal health sector

Chadia WANNOUS (c.wannous@woah.org)

World organization for animal health (WOAH), Paris, France

The presentation will discuss the OH approach and highlight its importance to deal with health threats at the animal-human-environment interface. It will also highlight the role of Veterinary Services and Animal Health Sector in adopting and implementing the OH approach and will provide examples of key OH initiatives supported by the World Health Organisation for Animal Health (WOAH).

Farmers' wellbeing significantly impacted by poor animal health in the Ghanaian livestock system

Francis Sena NUVEY (fsnuvey@gmail.com)

Afrique One - REACH, Centre Suisse de Recherches Scientifiques, Abidjan, Côte d'Ivoire

Introduction:

Although livestock production is a key livelihood source in developing countries, the high livestock infectious diseases burden hamper livestock productivity, threatening farmers' wellbeing and food security. This study estimates the effect of livestock mortalities attributable to disease on farmers' wellbeing.

Methods:

We conducted a survey involving 350 livestock farmers from three districts in Ghana. Mixed-effect linear regression models were used to estimate the relationship between animal health and farmer wellbeing. Farmer wellbeing was assessed using WHOQOL-BREF tool. Animal health was assessed as annual livestock mortalities to diseases adjusted for herd-size, and standardized in tropical livestock units. We adjusted for farmers' age, sex, educational attainment, farmland size, socio-economic status, herd disease risk perception, health satisfaction, herd disease outbreaks history, and social-support availability as fixed effects and community as random effects, in our pre-specified model.

Results:

The farmers had a median wellbeing score of 65.5 out of 100 (IQR: 56.6–73.2). On average farmers' reported 10% (IQR: 0–23%) annual herd mortalities to infectious diseases. We found a significant negative relationship between increasing disease-induced mortality levels and farmers' wellbeing. Specifically, our model predicted a difference of 7.9 (95%CI 1.50–14.39) wellbeing points between a farmer without any mortalities and a (hypothetical) farmer with 100% mortalities in a farming year. Thus, a reduction of 0.8 wellbeing points, for the 10% average disease-induced herd mortalities.

Conclusions:

Disease-induced livestock mortalities have a significant and negative effect on farmers' wellbeing. Thus, diseases risk mitigation measures like vaccination, could contribute to improving livestock farmers' wellbeing, and public food security.

Analysing dog movements in Southeast Asia and their epidemiological implications: a socio-ecological approach

Thibaut LANGLOIS^{1, 2} (thibaut.langlois@etu.umontpellier.fr), Areeya KRIENGUDOM^{3, 4}, Anamika KRITIYAKAN^{4, 5}, Wayan Tunas ARTAMA^{6, 7}, Muhammad Najib Arung Petana RAJA BONE⁶, Sopheak SORN⁸, Muhammad Nur Faiz MAHFUDZ⁶, Barandi Sapta WIDARTONO^{6, 7}, H  l  ne GUI^{1, 8, 9}, Serge MORAND^{4, 5}, Sylvie HURTREZ-BOUSS  S^{10, 2}, Michel DE GARINE-WICHATITSKY^{1, 3}

¹ ASTRE, Univ Montpellier, CIRAD, INRAE, Montpellier, France ; ² MIVEGEC, Univ Montpellier, IRD, CNRS, Montpellier, France ; ³ CIRAD, Kasetsart University, Bangkok, Thailand ; ⁴ HealthDEEP, IRL CNRS, Kasetsart University – Mahidol University, Bangkok, Thailand ; ⁵ Faculty of Veterinary Technology, Kasetsart University, Bangkok, Thailand ; ⁶ One Health Collaborating Center, Universitas Gadjah Mada, Yogyakarta, Indonesia ; ⁷ Faculty of Geography, Universitas Gadjah Mada, Yogyakarta, Indonesia ; ⁸ Epidemiology and Public Health Unit, Institut Pasteur du Cambodge, Phnom Penh, Cambodia ; ⁹ CIRAD, ASTRE, Phnom Penh, Cambodia ; ¹⁰ Department of Biology-Ecology, Faculty of Sciences, Univ Montpellier, Montpellier, France

Introduction & Objectives:

Free-roaming domestic dogs and their owners interact with their environment in very diverse and complex ways. The epidemiology and management of canine and zoonotic diseases in Southeast Asia must be addressed through an integrated multidisciplinary approach. By combining different methods, we seek to identify the factors driving the circulation of pathogens within dog populations in 3 village-sites in Thailand, Indonesia and Cambodia.

Materials & Methods:

We conducted longitudinal monitoring of the movements of 131 dogs in total, using GPS collars during 7-30 days sessions, between 2019 and 2023. Habitat use was estimated using land-use/land-cover maps characterising the available habitats in the study areas. Moreover, spatially-explicit semi-structured interviews explored dog owners' relationships with their animals, identifying links between their activities and canine spatial behaviours, and associated disease risks.

Results:

Based on the preliminary analysis of 187 dog/sessions, we illustrate various dog spatial profiles across sites, including ‘urban-sedentary’ dogs (confined in anthropized areas close to owners homes), ‘long-distance follower’ (travel long distances following owners to agricultural fields), ‘nature-explorer’ (independent visits to forests or semi-natural habitats). We explore the influence of geographic (e.g. village-site, topography), demographic (e.g. sex and age of dog and owner) and social factors (e.g. owner’s occupation, interactions with owners of other dogs) on dog movements.

Discussion & Conclusion:

The different “canine profiles” are likely to play very contrasted epidemiological roles as a reservoir of zoonotic pathogens close to humans and/or as “bridge hosts” at the wild-domestic interface.

Participatory workshops in Guinée Forestière to co-construct a pilot community-based surveillance system for the early detection of zoonotic diseases

Maxime TESCH^{1,2} (maxime.tesch@cirad.fr), Saa André TOLNO^{1,2,3}, Abdoulaye TOURÉ⁴, Mohamed Idriss DOUMBOUYA⁵, Alimou BARRY⁶, Erwan SACHET^{1,2}, Hélène DE NYS^{1,2,7}, Mathieu BOURGAREL^{1,2,8}, Momory LENO⁹, Marisa PEYRE^{1,2}, Marie-Marie OLIVE^{1,2}

¹ CIRAD, ASTRE, Montpellier, France ; ² ASTRE, Univ Montpellier, CIRAD, INRAE, Montpellier, France ; ³ Institut supérieur des sciences et de médecine vétérinaire de Dalaba, Dalaba, Guinea ; ⁴ CERFIG – Centre de recherche et de formation en Infectiologie de Guinée, Conakry, Guinea ; ⁵ DNSV – Direction Nationale des Services Vétérinaires, Conakry, Guinea ; ⁶ OGPNR – Office Guinéen des Parcs Nationaux et Réserves de Faune, Conakry, Guinea ; ⁷ CIRAD, ASTRE, Harare, Zimbabwe ; ⁸ Universidade Eduardo Mondlane - Campus Universitario Principal, Maputo, Mozambique ; ⁹ DNSV – Services Déconcentrés de Témessadou, Guéckédou, Guinea

The recurrent epidemics of zoonotic diseases, caused partly by increased proximity with wildlife, has highlighted the need to construct integrated zoonotic diseases surveillance systems, with communities as the primary source of information. The objective of the current study was to develop and conduct participatory workshops to co-construct a pilot community-based surveillance system for the early detection of zoonotic diseases in Guinée Forestière, while taking into account needs and constraints of stakeholders. Firstly, interviews conducted in two sous-prefectures of Guinée Forestière aimed to get an integrated vision of the local context and to build a relational network. A total of 80 participants were involved in this first stage. Then, a co-construction protocol was deployed over nine days, with three main stages: (i) mobilization of participants; (ii) participatory workshops; (iii) feedback in pilot sites.

A total of 42 stakeholders were invited for the coconstruction workshop, including representatives of community such as matrons, hunters or breeders, and human, animal and environmental health agents, resulting in 22 audio recordings and 28 collective work documents. The collaborative framework allowed participants to build concrete solutions for surveillance: which alarming events should be reported, how the health-related information should be passed on, and what equipment was needed. More generally, the discussions highlighted the importance of respecting local practices and knowledge, building trust with communities, and answering contextual issues like illiteracy. In conclusion, this work made it possible to test new methods while achieving significant progress towards the implementation of a community-based surveillance system.

Rapid response for zoonotic emergencies in Guinea: a study of barriers and opportunities

Saa André TOLNO^{1,2} (saa-andre.tolno@cirad.fr), Séverine THYS¹, Alpha-Kabinet KEITA^{3,4}, Léonce ZOGBELEMOU⁵, Marie-Marie OLIVE¹, Véronique CHEVALIER⁶

¹ ASTRE, CIRAD, Montpellier, France ; ² ISSMV Dalaba, Dalaba, Guinea ; ³ CERFIG, Conakry, Guinea ; ⁴ TransVIHMI, IRD, Montpellier, France ;

⁵ Direction Nationale des Services Vétérinaires, Macenta, Guinea ; ⁶ ASTRE, CIRAD, Antananarivo, Madagascar

Guinea has experienced several zoonotic emergencies with significant socio-economic impacts. Effective management of these epidemics requires the implementation of alert and multisectorial rapid response plans that consider socio-cultural contexts.

The objectives of this study were to describe the response mechanisms implemented in the context of the emergence of zoonotic diseases, and to identify the constraints and levers for making them more acceptable and adapted to the context and needs of the stakeholders involved in implementation of response plans, including communities.

Using a qualitative approach, individual interviews and focus group discussions (FGD) were conducted with stakeholders involved in epidemic management in Forest Guinea between 2022 and 2023. The topics discussed included the alert and response mechanisms in place, the needs, constraints and expectations of stakeholders. Data analysis was carried out using Nvivo2022 software.

Thirteen individual interviews and 13 FGD were conducted with 122 participants. The thematic analysis revealed that alerts are reported between different One-Health technical actors and communities on the basis of evocative signs that meet the case definitions of diseases and experiences. Needs for training, work tools and financial motivation were mentioned, and constraints such as crisis of confidence between the agents implementing response and the communities were expressed. The involvement of community leaders in awareness campaigns and the existence of village One-Health committees were identified as opportunities.

The understanding and consideration of needs and constraints of local stakeholders in the response of zoonotic emergencies would increase the acceptability and engagement of these actors in the epidemic response process.

Using ALERT serious board game to engage in One Health surveillance system: a pilot study of added-value in learning and engaging stakeholders

Mathias TALLA MBA¹ (mathias.talla_mba@cirad.fr), Saa André TOLNO^{1,2}, Mohamed Idriss DOUMBOUYA³, Mamadou Alimou BARRY⁴, Mathieu BOURGAREL⁵, Sophie MUSE⁶, Hélène DE NYS⁷, Marisa PEYRE¹, Marie-Marie OLIVE¹

¹ ASTRE, CIRAD, Montpellier, France ; ² ISSMV, Dalaba, Guinea ; ³ DNSV, Conakry, Guinea ; ⁴ OGPNR, Conakry, Guinea ; ⁵ ASTRE, CIRAD, Maputo, Mozambique ; ⁶ WOA, Paris, France ; ⁷ ASTRE, CIRAD, Harare, Zimbabwe

Stakeholders engagement in the surveillance of infectious diseases is a critical element to early detect emergence. Innovative tools, such as games, are being developed to strengthen the engagement of stakeholders in numerous fields, such as health. The serious board game ALERT was developed with the aim of increasing knowledge and engagement of stakeholders working at the human-animal-environment interface for the surveillance of zoonotic diseases.

The objectives of this study are to present the serious game and a pilot study aiming to evaluate its impact on knowledge acquisition and stakeholder willingness to engage in surveillance systems.

The study was implemented in Guinea among animal, public and environmental health workers and members of civil society. The game was used in two participant groups while more standard types of awareness materials were used in two other groups. Knowledge acquisition and willingness to engage in surveillance were assessed using participatory methodology.

The preliminary results suggested that compared to standard awareness materials, ALERT made players more aware of the diversity and the role of actors involved in a surveillance system of zoonotic diseases. In addition, players reported an increased awareness of the flow of information in a surveillance chain with multisectoral collaboration. Two weeks after ALERT was played, local initiatives emerged to improve collaboration between actors such as willingness to organize informational meetings between health workers and to involve citizens in surveillance.

By better understanding their role in the surveillance chain, stakeholders would feel more empowered to engage and communicate in One Health surveillance system.

A new contribution to epidemiological surveillance: presentation of the MOOD epidemic intelligence platform

Sarah HOUBEN¹ (shouben@avia-gis.com), Tom MATHEUSSEN¹, Mathieu ROCHE², Maguelonne TEISSEIRE³

¹ Avia-GIS, Zoersel, Belgium ; ² CIRAD, Montpellier, France ; ³ TETIS, INRAE, Montpellier, France

The MOOD project is committed to advancing epidemic intelligence (EI), encompassing early identification, verification, assessment, and investigation of potential health hazards by integrating both indicator-based and event-based components. This holistic approach involves utilizing structured data from routine surveillance systems and unstructured data from diverse sources.

Implemented as the MOOD platform, innovations within the project unfold through six case studies, facilitated and researched by case study experts. These studies are intricately linked to specific disease models, including West Nile virus infection (WNV), tick-borne encephalitis (TBE), antimicrobial resistance (AMR), COVID-19, Leptospirosis (LEPTO), Chikungunya (CHIK), Dengue (DEN), and highly pathogenic avian influenza (HPAI).

The platform, central to managing epidemic intelligence, encompasses a Core database housing covariates, vector data, and a disease database. Raster layers of covariates and disease models are stored reliably and with scalability.

Comprehensive metadata associated with disease and covariates data are stored in the MOOD GeoNetwork, with a selected subset directly accessible within the MOOD Core platform. The platform ensures open access to various datasources through an easily navigable interface.

This presentation will delve into the architecture of the information system and provide a platform demonstration, highlighting its capabilities in linking disease and non-disease data. The platform achieves consistency in disease and covariate datasets through the normalization of thematic, temporal, and geospatial dimensions, enhancing its ability to discern and consolidate related events for more insightful and streamlined analysis in the realm of epidemic intelligence.

Engaging farmers in the outbreak control of Rift Valley Fever in Rwanda and neighboring countries: a narrative review

Karen CEBALLOS¹ (kceballos@itg.be), Soledad COLOMBE¹, Wim VAN BORTEL¹, Anselme SHYAKA², Marie MEUDEEC¹

¹ *Institute of Tropical Medicine, Antwerp, Belgium* ; ² *University of Global Health Equity, Kigali, Rwanda*

Involving farmers in surveillance of zoonotic diseases allows early detection of potential outbreaks and timely interventions to help minimize disease spread, yet little is known about their role. We aimed to explore implemented strategies that involved farmers in the prevention, detection, and response of Rift Valley Fever (RVF) outbreaks mainly in Rwanda, while also considering its neighbouring countries (Uganda, Democratic Republic of Congo, Burundi, Tanzania, and Kenya). We conducted a narrative review after searching relevant articles and grey literature on PubMed and Google Scholar. Although no studies specified strategy implementation during an outbreak, promising approaches to disease control were described. Relevant strategies included farmer-focused extension programs to empower farmers and foster exchanges of knowledge and best practices, as well as the involvement of Community Animal Health Workers in disease surveillance, health service delivery, and community mobilization. Methods empowering women smallholder farmers to engage in the livestock vaccine value chain by training them on vaccinations and livestock management significantly helped them mitigate livestock losses and, consequently, financial losses. Gaps and biases in farmers' involvement were also noted, including prioritization of large-scale commercial cattle farming, neglecting the smallholder farmers and small ruminants. Recognizing the gap in access for small ruminants is very important. Small ruminants are often owned by women farmers who are also overlooked in accessing animal health information and services. In conclusion, disease control measures of RVF in Rwanda and neighbouring countries necessitate broader stakeholder involvement, emphasizing inclusivity to assess and address the socioeconomic needs of all farmers, especially women.

Modelling health information flows in event-based surveillance

Solene RODDE¹ (solene.rodde@yahoo.fr), Elena ARSEVSKA¹, Pachka HAMMAMI¹, Andrea APOLLONI¹, Asma MESDOUR¹, Bahdja BOUDOUA², Sarah VALENTIN²

¹ ASTRE, CIRAD, Montpellier, France ; ² TETIS, CIRAD, INRAE, Montpellier, France

In epidemic intelligence, health practitioners can monitor using non-official, non-verified data from various sources. Epidemic intelligence activities could be improved with a better understanding of the outbreak-related information flows through online media, and the identification of both factors involved.

We constructed a bipartite network of online media sources reporting news on avian influenza outbreaks to study the dynamics of health information flows in the media. To identify the drivers of such a network, we use the Exponential Random Graph Models (ERGM). We fitted an ERGM discriminating the covariates among 16 epidemiological, socio-economic, cultural and sources related covariates.

12 factors were identified as potential drivers of relationships and interactions in the network. Among the source covariates, the type of source, geographic focus, and media specialization were selected. Among the outbreak covariates, the reason for notification, host type, political stability, HDI, internet use, English, PFI, and geographic region seemed all significantly affect their notification into online media. The result indicates that the international organization is more likely to disseminate events than the other type of source. Similar results were estimated for international and specialized sources that are more likely to disseminate compared to local, national and general sources. These results highlight the importance of international and specialized animal health sources in events dissemination.

We attempt to assess the drivers of the dissemination of online health information in order to identify epidemic events more quickly, monitor their spread, and take appropriate measures.

Regional response to a natural disaster of volcanic origin: the experience of the Caribbean

Jennifer PRADEL^{1,2} (jennifer.pradel@cirad.fr), Lorelei CORSAUT^{1,3}, Karla GEORGES^{2,4}, Gavin PETERS^{2,5}, Coleen PHILIPS^{6,7}, Pastor ALFONSO^{2,8}, Victor GONGORA^{2,9}, Candice SANT^{2,4}, Maria Irian PERCEDO ABREU^{2,8}, Kathian HACKSHAW^{2,7}, Lila KHAN¹⁰, Paul CADOGAN^{11,12}, Keri JOHNSON¹³, Daryl BEST^{14,2}, Gil MANUEL¹⁵, Patricia D. BEDFORD^{16,17,2}

¹ ASTRE, Univ Montpellier, CIRAD INRAE, Montpellier, France ; ² CaribVET, Caribbean Animal Health and Veterinary Public Health, Petit Bourg, Guadeloupe ; ³ CIRAD INRAE, ASTRE, Petit Bourg, Guadeloupe ; ⁴ UWI-SVM, School of Veterinary Medicine, the University of the West Indies, Saint Augustine, Trinidad and Tobago ; ⁵ CAHFSA, Caribbean Agricultural Health and Food Safety Agency, Paramaribo, Suriname ; ⁶ VSPCA, Vincentian Society for the prevention of Cruelty to Animals, Kingstown, Saint Vincent and the Grenadines ; ⁷ Industry and labour, Ministry of Agriculture, Forestry, Fisheries, Rural Transformation,, Kingstown, Saint Vincent and the Grenadines ; ⁸ CENSA, Centro Nacional de Sanidad Agropecuaria, Mayabeque, Cuba ; ⁹ Belize Poultry Association, Belmopan, Belize ; ¹⁰ DRM Experts, San Juan, Trinidad and Tobago ; ¹¹ JVMA, Jamaica Veterinary Medical Association, Kingston, Jamaica ; ¹² CVA, Commonwealth Veterinary Association, Kingston, Jamaica ; ¹³ Attorney-at-law, Montego Bay, Jamaica ; ¹⁴ Ministry of Agriculture, Fisheries, Food Security and Rural Development, Castries, Saint Lucia ; ¹⁵ AVPLG, Association des Vétérinaires Praticiens Libéraux de Guadeloupe, Basse-Terre, Guadeloupe ; ¹⁶ BVA, Barbados Veterinary Association, Bridgetown, Barbados ; ¹⁷ FAO, Food and Agriculture Organisation of the United Nations, Bridgetown, Barbados

Introduction & Objectives:

The animal/livestock sector is often neglected in Caribbean countries hardest hit by natural disasters, prompting the mobilisation of veterinary networks to help. Very often, assistance is relegated to providing moral support, coupled with uncoordinated relief efforts, all due to a lack of regional plans, supporting tools, resources and agricultural sector expertise.

In 2021, the Saint-Vincent-and-the-Grenadines (SVG) volcano erupted, and subsequent ashfall, flooding from heavy rainfall and lahars severely affected SVG and neighbouring islands. Amid the COVID-19 pandemic, the veterinary community across several Caribbean countries/territories quickly coordinated an unprecedented mobilisation, with outstanding cross-sectoral collaborations resulting in the shipment of large quantities of emergency relief supplies for animals.

Understanding how this was made possible and how to facilitate further successful organisation of regional emergency aid for animals/livestock is key.

Materials & Methods:

An in-depth experience feedback analysis was conducted in 2023 to capture the conditions for success.

Results:

Multiple factors enabled this success: 1) the collaborative environment resulting from years of regional networking engendered trust, solidarity and mutual knowledge; 2) clear communication for the alert phase and efficient information sharing mechanisms allowed many persons who had never met to coordinate their actions quickly. Priorities were established, a Caribbean disaster group was formed through co-optation, relevant information was centralised, made accessible and updated in real time and both coordination and communications roles were designated.

Conclusion:

A cohesive approach to improve national and regional preparedness for future disasters, including climate-influenced ones, is being developed with a supporting tool and a regional disaster plan.



ABSTRACTS WEDNESDAY 22 MAY





Animal Health and Production



Novel developments in the management of bovine venereal diseases

Alicja (Ala) TABOR^{1,2} (a.tabor@uq.edu.au), Hannah V. SIDDLE¹, Zhetao ZHANG¹, Chian Teng ONG¹, Tony CAVALLARO¹, John Harvey SANTOS¹, Kieren MCCOSKER¹, Gry BOE-HANSEN^{1,3}

¹ Queensland Alliance for Agriculture & Food Innovation, The University of Queensland, Brisbane, Queensland, Australia ; ² School of Chemistry and Molecular Biosciences, The University of Queensland, Brisbane, Queensland, Australia ; ³ School of Veterinary Science, The University of Queensland, Gatton, Queensland, Australia

Venereal diseases bovine trichomonosis and genital campylobacteriosis (BGC) are transmitted to cows from infected asymptomatic bulls impacting cattle fertility globally. For trichomonosis, an accurate sensitive qPCR has been successfully detecting *Tritrichomonas foetus* in clinical preputial samples since 2006, whereas for BGC, the causative subspecies *Campylobacter fetus* subsp. *venerealis* is impossible to differentiate from other *C. fetus* not causing BGC. Commercial vaccines for BGC using two *C. fetus venerealis* biovars are well adopted globally, whereas *T. foetus* whole protozoan vaccines are less common.

We employed long read sequencing (Oxford Nanopore Technologies ONT) to characterize nine genomes of *C. fetus* subspecies compared to 16 previously reported, to identify potential core genome diagnostic targets, and three *T. foetus* isolates to confirm genomic conservation. A 'proof of concept' trichomonosis vaccine challenge trial in six unvaccinated and vaccinated bulls was undertaken using Australian strains.

An assay developed against the *MraY* SNP proved to be specific in qPCR experiments for the differentiation of the *C. fetus* subspecies. The vaccine and challenge *T. foetus* isolates were shown to be 99.2% similar yielding genome lengths of 110-111.7 Mbp from 194-226 contigs, respectively.

The trichomonosis vaccine trial initially demonstrated 67% efficacy in older mixed breed bulls with two of the six vaccinated animals remaining consistently positive immediately after challenge, but were presented as negative after six months.

Future research will confirm Australian *T. foetus* genomic conservation and undertake larger vaccine trials towards product registration. The *C. fetus* SNP assay will be further validated by veterinary diagnostic laboratories.

Characterization of reproductive tract microbiome and immune biomarkers for Bovine Genital Campylobacteriosis in vaccinated and unvaccinated heifers

Mst Sogra Banu JULI¹ (m.juli@uq.edu.au), Ali RAZA^{1,2}, Mehrnush FORUTAN¹, Hannah V. SIDDLE¹, Geoffry FORDYCE^{1,3}, Jarud MULLER³, Gry B. BOE-HANSEN^{1,4}, Ala E. TABOR^{1,5}

¹ Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, Queensland, Australia ; ² Department of Veterinary and Animal Sciences, University of Copenhagen, Frederiksberg, Denmark ; ³ Department of Agriculture & Fisheries, Charters Towers, Queensland, Australia ; ⁴ School of Veterinary Science, The University of Queensland, Brisbane, Queensland, Australia ; ⁵ School of Chemistry and Molecular Science, The University of Queensland, Brisbane, Queensland, Australia

Bovine Genital Campylobacteriosis (BGC) caused by *Campylobacter fetus* subspecies *venerealis* (CFV) is a globally important venereal disease responsible for reproductive failure in cattle. Diagnosis of BGC is highly challenging due to the lack of accurate diagnostic tests, hence the identification of biomarker(s) for BGC through omics may be useful for BGC management.

A total of 12 cycling heifers were selected with six vaccinated with VibroVax® (Zoetis) and six unvaccinated. Oestrous was synchronised following a double dose of PGF2a. Both groups were intravaginally challenged with live CFV and samples were collected before and after challenge. DNA extracted from vaginal mucus was screened using a *C. fetus* experimental qPCR method and 16S rDNA amplicon sequencing (V5-V8). Relative abundances of serum proteins were identified and compared using SWATH-MS at three timepoints- pre-challenge, post-challenge and post-recovery.

Heifers were CFV qPCR negative before and positive immediately after challenge. The mean abundances of vaginal microbiome changed significantly post-challenge with Firmicutes most abundant compared to Bacteroides, Proteobacteria and Actinobacteria in all heifers. *Streptococcus* spp. and *Arthrobacter* sp. were higher in abundance during oestrus than dioestrus. In unvaccinated heifers, *Campylobacter* spp. appeared sooner with increase of *Acinetobacter* sp. after challenge. Several significant serum proteins including Coglutinin, kininogen, GC, HP homologs, and Fetuin-B were identified post-challenge as potential biomarkers for BGC.

Vaccination didn't affect the vaginal microbiome of the heifers while changes were evident after challenge. The identified proteins were associated with challenge and further study is needed to validate their efficiency as putative immune biomarkers for BGC exposure.

Detecting venereal pathogens in cattle using long read sequencing and adaptive sampling

Hannah SIDDLE¹ (h.siddle@uq.edu.au), Zhetao ZHANG¹, Matthew KELLY², Ala TABOR^{1,3}

¹ Queensland Alliance for Agriculture and Food Innovation, University of Queensland, Brisbane, Queensland, Australia ; ² Australian Agricultural Company, Brisbane, QLD, Australia ; ³ School of Chemistry & Molecular Biosciences, University of Queensland, Brisbane, Queensland, Australia

Introduction:

Venereal diseases (VDs) cause significant fertility issues in cattle. The ability to monitor VD in extensive cattle herds is problematic where causative pathogens have highly related sub-species. For example, *Campylobacter fetus subsp. venerealis* and *Campylobacter fetus subsp. fetus* are difficult to distinguish, but *C. fetus venerealis* is more likely associated with fertility issues. Further, multiple testing tools are required to identify bacterial and parasitic pathogens, such as *Tritrichomonas foetus*, a protozoan which also causes VD. These issues lead to misdiagnoses and inhibitory expense.

Material & Methods:

Here we developed a PCR-free testing strategy using adaptive sampling with long read sequencing on Oxford Nanopore Technology platforms. Pre-putial swab samples from bulls were used to optimise the detection of known quantities of bacterial and protozoal DNA. A bioinformatic pipeline utilising BLAST was developed to produce a threshold of reads for positive samples.

Results & Discussion:

The method was used to detect and distinguish between *C. fetus venerealis* and *C. fetus fetus* DNA in a panel of 24 animals, demonstrating sensitivity to 4 pg of *C. fetus venerealis* DNA. Read depth was identified as the limiting factor in detection with 6×10^5 reads required to identify 4 pg of *C. fetus venerealis* DNA with 5% coverage of informative SNPs. The technique can detect *T. foetus* and *C. fetus venerealis* DNA in a single test.

Conclusion:

These results demonstrate that sequencing technologies can be used to test for multiple pathogenic species, reducing misdiagnosis, improving disease monitoring and the management of cattle fertility.

Community animal health workers (CAHWs) can provide quality animal health services to livestock keepers living in remote rural areas of the Global South

Alexia RONDEAU (a.rondeau@vsf-international.org)

Vétérinaires Sans Frontières International, Cenon, France

In the 80's-90's, structural adjustments led governments to withdraw from the provision of free animal health services to livestock keepers to focus resources on regulatory functions. It was assumed that the private sector would take over to fill the gap, but privatization was poorly incentivized and took long to gain traction, leaving livestock keepers in remote and hard to reach areas without reliable access to quality animal health services.

Indeed, Veterinarians and Veterinary Paraprofessionals (VPPs) are in insufficient numbers to adequately meet livestock keepers' needs. They concentrate in urban and peri-urban areas for better employment opportunities. As a result, smallholders and pastoralists lack access to animal health services in many areas of the world. This threatens not only animal health, but also public health, food and income security, and livelihoods.

To fill this gap, community animal health workers (CAHWs) are trained and deployed by NGOs, governments, and development partners in areas where veterinarians and VPPs can't operate. They provide basic animal health care to animals, participate in vaccination campaigns and in disease surveillance and reporting, advise and sensitize their communities on animal health and good husbandry practices, etc.

In view of strengthening animal health systems globally, WOA and VSF International are implementing a joint project to develop competency and curricula guidelines for CAHWs and recommendations for sustainable CAHW programming. Project's results will support the recognition, regulation and integration of CAHWs in animal health systems for strengthened veterinary workforce and more resilient livestock keeping communities in rural areas.

Unlocking potential: Investigation into non-specific effects of veterinary vaccines for enhanced animal health and production

Sintayehu AREGA¹ (sintmulberg@gmail.com), Darryn KNOBEL², Anne CONAN³, Felix TOKA²

¹ Department of Public and Community Health, Jaramogi Oginga Odinga University of Science and Technology, Bondo, Siaya, Kenya ;

² Department of Biomedical Sciences, Ross University School of Veterinary Medicine, Basseterre, Saint Kitts and Nevis ; ³ CIRAD, Harare, Zimbabwe

Recent research has expanded our understanding of the effects of vaccines beyond their intended targets, known as nonspecific effects (NSEs) or heterologous effects. While NSEs in human vaccines have gained attention, similar studies in veterinary medicine are relatively rare. To address this gap, we conducted a systematic review by screening 8412 titles from PubMed and CABI databases and identified 45 relevant articles. Our review included various vaccines tested against various pathogens and diseases, with both positive and harmful NSEs. Contrary to the belief that only live vaccines exhibit beneficial NSEs, our results show a mixed pattern across vaccine types. For example, while live BCG vaccines consistently show positive NSEs in animal models, non-live vaccines and subunit vaccines also demonstrate notable effects. Factors affecting NSE include vaccine strain and type, method of administration, time interval between vaccination and challenge, dose, maternal immunity, and recipient host characteristics (such as sex and stress level). Despite the limitations of the study, our synthesis provides valuable insights into the NSEs of veterinary vaccines. Further research, particularly randomized controlled trials in natural animal populations, is critical to fully understand and exploit the potential benefits of NSEs in optimizing vaccination strategies for animal health and production.

Supporting vaccine development for tropical animal health through the refinement of animal models

Alec EVANS (alec.evans@clinglobal.com)

Clinglobal, Tamarin, Mauritius

Developing effective vaccines for vector borne diseases requires robust preclinical testing and validation. Animal models play a pivotal role in assessing vaccine candidates, elucidating immune responses, and optimizing formulations.

African Animal Trypanosomosis (AAT) and Bovine babesiosis are two such diseases affecting large parts of the tropical world and for which there is a need for improved control measures. Whilst live vaccines exist for *Babesia bovis*, significant limitations exist, such as the short shelf life and risk of reversion to resistance. On the other hand, there is no vaccine for AAT and no new therapeutic agents have been developed in the last 50 years.

Our objective was to refine the currently available models for these diseases to reduce the number of animals required whilst adapting the method to be more appropriate for the evaluation of vaccines.

We demonstrated the potential for the elimination of splenectomised cattle in a *B. bovis* challenge model by incorporating an *in vitro* culture system and the effective cryopreservation of *B. bovis* stabilates as an inoculum. This methodology allows the 'cleaning' of field stocks with potential multiple infections whilst reducing the need for intermediate donor animals.

By adapting the cattle challenge model for *Trypanosoma congolense*, we were able to titrate down the infective dose to a number similar to an infected tsetse bite, whilst still obtaining 100% infectivity. We further statistically evaluated the variation in multiple parameters to better define group sizes.

Details of both models and their application in clinical research will be further presented.

Genomic variation in *Cyprinus cyprinidallo3* and its implications for their evolution

Nurul FUANDILA¹ (nurul.fuandila@umontpellier.fr), Marie-Ka TILAK², Anna-Sophie FISTON-LAVIER¹, Emira CHERIF³, Angela Mariana LUSIASTUTI⁴, Munti YUHANA⁵, Anne-Sophie GOSSELIN-GRENET⁶, Jean-Christophe AVARRE³

¹ ISEM, University of Montpellier, Montpellier, France ; ² ISEM, CNRS, University of Montpellier, Montpellier, France ; ³ ISEM, IRD, University of Montpellier, Montpellier, France ; ⁴ Research Center for Veterinary Science, National Research and Innovation Agency, Jakarta, Indonesia ; ⁵ Faculty of Fisheries and Marine Sciences, IPB University, Bogor, Indonesia ; ⁶ DGIMI, University of Montpellier, Montpellier, France

Cyprinus cyprinidallo3 (CyHV-3) is a highly virulent virus, causing high mortalities in common carp. CyHV-3 exists within its host as a diverse population of closely related genetic variants, or haplotypes. Such an haplotype diversity poses challenges in terms of antiviral therapies and vaccination strategies. Adapting a CyHV-3 strain to cell culture resulted in a less virulent form, making it a promising candidate for vaccine development. Its genome analysis revealed a viral haplotype carrying a 1363-bp deletion in the open reading frame (ORF) 150 (ORF150-del).

We thus investigated whether this deletion occurred naturally *in vivo* by screening 236 fish from 43 different farms in Indonesia. It revealed a high prevalence of CyHV-3 (nearly 70%), both in symptomatic and asymptomatic common carp. However, long-read sequencing of the ORF150 showed a low level of genetic variations and the absence of the ORF150-del.

To understand whether this deletion could be reproduced *in vitro*, an isolate of CyHV-3 was propagated in 10 subcultures and serially passaged 65 times under identical conditions. At passage 26 (P26), a thermal stress was applied to evaluate its effect on the accumulation of variations. Long-read sequencing of all subcultures from P15, P30, P50 and P65 evidenced a dynamic accumulation of structural variations: their number was relatively low at P15, decreased at P30 to significantly increase again at P50 and P65. However, the 1363-bp deletion was not detected. These results indicate that the ORF150-del haplotype is a good vaccine candidate as it can be monitored and differentiated from naturally-occurring CyHV-3 haplotypes.



Transboundary Animal Diseases



S3-01

A highly performant ELISA for the detection of specific CCHFV antibodies in multiple species, including humans

Loïc COMTET (loic.comtet@innovative-diagnostics.com), Fabien DONNET, Muriel MALZAC, Philippe POURQUIER

Innovative Diagnostics, Grabels, France

Introduction:

Crimean-Congo hemorrhagic fever (CCHF) is a tick-borne illness caused by the Crimean-Congo hemorrhagic fever virus (CCHFV). It sporadically affects humans in Africa, South Asia, and Southern Europe, causing a potentially fatal hemorrhagic illness. While infected animals are asymptomatic, viraemia and anti-CCHFV antibodies can be detected. This study validates a new CCHF double antigen ELISA for anti-CCHFV nucleoprotein antibodies detection on serum/plasma and filter paper (FPS)/dried blood spot (DBS) samples. This recombinant protein-based ELISA can be run under standard biosafety conditions.

Materials & Methods:

Sensitivity was assessed on 95 cattle and 176 small ruminants' sera with confirmed antibody status with 3 serological assays. Specificity was evaluated on 402 cattle and 804 small ruminants' sera from CCHFV-free areas (France, Germany). Monkeys, camels, rats, ferrets, raccoon dogs, raccoons, foxes, hares, pigs, and humans' negative sera were tested to ensure the ELISA's efficacy across multiple species. FPS/DBS application was validated by testing 8 CCHF-negative samples and serial dilution of 4 CCHF-positive samples.

Results:

All negative sera (n=2136) were confirmed by this new ELISA, indicating a specificity of 100% [99.8-100]. Measured diagnostic sensitivity was 98.9% [96.8-99.8]. Analytical sensitivity obtained with DBS is slightly inferior compared to serum application, which does not affect diagnostic sensitivity of the FPS/DBS application. All samples tested in parallel with serum and filter paper protocols gave the same results.

Conclusion:

This novel ELISA demonstrates excellent specificity and sensitivity, adapted to the accurate detection of anti-CCHFV antibodies in animals and humans, on serum/plasma or filter paper/dried blood spot samples.

Assessing interactions between domestic and wild pigs and implications for the transmission of African swine fever and other pathogens in rural habitats of Madagascar

Rianja RAKOTOARIVONY (rianjarakotoarivony@gmail.com)

Joint Research Unit-Animal-Health-Territories-Risks-Ecosystems (ASTRE), CIRA, CIRAD, Antananarivo, Madagascar

In some rural anthropized areas of Madagascar, domestic pigs are reared in free-ranging conditions sharing their natural environment and resources with sympatric wildlife species, including bushpigs, *Potamochoerus larvatus* the largest mammal species in the country. Since 1998, African swine fever (ASF) is endemic in Madagascar and the bushpig is considered one of its natural reservoirs in sub-Saharan Africa. To assess the potential for ASF transmission between domestic pigs and bushpigs, 25 camera-traps were deployed in two different regions of Western Madagascar over a 3-month period. The traps were placed around three types of animal attraction points near nine villages: water sources (n=7), attractive plants (n=11), and resting areas (n=8) and total of 17,804 images were collected and analysed.

During the study period, no direct interaction between domestic and wild species was observed. However, a total of 0.29 indirect interactions occurred within 24-hour interval, involving domestic pigs, bushpigs, and other sympatric species. The study revealed a median time interval of 420 minutes [300-1410] time interval for indirect interactions between domestic pigs and bushpigs, indicating potential indirect ASF transmission through shared resources or habitat. Additionally, on average 11.6 indirect interactions with other sympatric domestic species occurred daily, with a minimum observed time interval of 30 minutes, potentially facilitating the sharing of multi-host pathogens like tuberculosis or toxoplasmosis.

Our research provides valuable insights into the use of camera-traps to assess habitat sharing between domestic and wild species in rural Madagascar, and establish hypothesis about interspecific pathogen spillover, which can impact the health of wild, domestic animals but also humans.

Clinico-pathological study of Peste des petits ruminants' virus on rural indigenous sheep and goats in Plateau State, North Central Nigeria

Ladi Amos CHABIRI¹ (ladichabiri@yahoo.com), Sohnap James SAMBO², Sani ADAMU², Timothy Yusufu WOMA³, Maryam MOHAMMED⁴, Marion BORDIER⁵, Muhammad Bashir BOLAJOKE⁶, Alexis DELABOUGLISE⁷

¹ Diagnostic Services, National Veterinary Research Institute (NVRI), Vom., Jos, Plateau State, Nigeria ; ² Veterinary Pathology, Ahmadu Bello University, Zaria, Kaduna, Nigeria ; ³ Viral Research, National Veterinary Research Institute (NVRI), Vom., Jos, Plateau, Nigeria ; ⁴ Directorate, National Veterinary Research Institute (NVRI), Vom., Jos, Plateau, Nigeria ; ⁵ Dakar, CIRAD, ASTRE, Dakar-Etoile, Dakar, Senegal ; ⁶ Diagnostic Services, National Veterinary Research Institute (NVRI), Vom., Jos, Plateau, Nigeria ; ⁷ CIRAD, ASTRE, CIRAD, ASTRE, Montpellier, Southern France, France

Introduction:

A large part of mortality in small ruminant populations is attributed to PPRV infection in Plateau State. Most information on pathology of PPR is based on results obtained following experimental infections. This study intended to fill this gap.

Methods:

A rapid field test is carried out to confirm PPRV infection using the ID Rapid PPR antigen detection test. Blood and serum samples were obtained from sick animals and analysed. Postmortem examination was conducted on animals that died of PPR, and tissue samples were obtained for histopathology. Apparently healthy animals seropositive to PPR were equally sampled to serve as control.

Results:

A total of 303 sheep and goats were sampled showing respiratory signs, and symptoms of gastrointestinal disturbances. There were significant variations in haematological and serum biochemical values. Infected sheep and goats had significantly higher mean lymphocyte and monocyte count, mean corpuscular volume, mean corpuscular haemoglobin, and platelet distribution width than the control. The mean values of alkaline phosphate, gamma-glutamyl transferase, total bilirubin, direct bilirubin, potassium, cholesterol, uric, and creatinine in the infected group were significantly higher than in the control group.

Discussion:

The ID Rapid PPR antigen detection is most ideal field diagnosis of PPR. Lymphocytosis observed in infected sheep and goats contrast with previous findings which observed lymphopenia and attribute it to possible degenerative changes of bone marrow. Hypernatremia is a significant finding which maybe due to diarrhoea or low fluid intake. Postmortem examination less severe lesions possibly because of virulence of the virus and the infective dose.

Combining animal mobility field surveys and Expert knowledge to map the risk of the spread of Peste des petits ruminants in three states in Northern Nigeria

Sandra IJOMA (sandraijomaifeoma@gmail.com)

Veterinary Public health and Preventive Medicine, National Veterinary Research institute, Vom., Jos, Plateau, Nigeria

Introduction & Objectives:

Peste des petits ruminants (PPR) outbreaks persist in Nigeria despite vaccination, particularly during dry-season animal migrations. Understanding the animal network, risk factors, and high-risk transmission areas is crucial for targeted PPR surveillance and control.

Materials & Methods:

A cross-sectional survey on animal mobility was carried out across three states in Nigeria (Bauchi, Kano, Plateau) among 10 major livestock markets in 10 Local Government Areas (LGAs) for a total of 1065 respondents. Twenty Focus Group Discussions (FGD) with market actors, transhumance farmers and PPR experts were done to complete information on animal network. Global and centrality measures were calculated of the reconstructed network.

A multi-Criteria Decision Analysis approach was used to produce risk maps for PPR occurrence. Risk factors for PPR occurrence were identified by experts and their importance assessed during workshops.

Results:

The network is connected, has a very low density and is highly heterogeneous and the presence of hubs increases the risk of PPR spread. Gwarzo, Wudil (Kano state) and Alkalari (Bauchi state) LGA receives the most of sheep and goats, while Jos North (Plateau) and Gwarzo supplies more small ruminants. Bukuru and Alkalari markets are superspreaders with a higher probability of detecting virus circulation. Six communities were identified.

Highest risk LGAs for disease occurrence were Alkalari and Ningi (Bauchi state), Gwarzo and Wudil (Kano state) and Barkin Ladi, Kanam, Lantang north, Quaanpan, Riyom, Shendam, Wase LGAs.

Discussion & Conclusion:

These findings inform risk-based PPR control policies focused on high-risk markets and movement corridors.

Comparative evolutionary analyses of Peste des petits ruminants virus genetic lineages

Arnaud BATAILLE¹ (arnaud.bataille@cirad.fr), Maxime COURCELLE¹, Kadidia TOUNKARA¹, Moustapha LO², Aminata BA², Mariam DIOP², Mamadou NIANG³, Chieck ABOU KOUNTA SIDIBE³, Amadou SERY³, Marthin DAKOUO³, Lancei KABA⁴, Youssouf SIDIME⁴, Mohammed KEYRA⁴, Alpha OUMAR SILY DIALLO⁴, Ahmed BEZEID EL MAMY⁵, Ahmed SALEM EL ARBI⁵, Yahya BARRY⁵, Ekaterina ISSELMOU⁵, Habiboullah HABIBOULLAH⁵, Baba DOUMBIA⁵, Mohamed BABA GUEYA⁶, Joseph AWUNI⁷, Theophilus ODOOM⁷, Patrick ABABIO TETTEH⁷, Daniel TAWIAH YINGAR⁷, Caroline COSTE¹, Samia GUENDOZ¹, Olivier KWIAK¹, Geneviève LIBEAU¹

¹ CIRAD, Montpellier, France ; ² LNERV, Dakar, Senegal ; ³ LCV, Bamako, Mali ; ⁴ Institut Supérieur des Sciences et de Médecine Vétérinaire, Dalaba, Guinea ; ⁵ ONARDEL, Nouakchott, Mauritania ; ⁶ Mauritania, ONARDEL, Nouakchott, Mauritania ; ⁷ Accra Veterinary Laboratory, Accra, Ghana

Peste des petits ruminants virus (PPRV) causes a highly infectious disease affecting mainly goats and sheep and has an important impact on the global economy and food security. Full genome sequencing of PPRV strains has proved to be critical to increasing our understanding of PPR epidemiology and to inform the on-going global efforts for its eradication. However, the number of full PPRV genomes published is still limited and with bias towards recent samples and genetic lineage IV, which is only one of the four existing PPRV lineages. Here, we generated genome sequences for 25 recent and 7 historical PPRV samples, focusing mainly on lineage II in West Africa. This provided the first opportunity to compare the evolutionary pressures and history between the globally dominant PPRV genetic lineage IV (LIV) and lineage II (LII), which is endemic in West Africa. Phylogenomic analysis showed that the relationship between PPRV LII strains was complex and supported the transboundary circulation of the virus within West Africa. In contrast, lineage IV sequences were clearly separated per region, with strains from West and Central Africa branched as a sister clade to all other LIV sequences, suggesting this lineage also has an African origin. Molecular evolution analyses show that strains belonging to LII and LIV have evolved under different selection pressures. Differences in codon usage and adaptative selection pressures were observed in all viral genes between the two lineages. Our results confirm that comparative genomic analyses can provide new insights into PPRV's evolutionary history and molecular epidemiology.

Modelling RVF vector population dynamics in a tropical setting in South-Eastern Madagascar

Laure J.G. CHEVALIER¹ (laure.chevalier@cirad.fr), Thomas BALENGHIEN¹, Benoît DURAND², Luciano TANTELY³, Véronique CHEVALIER^{1,4}, Pauline EZANNO⁵

¹ ASTRE, CIRAD, Montpellier, France ; ² Epidémiologie (EPI), ANSES, Maisons-Alfort, France ; ³ Unité d'entomologie, Institut Pasteur de Madagascar, Antananarivo, Madagascar ; ⁴ Unité d'épidémiologie, Institut Pasteur de Madagascar, Antananarivo, Madagascar ; ⁵ Biologie, épidémiologie et analyse de risque en santé animale (BIOEPAR), INRAE, Nantes, France

Introduction & Objectives:

Rift valley fever (RVF) is an emerging zoonotic arbovirolosis circulating in Africa, the Middle East and the Indian Ocean. It has been identified by the WHO as a priority disease for research, surveillance and prevention. The RVF virus (RVFV) causes abortive fever and juvenile mortality in ruminants, and potentially haemorrhagic fever in humans, with a high human, animal and economic toll on affected communities. Three large epizootic waves have hit Madagascar since RVFV was introduced there, and interepizootic circulation has been demonstrated. We studied the population dynamics of suspected vector species for RVFV in South-Eastern Madagascar, which was hit by a RVF wave in 2021, in order to use the outputs to model RVFV transmission in the area.

Materials & Methods:

Anopheles coustani and *Culex antennatus* were identified as potential significant vectors from a literature review. A generic mechanistic compartmental model, driven by temperature and rainfall, was simplified and adapted to these species. This model was used to estimate relative abundances of host-seeking mosquitoes, which we then compared to observed mosquito captures.

Results, Discussion & Conclusion:

We present here a simple model predicting vector populations according to climate variables. The predictions seem coherent with field observations, especially for *Anopheles coustani* population dynamics. Peaks in predicted mosquito abundance occur at the end of the wet season, which is concurrent to when RVFV circulation is high. These first results are promising when it comes to incorporating the population dynamic model into a transmission model for RVFV in Madagascar.

West Nile virus virulence and transmission in vertebrate hosts and mosquitoes is modulated by different regions of the virus genom

Sylvie LECOLLINET (sylvie.lecollinet@cirad.fr)

ASTRE, CIRAD, Petit Bourg, Guadeloupe

West Nile virus (WNV) is a neurotropic mosquito-borne virus belonging to the *orthoflavivirus* genus. WNV amplification cycle involves birds as amplifying hosts and mosquitoes, mainly of the genus *Culex*, as vectors. Subsequent to WNV emergence in New York in 1999, a fast WNV spread occurred in the Americas with apparently a lower health impact in Latin America and Caribbean.

WNV induces outbreaks of varying intensity in humans, horses and birds. Beyond environmental variables, the different incidence of WNV epizootics or epidemics could be explained by differences in strain virulence and transmission. To characterize the genetic determinants of WNV pathogenesis and transmission in vertebrates and arthropods, we generated by reverse genetics several chimeras between two WNV strains differing in their levels of virulence. The replicative capacity of the chimeras was assessed *in vitro* in mammalian Vero, avian CCL141 and C6/36 mosquito cells. Infection of Vero cells suggests a role for NS1, NS3 and NS4A proteins in viral replication 24 and 48 h post-infection, whereas NS5 and the 3'UTR region modulate viral fitness in C6/36. Infection of BALB/c mice, 1-day old chickens as well as *Culex pipiens* mosquitoes extends these observations: the virulence in mammals and birds and the vector competence in mosquitoes are clearly modulated by different regions of the virus genome. Precise mapping of WNV virulence determinants will allow for more rapid assessment of emerging strains epidemic potential, as well as the development of effective preventive or control solutions.



SESSION 4

Veterinary Parasitology



Multiresistance of *Haemonchus contortus* (Nematoda: Trichostrongylidae) to anthelmintics: a global threat to small ruminant farming

Philippe JACQUIET (philippe.jacquiet@envt.fr)

Parasitology, National Veterinary School of Toulouse, Toulouse, France

Haemonchus contortus is a nematode of the Haemonchinae subfamily, a parasite of the abomasum of small ruminants. Haemonchinae probably originated in Africa, but the *H. contortus* species has conquered all the world's small ruminant breeding areas, including cold regions such as Canada and Sweden, thanks to its high genetic variability, ecological plasticity and ability to adapt to diverse environments. Among the nematodes that parasitize the digestive tract of small ruminants, *H. contortus* is the most pathogenic species. Hematophagous, this species causes severe anemia and even mortality in massive infections. Control of this parasite has long relied on the repeated use of anthelmintic molecules (AH) such as benzimidazoles, macrocyclic lactones, imidazothiazoles, salicylanilides or aminoacetonitrile derivatives. However, this monolithic strategy is now facing the emergence of resistance, or even multi-resistance to several families of AHs, and the need to take into account of the ecotoxicity of macrocyclic lactones. A complete revision of our control approach is therefore necessary. To achieve this, there are three possible courses of action: i) rational and sparing use of molecules that are still effective on a farm, ii) increasing the resistance and resilience of sheep and goats through feeding and genetic selection, and iii) new grazing management approach to limit pastures' contamination (cell grazing, mixed grazing with cattle). This integrated pest management is currently being evaluated in several countries. Its acceptability to farmers is also a crucial point, requiring major awareness-raising/training efforts and a relationship of trust between the farmer and his veterinarian.

S4-01

Immunization of cattle with a *Rhipicephalus microplus* chitinase peptide containing predicted B-cell epitopes reduces tick biological fitness

Juan MOSQUEDA (joel.mosqueda@uaq.mx)

Faculty of Natural Sciences, Universidad Autonoma de Queretaro, Queretaro, Mexico

Rhipicephalus microplus, the cattle fever tick, is the most important ectoparasite impacting the livestock industry worldwide. Overreliance on chemical treatments for tick control has led to the emergence of acaricide-resistant ticks and environmental contamination. An immunological strategy based on vaccines offers an alternative approach to tick control. To develop novel tick vaccines, it is crucial to identify and evaluate antigens capable of generating protection in cattle. Chitinases are enzymes that degrade older chitin at the time of molting, therefore allowing interstadial metamorphosis. In this study, one *R. microplus* chitinase was identified and its capacity to reduce fitness in ticks fed on immunized cattle was evaluated. First, the predicted amino acid sequence was determined in four isolates and their similarity were analyzed by bioinformatics. Four peptides containing predicted B-cell epitopes were designed. The immunogenicity of each peptide was assessed by inoculating two cattle, four times at 21-days intervals, and the antibody response was verified by indirect ELISA. A challenge experiment was conducted with those peptides that were immunogenic. The *chitinase* gene was successfully amplified and sequenced, enabling comparison with reference strains. Notably, a 99.32% identity and 99.84% similarity were ascertained among the sequences. Furthermore, native protein recognition was demonstrated through western blot assays. Chitinase peptide 3 reduced the weight and oviposition of engorged ticks, as well as larvae viability, exhibiting a 71 % efficacy. Therefore, chitinase 3 emerges as a viable vaccine candidate, holding promise for its integration into a multiantigenic vaccine against *R. microplus*.

Integrating ROS-tolerant entomopathogenic fungi with a vaccine targeting tick immunity decreases infestations in a semi-field pasture test

Isabel Kinney Ferreira DE MIRANDA SANTOS (imsantos@fmrp.usp.br)

Ribeirão Preto Medical School, University of São Paulo, Ribeirão Preto, SP, Brazil

Entomopathogenic fungi (EPF) present low virulence for ticks, possibly related to their susceptibility to reactive oxygen species (ROS) derived from the parasite's blood meal. We thus evaluated EPF for tick control by addressing this issue as well as targeting the parasite's innate immune system. We generated ROS-tolerant EPF (EPF-T) by successive passages in medium containing a pro-oxidant agent. Compared to EPF, EPF-T show similar germination, conidiogenesis and tolerance to UV-B, but significantly increased antioxidant defenses. In an incubator assay, blood-fed female *R. microplus* ticks were then treated with EPF or EPF-T, after which they exhibited increased ROS production when challenged by EPF. Overall biological parameters were significantly reduced, by 84.44%, in ticks challenged with EPF-T, including weights of egg masses and reproductive indices, the latter by 70%. We then vaccinated cattle with antigens targeting tick innate immunity. Compared to ticks fed on control animals, expression of genes *Stat*, *Toll*, *Trx* was significantly downregulated in their hemocytes and fat bodies. When these ticks were challenged with EPF-T, the arthropod's immune pathways were activated. We then exposed ticks fed on vaccinated or on unvaccinated cattle to EPF-T-infected or uninfected soil in pots where *Urochloa decumbens* was growing. EPF-T significantly reduced larvae derived from ticks fed on unvaccinated cattle by 30% on pasture leaves and by 75% when derived from ticks fed on vaccinated cattle. We show that harmful chemicals used to control tick infestations can be replaced by associating entomopathogens with vaccines that neutralize tick immunity. Funding: FAPESP and FAPERJ

Long Read Whole Genome Sequencing and Assembly of two *Tritrichomonas foetus* strains isolated from Queensland and Northern Territory in Australia

Harvey SANTOS¹ (johnharvey.santos@uq.edu.au), Antonino CAVALLARO¹, Elizabeth ROSS¹, Gry BOE-HANSEN^{1, 2}, Hannah SIDDLE¹, Loan NGUYEN¹, Ali RAZA¹, Ala TABOR^{1, 3}

¹ Centre for Animal Science, Queensland Alliance for Agriculture & Food Innovation, The University of Queensland, St Lucia, Queensland, Australia ; ² School of Veterinary Science, The University of Queensland, Gatton, Queensland, Australia ; ³ School of Chemistry & Molecular Biosciences, The University of Queensland, St Lucia, Queensland, Australia

Bovine trichomonosis, caused by *Tritrichomonas foetus*, is a venereal disease that poses significant challenges to cattle reproductive health, resulting in suboptimal breeding outcomes. Conventional vaccine strategies have been limited to whole inactivated *T. foetus* which depends upon large-scale culture. As an alternative, this study aims to employ reverse vaccinology by sequencing Australian *T. foetus* strains to identify subunit candidates against bovine trichomonosis.

In 2020-2021, *T. foetus* was detected with qPCR and two isolates were selected (TfOz5 and TfOz-N36) from preputial samples collected from various herds in Queensland and the Northern Territory. Genomic DNA was extracted via cold alkaline lysis and the sequencing library was prepared using the SQK-LSK110 kit. The library was then sequenced using a MinION flow cell (FLO-MIN106, R9.4.1) on a MinION Mk1C for 48 hours. Base calling was performed at super-high accuracy model using Guppy version 6.5.7. Reads under 20 Kilobase pairs with an average Q-score under 12 were removed using NanoFilt v2.8.0. For genome assembly, Flye v2.9.1.

The genome assembly of Australian *T. foetus* TfOz5 strain showed a total of 194 contigs (110 Mb), with a GC content of 30.56%, an N50 value of 1.49 Mb. For TfOz-N36, the sequencing coverage was 59x composed of 368 contigs (105 Mb), with a GC content of 30.93%, and an N50 value of 0.48 Mb. These two isolates have 99.2% similarity, and these genome assemblies have improved previous *T. foetus* genomes with 10 to 100-fold fewer contigs assembled.

These genomes can be mined to identify putative candidates for vaccine development.

Novel genomic technologies for tick control in Australian beef cattle

Hannah SIDDLE¹ (h.siddle@uq.edu.au), Chuning WANG², Ala TABOR^{2,3}

¹ Queensland Alliance of Agriculture and Food Innovation, University of Queensland, Brisbane, QLD, Australia ; ² Queensland Alliance of Agriculture and Food Innovation, University of Queensland, Brisbane, Queensland, Australia ; ³ School of Chemistry & Molecular Biosciences, University of Queensland, Brisbane, Queensland, Australia

Introduction & Objectives:

Cattle ticks and tick-borne diseases are a global problem, predicted to worsen with climate changes. *Rhipicephalus australis* (Australian cattle tick) was introduced into Australia and belongs to a broader cryptic species of *R. microplus*, with a global distribution causing USD\$22–30b per annum in losses. The tick microbiome is a target for potential control strategies, but few studies have investigated *R. microplus* and no studies have utilised unbiased metagenome approaches.

Materials & Methods:

Gut and salivary gland (SG) tissues were dissected from 60 semi engorged adult female ticks, with 3 replicates for each tissue. Extracted DNA was sequenced using long read Oxford Nanopore platforms with adaptive sampling to deplete host (tick) DNA, utilising a draft genome of *R. australis*.

Results & Discussion:

No statistical difference in alpha diversity between gut and SG samples ($p = 0.12$) was observed, however differences between genera and species present were evident. The dominant genus in SG is *Coxiella* spp. (mean abundance, 87%), contrasting with the gut samples where *Staphylococcus* spp. (mean abundance, 49%) and *Escherichia* spp. (mean abundance, 31%) dominate. *Staphylococcus* spp., *Xylosus* spp., *S. chromogenes* and *E. coli* were prevalent in gut, while *C. mudrowiae* was the most prevalent *Coxiella* spp. in SG. Potential pathogenic species included *Corynebacterium resistens* and *Borrelia* spp.

Discussion:

Analysis of the gut and SG tissues has revealed genera and species present in each niche, most interestingly the dominance of the endosymbiotic *Coxiella* spp. in SG. These findings will allow crucial endosymbiotic species to be targeted for control of ticks.

Pre-existing antibodies to antigens affect efficacy of a vaccine for the cattle tick, *Rhipicephalus microplus*

Isabel Kinney Ferreira DE MIRANDA SANTOS (imsantos@fmrp.usp.br)

Ribeirão Preto Medical School, University of São Paulo, Ribeirão Preto, SP, Brazil

Tick-infested cattle develop antibodies to the parasite's salivary proteins but are still susceptible to reinfestations. We formulated a vaccine based on 13 chimerized salivary antigens and examined if pre-vaccination, vaccine-specific antibodies (PV-Abs) affected its efficacy. We assigned 21 bovines to two experimental groups according to innate tick loads and previous exposure to ticks (high [HE] or low [LE]). They were vaccinated with chimeras adjuvanted in Alhydrogel or with Alhydrogel alone, maintained in tick-infested pastures for 14 weeks, and fed ticks were counted weekly 12 times. Sera from individual animals collected on day 0 of vaccination were reacted in an ELISA with 4 pools of individual antigens that formulated the chimeras. Counts of fed female ticks on vaccinated LE bovines (60.2 ± 69.73) were significantly ($P=0.001$) lower compared to LE controls (133 ± 141.54). Conversely, animals with previous high exposure did not present significant ($P=0.13$) differences of tick loads between vaccinated (46.6 ± 65.40) and control bovines (38.14 ± 52.14). In a heat map of reactivities to each antigen pool generated with unsupervised clustering of ELISA optical densities, the reactivities of PV-Abs from 4 of 6 LE animals presented a negative z score; PV-Abs of all 5 HE animals presented a positive z score. Hypotheses to explain these results are antigenic imprinting, antigen masking by PV-Abs and/or dermatopathic lymphadenopathy. These data indicate that it may be necessary to employ tick vaccines before the Spring Rise of tick infestations and to determine that levels of PV-ABs to antigens are below a certain threshold before vaccination.

Funding: FAPESP and IEL.

Trials and tribulations of cattle tick vaccines - an Australian update

Hannah SIDDLE (h.siddle@uq.edu.au), Nimitha RAMACHANDRAN, Alicja (Ala) TABOR

Queensland Alliance of Agriculture & Food Innovation, The University of Queensland, Brisbane, Queensland, Australia

The *Rhipicephalus microplus* species complex transmits babesiosis and anaplasmosis to cattle in tropical and sub-tropical regions of the world costing ~\$US22-30b losses per annum. A cattle tick vaccine program commenced in 2005 with the objective to use a novel reverse vaccinology approach to identify antigens from a *R. microplus* EST library.

The *R. microplus* EST library (BmGI) of 13,643 sequences were screened using trans-membrane, secreted and B cell epitope software. Gene expression analyses identified tick genes expressed when sensing tick resistant cattle (*Bos indicus*). Pooled sera from tick resistant (n=6) and tick susceptible (n=6) cattle were screened against tick B cell epitopes using ELISA. Antibodies against peptides recognized by resistant sera were screened in vitro by feeding semi-engorged females. A final dual vaccination trial consisting of two recombinant proteins in two groups of vaccinated and unvaccinated 6 tick naïve steers were exposed to two larval tick challenges.

Efficacy of the dual vaccination after the first challenge was 83% and increased after the second tick challenge to 90%. Under the same conditions, Bm86 efficacies were 74% and 64% respectively. The adult female ticks from vaccinated cattle presented as a black phenotype which did not lay eggs. Transcriptome analyses of the black ticks revealed diminished expression of one of the candidates with pathways associated with stress response and cell death upregulated.

Although the results are excellent, pharma are looking for tick knockdown as observed with acaricides. Funding to undertake a larger trial using 40 cattle will improve our data for product registration.

Vaccination against cattle ticks in Mexico: Current status and Perspectives

Consuelo ALMAZÁN¹ (c_almazan_g@hotmail.com), Delia Inés DOMÍNGUEZ-GARCÍA², Rodrigo ROSARIO², Juan MOSQUEDA¹

¹Immunology and Vaccines Laboratory, College of Natural Sciences, Autonomous University of Queretaro, Queretaro, Mexico ;

²Biotechnology in Health and Environmental Sciences Research Laboratory, Autonomous University of Guerrero State, Chilpancingo, Mexico

Ticks negatively impact humans and animals directly through tick bites and blood feeding, and indirectly by transmission of viral, bacterial, and protozoan pathogens. The use of chemical acaricides during long periods of time has contributed to genetical selection of resistant tick populations. In addition, acaricides contaminate the environment and products destined for human consumption. The increase in occurrence of tick-borne diseases in cattle has stimulated research focused on the development of new tools for prevention and control of tick infestations. Anti-tick vaccines represent a feasible alternative for tick control. In Mexico more than 20 vaccination trials testing different antigens against the cattle tick *Rhipicephalus microplus* have been conducted and results have demonstrated a decrease on tick feeding, tick survival, oviposition, and fertility. Although commercial vaccines against the cattle tick, *R. microplus* have been developed, vaccines against other tick species do not exist yet. In this presentation, the need for a vaccine that targets both *R. microplus* and *Amblyomma mixtum*, the most important ticks affecting cattle in Mexico will be addressed. Efforts to develop new anti-tick vaccines, and strategies of tick control using anti-tick vaccines in areas with multi-tick resistance will be presented. Effective broad-spectrum anti-tick vaccines against *R. microplus* and *Amblyomma* spp. are still required in tropical areas where both ticks are found co-infesting cattle.



ABSTRACTS THURSDAY 23 MAY





Vector-Borne Diseases



A new cell line derived from the tsetse fly *Glossina morsitans morsitans*

Lesley BELL-SAKYI¹ (L.Bell-Sakyi@liverpool.ac.uk), Lee HAINES², Catherine HARTLEY¹, Alexandra BELIAVSKAIA¹, Jing Jing KHOO¹, Benjamin MAKEPEACE¹, Alistair DARBY¹

¹ Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, Liverpool, United Kingdom ; ² Vector Biology Department, Liverpool School of Tropical Medicine, Liverpool, United Kingdom

Insect cell lines play a vital role in many aspects of research on disease vectors and agricultural pests. The tsetse fly *Glossina morsitans morsitans* is an important vector of salivarian trypanosomes in sub-Saharan Africa and, as such, is a major constraint on livestock production, agricultural development and human health in the region. We have recently established a new cell line, GMA/LULS61, derived from tissues of adult female *G. m. morsitans*. The tsetse cells are grown at 28 °C in L-15 (Leibovitz) medium supplemented with foetal bovine serum and tryptose phosphate broth. Karyotyping at passage 17 revealed a predominantly haploid chromosome complement. PCR amplification and sequencing of fragments of the COI gene and pan-bacterial 16S rRNA gene confirmed, respectively, species origin and absence of contaminating bacteria. GMA/LULS61 cells supported infection and growth of several insect-derived strains of the intracellular bacterial symbiont *Wolbachia*. The GMA/LULS61 cell line, available from the Tick Cell Biobank at the University of Liverpool, has potential for application in a variety of studies investigating the biology and control of *G. m. morsitans* and its associated pathogenic and symbiotic microorganisms.

Application of SHERLOCK detection for epidemiological surveys of Animal African Trypanosomiasis

Roger ELOIFLIN¹ (roger.eloiflin@ird.fr), Elena PEREZ ANTON², Aïssata CAMARA³, Annick DUJEANCOURT-HENRY², Martial Kassi N'DJETCHI⁴, Mathurin KOFFI⁴, Vincent JAMONNEAU¹, Sophie THEVENON¹, Mamadou CAMARA⁵, Jean-Mathieu BART¹, Lucy GLOVER⁶, Brice ROTUREAU⁷

¹ UMR INTERTRYP, IRD, Montpellier France ; ² Trypanosome Molecular Biology, Department of Parasites and Insect Vectors, Pasteur Institute, Paris, France ; ³ Parasitology Unit, Pasteur Institute, Conakry, Guinea ; ⁴ Génétique et Épidémiologie Moléculaire, Laboratoire de Biodiversité et Gestion des Écosystèmes Tropicaux, Daloa, Côte d'Ivoire ; ⁵ Programme National de Lutte contre la Trypanosomiose Humaine Africaine, Ministère de la Santé, Conakry, Guinea ; ⁶ Trypanosome Molecular Biology, Department of Parasites and Insect Vectors, Pasteur Institute, Paris, France ; ⁷ Trypanosome Transmission Group, Trypanosome Cell Biology Unit, Pasteur Institute, Paris, France

Animal African trypanosomiasis (AAT) is a disease caused by parasites of the genus *Trypanosoma*. After the successful development of a diagnostic test for human African trypanosomiasis, we have adapted the CRISPR-based detection toolkit SHERLOCK (Specific High-sensitivity Enzymatic Reporter unlocking) for trypanosomatid parasites responsible for AAT. SHERLOCK first amplifies nucleic acid using recombinase polymerase amplification (RPA), which is then combined with the Cas13a nuclease for RNA target recognition via specific guides (crRNAs) and a fluorescent reporter linked to a quencher. Target sequence recognition by Cas13a results in promiscuous ribonuclease activity which cleaves the fluorescent reporter, emitting fluorescence used for detection. To test the applicability of this technique in the field, we analysed domestic animal samples (sheep, goat, pig and dog) from surveys in Cameroon, Côte d'Ivoire and Guinea. The preliminary results of this pilot study show that the SHERLOCK4AAT method is able to detect and discriminate between trypanosome species involved in multiple infections with a high sensitivity, especially in blood samples. In Côte d'Ivoire, we determined that approximately 60% of the Trypanozoon-positive blood samples collected on free-ranging pigs were co-infected with *T. congolense*, while no *T. vivax* infections were detected. We are now focussing on further improving the sensitivity of the assay and developing a multiplex version for species discrimination in a single test.

First epidemiological and molecular report of ticks and tick-borne pathogens in small ruminants across North and North-western Pakistan

Olivier SPARAGANO¹ (olivier.sparagano@rau.ac.uk), Jehan ZEB², Baolin SONG³, Munsif ALI KHAN⁴, Haytham SENBILL⁵, Sabir HUSAIN³, Muhammad UMAIR³, Alejandro CABEZAS-CRUZ⁶

¹ Agricultural Sciences and Practice, Royal Agricultural University Cirencester, G, Cirencester, United Kingdom ; ² Hong Kong Science and Technology Park, Center for Immunology and Infection, New territory, Hong Kong SAR China ; ³ Department of Infectious Diseases and Public Health, City University of Hong Kong, Kowloon, Hong Kong SAR China ; ⁴ Department of Public Health, The University of Hong Kong, Kenedy town, Hong Kong SAR China ; ⁵ Department of Zoology, Alexandria University, Alexandria, Egypt ; ⁶ UMR BIPAR, Laboratoire de Santé Animale, Maisons-Alfort, ANSES, INRAE, Ecole Nationale Vétérinaire d'Alfort, Inrae, France

The current study aims to shed light on the zoonotic and veterinary significance of ticks and tick-borne infections by getting essential data about their distribution and genetic characteristics in previously unexplored areas. A total of 1,587 ixodid ticks were collected from goats and sheep (n = 600) followed by morphological and molecular identification using 16S rRNA and *COI*. Tick-borne pathogens were assessed by PCR targeting the genetic markers 16S rRNA and *gltA* for bacterial pathogens, and 18S rRNA for Apicomplexan. The morpho-molecular detection revealed three ixodid tick genera (*Hyalomma*, *Haemaphysalis*, and *Rhipicephalus*), which included 11 tick species viz. *Hy. anatolicum* (5.9%), *Hy. dromedarii* (9.1%), *Hy. excavatum* (2.8%), *Hy. isacchi* (5.1%), *Hy. scupense* (7.7%), *Hae. montgomeryi* (18.3%), *Hae. sulcata* (6.5%), *Rh. decoloratus* (4.4%), *Rh. haemaphysaloides* (13.2%), *Rh. microplus* (10.8%), and *Rh. turanicus* (16.2%). Amplified tick 16S rRNA and *COI* nucleotide sequences clustered phylogenetically with similar isolates from other regions of the world. The 16S rRNA, 18S rRNA and *gltA* nucleotide sequences of detected *R. massiliae* (24.5%) followed by *T. ovis* (16.4%), *A. capra* (9.1%), *T. luwenshuni* (6.4%), *A. ovis* (5.9%), *R. hoogstraalii* (5.0%), *Anaplasma* spp. (4.5%), *Ehrlichia* spp. (4.5%), *Rickettsia* spp. (4.5%), *T. annulata* (4.1%) and *A. marginale* (3.6%), shared 99.48-100% similarity with sequences previously reported species. Our results are the first available report documenting important ticks and tick-borne pathogens of veterinary and public health concern from previously neglected parts of Pakistan which can provide a baseline to facilitate future large-scale epidemiological and molecular studies about TTBP at the local and global levels.

SSR-seq loci to study the population genetics of vectors: tsetse flies in three sleeping sickness foci: Boffa (Guinea), Bonon (Côte d'Ivoire) and Maro (Chad)

Thierry DE MEEUS¹ (thierry.demeus@ird.fr), Sophie RAVEL¹, Moise KAGBADOUNO², Djakaridja BERTE³, Hissène MAHAMAT⁴, Adeline SÉGARD¹, Emilie CHANCEREL⁵, Erwan GUICHOUX⁵, Olivier LEPAIS⁵

¹ Intertryp, IRD, Montpellier, France ; ² PNLTHA, Conakry, Guinea ; ³ IPR, IBouaké, Côte d'Ivoire ; ⁴ IRED, Ndjamena, Chad ; ⁵ PGTB BIOGECO, INRAE, Bordeaux, France

In Subsaharan Africa, tsetse flies are vectors of trypanosomes causing Human African Trypanosomiasis (HAT) and Animal African Trypanosomosis (AAT). To evaluate the efficiency of and/or design most efficient vector control campaigns requires, as far as possible, a good knowledge of the population biology of the targeted species. To date this was made with microsatellite markers developed in a classical way. Such markers suffer from difficulties of interpretation due to the frequent occurrence of amplification issues, and their frequent occurrence in the X chromosome, rendering useless the genotyping of males. In this paper, we present the development of a new method to design and genotypes microsatellites with high-throughput sequencing technology: SSR-seq. We applied this new technology and developed 26 new loci on three species of tsetse flies: *Glossina palpalis gambiensis*, *G. p. palpalis*, and *G. fuscipes fuscipes* from three foci of HAT in Guinea, Côte d'Ivoire and Southern Chad, where programs of tsetse control was started against the local vector. We analyzed flies captured before and after the beginning of vector control and we compare different statistics and estimators obtained with these new markers and «classic ones».

Whole blood transcriptome of trypanotolerant and trypanosusceptible cattle during trypanosome infection highlights modulation of genes involved in immuno-metabolism

Sophie THEVENON¹ (sophie.thevenon@cirad.fr), David BERTHIER², Isabelle CHANTAL², Laurence FLORI³, Moana PEYLHARD², Guilhem SEMPÉRÉ², Roger Junior ELOIFLIN⁴, Guiguigbaza-Kossigan DAYO⁵, Souleymane SYLLA⁵

¹ BIOS UMR INTERTRYP, CIRAD, Montpellier, France ; ² CIRAD, Montpellier, France ; ³ INRAE, Montpellier, France ; ⁴ IRD, Montpellier, France ;

⁵ CIRDES, Bobo Dioulasso, Burkina Faso

Introduction & Objectives:

African Animal trypanosomosis, caused by blood protozoan parasites transmitted mainly by tsetse flies, represents a major constraint for millions of cattle in sub-Saharan Africa. Exposed cattle include trypanosusceptible indicine breeds, severely affected by the disease, and West African taurine breeds called trypanotolerant owing to their ability to control parasite development, survive and grow in enzootic areas. Cattle trypanotolerance is an emblematic example of local adaptation of livestock to a natural selective pressure embodied by a parasitic disease. Our objective was to improve knowledge on gene regulations involved in trypanotolerance by investigating whole blood transcriptome of tolerant and susceptible cattle.

Materials & Methods:

We performed an experimental infection of five cattle breeds, three trypanotolerant taurine breeds (N'Dama, Lagune and Baoulé), one susceptible zebu (Zebu Fulani) and one African taurine x zebu admixed breed (Borgou) by *Trypanosoma congolense*. Whole blood genome-wide transcriptomes were profiled by RNA sequencing at four time points, one before and three during infection.

Results, Discussion & Conclusion:

As expected, infection had a major impact on cattle blood transcriptome regardless of the breed. We confirmed previous findings, naming an early activation of the innate immune response, followed by an activation of the humoral response and an inhibition of T cell functions at the chronic stage of infection. We also highlighted a strong disturbance in host metabolism and cellular energy production that seems to differentiate trypanotolerant and trypanosusceptible breeds. This study showed the strong interplay between immunity and metabolism that could be involved in trypanotolerance.

Vectorial capacity of *Aedes aegypti* in transmitting Lumpy Skin Disease Virus: Insights from experimental infection studies

Elizabeth RIANA^{1, 2, 3} (elizabethriana1994@gmail.com), Chalida SRI-IN³, Sonthaya TIAWSIRISUP³

¹ Parasitology Unit, Department of Pathology, Faculty of Veterinary Science, Chulalongkorn University, Bangkok, Thailand ; ² The International Graduate Program of Veterinary Science and Technology (VST), Faculty of Veterinary Science, Chulalongkorn University, Bangkok, Thailand ; ³ Center of Excellence in Animal Vector-Borne Diseases, Parasitology Unit, Department of Pathology, Faculty of Veterinary Science, Bangkok, Thailand

Introduction & Objectives:

Lumpy skin disease virus (LSDV) is a transboundary viral disease affecting cattle, water buffalo, and wild ruminants. It has recently spread in Asia and Europe, with limited knowledge of its transmission. Thereby, we aim to explore the vectorial capacity of *Aedes aegypti* in transmitting LSDV.

Materials and Methods:

Unfed female *Ae. aegypti* were exposed to an infected blood meal with three concentrations ($10^{2.7}$, $10^{3.7}$, $10^{4.7}$ TCID₅₀/mL). After an hour of feeding, fully engorged mosquitoes were kept in cardboard cups for up to 14 days. A total of 30 mosquitoes were collected at each time point until 14 days post-infection (dpi). LSDV detection utilized conventional PCR targeting the B22R gene. Infection, dissemination, and transmission rates from different titers were compared using Chi-Square in GraphPad Prism.

Results, Discussion & Conclusion:

LSDV was detectable at each time point up to 14 dpi. The infection, dissemination, and transmission rates of $10^{4.7}$ TCID₅₀/mL were significantly higher than $10^{2.7}$ and $10^{3.7}$ TCID₅₀/mL at 2 dpi (p -value < 0.05). From 8 to 14 dpi, transmission and infection rates at $10^{4.7}$ TCID₅₀/mL were significant compared to those at $10^{2.7}$ TCID₅₀/mL. LSDV DNA was present in the saliva from 2 dpi onward, after ingested blood meal concentrations of $10^{3.7}$ and $10^{4.7}$ TCID₅₀/mL. The sustained presence of the virus until 14 dpi suggests a complex interaction between the virus and the mosquito. These findings highlight the potential vector competence of *Ae. aegypti* for LSDV.

Investigation of African Trypanosomiasis in the ruminant population of Trinidad and Tobago

Karla GEORGES¹ (karla.georges@sta.uwi.edu), Candice SANT², Winthrop HAREWOOD², Anil PERSAD², Marc DRISCOLL², Michael MORRIS², David KANGALOO³, Simone TITUS⁴, Christopher OURA²

¹ School of Veterinary Medicine, University of the West Indies, Mt Hope, Trinidad and Tobago (+1 868), Trinidad & Tobago ; ² School of Veterinary Medicine, University of the West Indies, Mt Hope, Trinidad & Tobago ; ³ Ministry of Agriculture Land and Fisheries, Port of Spain, Trinidad & Tobago ; ⁴ Ministry of Agriculture Land and Fisheries, Chaguana, Trinidad & Tobago

Introduction & Objectives:

The ongoing humanitarian crisis in Venezuela precipitated an increase in movement of people and livestock from Venezuela to Trinidad, a distance of seven kilometers. Two predominant species of African trypanosomes of ruminants in South America are *T. evansi* and *T. vivax*, both transmitted by biting dipteran flies. This study is of importance as both *T. vivax* and *T. evansi* have been detected in man. The objective of this study was to determine whether these African trypanosomes are present in the ruminant population of Trinidad and Tobago.

Materials & Methods:

Blood was collected from 371 goats, 331 sheep and 435 cows throughout Trinidad and Tobago and analysed by microscopy, PCR followed by sequencing.

Results:

Trypanosomes were detected on microscopic examination of blood smears from two goats and one sheep. Examination of the wet mount showed progressive forward motility characteristic of *T. vivax*. Conventional PCR and sequencing revealed that 6 goats (1.62%), 5 sheep (1.51%) and 3 cows (0.69%) were positive for *T. vivax*. Positive animals were located at 3 different sites in Trinidad. *T. evansi* was not detected.

Discussion & Conclusion:

This is the first investigation of African trypanosomiasis in the ruminant population of Trinidad and Tobago. Positive animals were suspected of being illegally imported or in close association with animals suspected of arriving illegally into Trinidad. The results demonstrate the need to establish early warning systems which include ongoing surveillance to detect transboundary diseases that have the potential to affect the health of both animals and humans.

Rodents as potential reservoir hosts for *Anaplasma* spp. at the human-livestock-wildlife interface of the Mnisi community, South Africa

S. Marcus MAKGABO^{1,2} (marcusmakgabo.mm@gmail.com), Gilbert KAMGAN-NKUEKAM¹, Kelly A. BRAYTON^{1,3}, Dina M. FAGIR¹, Marinda C. OOSTHUIZEN^{1,4}, Nicola E. COLLINS^{1,4}

¹ Department of Veterinary Tropical Diseases, University of Pretoria, Pretoria, South Africa ; ² Department of Life and Consumer Sciences, University of South Africa (UNISA), Roodepoort, South Africa ; ³ Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, Washington, United States ; ⁴ Centre for Veterinary Wildlife Research, University of Pretoria, Pretoria, South Africa

Rodents are reservoir hosts for many pathogens and play a key role in the circulation of viral, bacterial, and parasitic infections. *Anaplasma* species are widely distributed in a variety of vertebrate hosts. Although *A. bovis* and *A. phagocytophilum* have previously been reported in rodents in South Africa, the role of small mammals in the distribution of *Anaplasma* spp. has yet to be extensively explored. In the Mnisi Community, Mpumalanga, rodents are widespread and frequently found in and around households. The presence of *Anaplasma* species in rodents in the Mnisi Community over three years (2019-2021) was examined. Genomic DNA was extracted from 168 rodents of various species captured from villages and the Manyeleti Game Reserve. The full-length 16S rRNA gene was amplified for sequencing on a Pacific Biosciences platform. More than 31,000 sequence reads classified in the genus *Anaplasma* from 35 *Anaplasma*-positive samples revealed the presence of 16S rRNA sequences with 99.77% and 99.85% sequence identity to those from the *A. centrale* vaccine strain and *A. platys*, respectively, as well as a sequence closely related to the *A. bovis* 16S rRNA sequence, with 98.15% identity. Since some distinct *Anaplasma* spp. have more than 98.7% sequence identity, whether these sequences represent novel species or variants of known species must be clarified. Sequence data from other genes will clarify the phylogenetic classification of the species identified. Our findings demonstrate abundant *Anaplasma* sequences in rodents and contribute to the limited information on rodents as potential reservoir hosts of *Anaplasma* spp. in South Africa.

Expanding the detection and surveillance of ticks and tick-borne diseases in the Caribbean region

Roxanne CHARLES¹ (roxanne.charles@sta.uwi.edu), Mathilde GONDARD², Clemence GALON², Dane HARTLEY³, Paul CROOKS⁴, Patricia POW-BROWN¹, Christopher OURA¹, Emmanuel ALBINA⁵, Sara MOUTAILLER⁶, Karla GEORGES¹

¹ The University of the West Indies, Port of Spain, Trinidad & Tobago ; ² ANSES, Maisons-Alfort, France ; ³ Guyana Livestock Development Authority, Mon Repos, Guyana ; ⁴ Tobago House of Assembly Division of Food Security, Scarborough, Trinidad & Tobago ; ⁵ CIRAD, DGDRS, F-Montpellier, France ; ⁶ Anses, INRAE, EnvA, UMR BIPAR, Maisons-Alfort, France

Introduction:

Ticks and the pathogens they transmit are prevalent in many animal populations across the Caribbean region. There is, however, limited information on the abundance and diversity of the ticks and the tick-borne pathogens they transmit. Therefore, there is a need for a regional surveillance system to obtain epidemiological data that can aid in the management and control of ticks and tick-borne diseases of animals, and by extension humans, in the Caribbean.

Materials & methods:

Four Caribbean/associated territories (St. Lucia, Trinidad, Tobago and Guyana) were targeted in this study. A total of 217 *Rhipicephalus sanguineus*, 244 *Rhipicephalus microplus*, three *Amblyomma cajennense*, 21 *Amblyomma ovale* and one *Amblyomma variegatum* were screened for pathogens using a high-throughput microfluidic real-time PCR system, designed for screening known bacterial and protozoan tick-borne pathogens.

Results:

The system detected 15 species of pathogens belonging to eight genera including bacteria (*Anaplasma marginale*, *Anaplasma platys*, *Borrelia* spp., an uncultured *Ehrlichia* spp., *Ehrlichia canis*, *Francisella* spp., *Rickettsia felis* and *Rickettsia africae*) and protozoa (*Babesia bovis*, *Babesia bigemina*, *Babesia vogeli*, *Theileria equi*, *Theileria mutans*, *Theileria velifera* and *Hepatozoon canis*). Further, conventional PCR and sequencing confirmed the presence of DNA of most of the aforementioned pathogens.

Conclusion:

The high diversity of pathogens detected in this study, some with veterinary and public health importance, highlights the need for an efficient and rapid Caribbean regional surveillance system to be set up for the detection of ticks and tick-borne microorganisms. This would better inform and improve disease control and prevention strategies.

Development of a pan-species ELISA test for detection Heartwater across mammals

Valérie RODRIGUES^{1, 2} (valerie.rodrigues@cirad.fr), Laetitia VIRY¹, Alexis MONTEIL³

¹ ASTRE, CIRAD, Petit Bourg, Guadeloupe, France ; ² Université de Montpellier, CIRAD, Montpellier, France ; ³ IUT Lyon, Villeurbanne, France

Heartwater is a fatal disease of ruminants, caused by an intracellular bacterium *Ehrlichia ruminantium*, and transmitted by the *Amblyomma* tick in Africa, Indian Ocean and Caribbean Islands, especially Guadeloupe and Antigua. The disease impacts both domestic animals and wildlife, including giraffes, antelopes, and buffaloes. Traditionally, diagnosis relies on pathogen detection during the symptomatic phase, with serological response observed in animals that recover or exhibit mild effects. Current epidemiological studies and disease surveillance are limited to domestic cattles, goats and sheep with no tests available for other mammalian species. In this study, we develop a pan-species ELISA test capable of detecting antibodies against the MAP1-B protein of *Ehrlichia ruminantium*, applicable to all mammal species except felines. We validated this test on cattle, goat and sheep and also tested it on known negative wildlife samples. The analytical sensibility of the new test is very close to that of existing ELISA tests, maintaining identical specificity. This advancement 1) simplifies the surveillance operations for domestic ruminants and 2) enables the assessment of heartwater seroprevalence worldwide, contributing to improved disease prevention and control strategies.

Epidemiology of livestock-associated ticks and tick-borne pathogens in northern Nigeria

Richard BIRTLES¹ (r.j.birtles@salford.ac.uk), Adamu Haruna MAMMAN², Vincenzo LORUSSO¹, Bushra ALMATROUD¹, Rachael Noyelum AZIKE¹, Kevin BOWN¹, Konto MOHAMMED³, Abraham DOGO²

¹ Human and Natural Sciences, University of Salford, Salford, Greater Manchester, United Kingdom ; ² Department of Veterinary Parasitology and Entomology, University of Jos, Jos, Plateau, Nigeria ; ³ Department of Veterinary Parasitology and Entomology, University of Maiduguri, Maiduguri, Borno, Nigeria

Northern Nigeria is an important hub within a vast regional transboundary livestock trade network through which thousands of animals raised in the semi-arid Sahel pass each year en route to markets in the densely populated coastal regions to the south. This network can facilitate the rapid spread of pathogens across large distances, especially in the absence of any form of importation control at borders. Ticks and tick-borne pathogens present a well-established threat to livestock and human health in the region but almost no work has been done to assess the impact of transboundary livestock trading on their diversity, distribution and epidemiology. This study aimed to establish fundamental information about the diversity of ticks and tick-borne pathogens infesting cattle, camels and equids in key livestock markets in the region. Surveys were carried out in Sokoto, Zamfara and Borno states in Northern Nigeria between 2017 and 2021. The ticks were identified by reference to taxonomic keys and molecular methods (mass spectrometry and DNA barcoding) then screened for apicomplexan parasites and rickettsial pathogens using PCR. A remarkable diversity of ticks were encountered, including numerous *Hyalomma* species typically associated with the Sahel or Saharan regions of north Africa. Numerous *Theileria*, *Babesia* and *Rickettsia* species were detected in these ticks, including *Theileria annulata*, the agent of tropical theileriosis. These results suggest that transboundary livestock trade is playing a role in the distribution of ticks and the pathogens in the region and should therefore be considered in the development of meaningful and effective disease control strategies.

Defining the impact of *Theileria* infection on the regulatory landscape of bovine lymphocytes

Rachel OWEN¹ (rowen2@exseed.ed.ac.uk), Chumeng ZHU¹, Liam MORRISON^{1,2}, Tim CONNELLEY^{1,2}, Musa HASSAN^{1,2}, James PRENDERGAST^{1,2}

¹ The Roslin Institute, University of Edinburgh, Edinburgh, Midlothian, United Kingdom ; ² The Roslin Institute, Centre for Tropical Livestock Genetics and Health, Edinburgh, Midlothian, United Kingdom

Theileria parva, a tick-borne parasite prevalent across sub-Saharan Africa, is the causative agent of East Coast fever, a severe lymphoproliferative disease of cattle responsible for the deaths of over 1 million animals each year [1]. The mechanisms underlying the cellular transformation and associated pathology caused by *T. parva* are poorly understood, and how the parasite co-opts the host proliferative machinery is not well defined. Heritable tolerance to *T. parva* infection has been described, but the mechanisms of this tolerance are not known, limiting the implementation of effective selective breeding [2].

Most phenotypic variation is driven by variation in regulatory regions of the genome [3], and consequently understanding the relationship between important phenotypes and their regulatory control is key to implementing effective measures to improve livestock health and production. Using PRO-Cap, an RNA sequencing method effective at capturing enhancer activity, we have generated matched libraries for naïve and *T. parva* infected CD4+, CD8+ and $\gamma\delta$ T-cells; and B cells. This has allowed us to define the regulatory landscape of bovine immune cell subsets, and identify which regulatory elements respond to infection with *T. parva* in different cell types. This data provides important insights into the mechanisms of *Theileria* induced cellular transformation and the host immune response, and aids in the prioritisation of key genomic regions for targeted downstream analysis to improve treatment, vaccination and selective breeding programmes.

References:

1. Surve et al. (2023) Front Vet Sci.
2. Wragg et al. (2022) PLoS Genet.
3. Albert and Kruglyak (2015) Nat Rev Genet.

Secreted *Theileria annulata* effector protein Ta9 binds and potentially activates proto-oncogenic macrophage Hck

Shahin TAJERI¹ (shahin.tajeri@fu-berlin.de), Andreas NERLICH², Jane KINNAIRD³, Khawla ELATI¹, Brian SHIELS³, Gordon LANGSLEY⁴, Ard NIJHOF¹

¹ Freie Universität Berlin, Institute for Parasitology and Tropical Veterinary Medicine, Berlin, Germany ; ² Veterinary Centre for Resistance Research, Berlin, Germany ; ³ University of Glasgow, School of Biodiversity, One Health and Veterinary Medicine, Glasgow, United Kingdom ;

⁴ Laboratoire de Biologie Comparative Des Apicomplexes, Faculté de Médecine, Cochin Institute, Paris, France

In tropical theileriosis of cattle, a major driver of pathology is the transformation of host macrophages by the intracellular apicomplexan parasite *Theileria annulata*. In *Theileria*-transformed leukocytes several oncogene-associated signalling pathways, such as Activator Protein 1 (AP-1) and c-Myc are constitutively activated in a parasite-dependent manner. We have previously shown that the proto-oncogene haematopoietic cell kinase (Hck) of the Src family of non-receptor tyrosine kinases is constitutively active in *T. parva*-transformed B cells and contributes to AP-1-driven transcription. Ta9 is a *T. annulata* secreted protein that we have shown capable of stimulating AP-1-driven transcription raising the possibility that Ta9 might do so by augmenting Hck signalling. Using two independent anti-Hck antibodies we now demonstrate co-localization of Ta9 with the active form of Hck in/on cytoplasmic vesicle-like structures that we have shown to be the host mitochondria. Overexpression of full-length GFP-tagged Ta9 in mouse 3T3 cells results in the appearance of numerous spike-like membrane protrusions ('hairy phenotype') and dorsal ruffles. These results are consistent with Ta9 binding to and activating Hck. Treatment of *T. annulata*-infected macrophages with a selective Hck inhibitor (A419219) negatively impacted on the parasite-dependent transformed phenotype, as estimated by cell proliferation and soft agar colony formation assays. Potential modulation of host mitochondria function by the Ta9/Hck complex is currently being investigated.



ABSTRACTS FRIDAY 24 MAY





Teaching and continuing Education in Tropical Veterinary Medicine



One Health and Veterinary Medicine Education: when research meets co-learning

Olivier SPARAGANO (olivier.sparagano@rau.ac.uk)

Agricultural Sciences and Practice, Royal Agricultural University, Cirencester, United Kingdom

Veterinary Medicine Education has been evolving not only because of new knowledge being created but also because new clinical techniques and teaching methods. Teaching methods have evolved due to pedagogical research on student learning outcomes taking them from passive learning to directed learning to co-learning alongside self-learning. Peer and self-assessment are now being introduced to prepare them to assess each other and their future peers and staff (Mills *et al*, 2022). Finally, AI and virtual reality have entered the curriculum to help students towards complex and international situations through virtual reality (VR) and augmented reality (AR).

A different educational/reputational/commercial driver would be if veterinary education establishments (VEEs) have the resources (staff, facilities, funding) to develop modern learning environment. Sometimes such drivers could be due to a strategic goal to get international accreditations (AVBC, RCVS, AAVMC, EAEVE), then non-curriculum standards and criteria are added to obtain such accreditation to recognize the Day 1 competencies (D1Cs) of our graduates.

Veterinary medicine has also co-evolved due to the changes in the relationship we had with animals (from cancer-, covid19- sniffing dogs to the use of animals in hospitals for palliative and end-of-life patients creating also new risks of diseases and traumas for animals not experienced before by veterinarians) and how the society changed its perception on animals, humans and the environment (One Health concept).

One Health can now be fully integrated into our Veterinary Medicine curriculum while veterinarians and animal scientists can support the One Health Agenda in return (VSC, 2014).



SESSION 8

Drug Resistance



Characterization of antimicrobial resistance integrated surveillance in CaribVET's network

Tennille AUGUSTE¹ (Tennille.Auguste@sta.uwi.edu), Joel CAMACHO², Eric ETTER³, Lisa BENJAMIN¹, Devon SEUNARINE⁴, Robyn JOSEPH⁵, German VASQUEZ⁶

¹ CaribVET/The University of the West Indies, Champs Fleurs, Trinidad & Tobago ; ² CaribVET, Mexico City, Mexico ; ³ CIRAD/CaribVET, Petit Bourg, Guadeloupe ; ⁴ CaribVET/Tuskegee University College of Veterinary Medicine, Tuskegee, USA ; ⁵ Ministry of Agriculture, Fisheries, Food Security and Rural Development, Castries, St. Lucia ; ⁶ CaribVET, Rio de Janeiro, Brazil

Introduction & Objectives:

Antimicrobial resistance (AMR) represents a global health problem due to the impact on human, animal, and environmental health. Integrated surveillance is one of the fundamental methods to obtain information to measure the magnitude of the problem and design and implement actions to contain it, under a One Health approach. The objective of this study was to analyze the level of advancement of different sectors to achieve integrated surveillance on AMR in the Caribbean Animal Health Network (CaribVET) countries.

Material & methods:

Instruments were designed to characterize the progress in integrated surveillance on AMR, as well as the main challenges for its formalization related to animal, food, and/or the environmental sectors. Ninety participants from various Caribbean countries and territories received questionnaires. Participants were sampled using a combination of convenience and snowballing techniques. Data was analyzed using a combination of quantitative and qualitative analytical methods.

Results:

Partial results have been obtained to date. Stakeholders from twelve countries replied to the different questionnaires. Only four countries reported having an integrated AMR monitoring protocol or are working on a draft. The main challenges faced by all participating countries or territories are availability of financial resources as well as governance in the field of One Health and AMR.

Conclusions:

The formalization of antimicrobial resistance surveillance requires specific governance for each sector. The National Action Plans to control AMR developed by each country are key documents that might foster each sector's governance and capabilities in order to have structured resources and ensure sustainability.

S8-02

Domestic carnivores as sentinel for antimicrobial resistance surveillance in French overseas territories; example of La Réunion

Cécile SQUARZONI¹ (cecile.squarzoni@cirad.fr), Katerina ALBRECHTOVA², Clement RABALY², Axelle SELLIER², Cléa MARINES--CARBONEILL², Anaïs ETHEVES², Olivier BELMONTE³, Thomas GARRIGOS³, Guillaume MILTGEN³, David WILKINSON²

¹ ASTRE, Cirad, Saint-Denis, La Réunion, France ; ² ASTRE, Cirad, Saint-Denis, France ; ³ Centre Hospitalier Universitaire, Saint Denis, France

The sentinel potential of domestic carnivores in frame of antimicrobial resistance monitoring had recently received considerable attention. Analogical approaches are used to surveillance of antimicrobial resistance; dogs and cats can stand at the crossroads between human and animal life and the environment, facilitating the inter-compartmental transmission of antimicrobial resistance. Geographically speaking, La Réunion also stands at the crossroads ; a small island in the south-west part of the Indian Ocean represents a fusion of African, Asian and European cultures, trade routes and microbes. Its population of dogs and cats is a phenomenon not to be ignored by epidemiologists; the ratio of domestic carnivores to the human population is 4 times higher as compared to Europe. These animals often roam free, interact with rodents and birds and scavenge for food in waste disposal before regaining close proximity to people.

Using the Nanopore sequencing we explored the role of domestic carnivores (study population of 950 individuals, including stray, free-roaming and home-confined animals) in the transmission and dissemination of antibiotic resistance genetic determinants. We found that 8 % of healthy dogs and cats living in the island carry extended-spectrum beta-lactamases-producing Enterobacteriaceae. More alarmingly, carbapenemases were detected in two dogs. Our comparison of the genetic background of these animal-originating multiresistant isolates to phenotypically similar Enterobacteriaceae detected in human population indicates that a substantial part of animal-carried resistant strains might originate from human population. These findings highlight the importance of environmental contamination as a pathway of antimicrobial resistance spread, and the role of domestic carnivores therein.

CANCELED

Medically rational use of antibiotics for reducing resistance and supporting effective animal production in low- and middle-income countries

Ulf MAGNUSSON (ulf.magnusson@slu.se)

Department of Clinical Science, Swedish University of Agricultural Sciences (SLU), Uppsala, Sweden

Antibiotic resistance is a kind of drug resistance that threatens both human and animal health as the same kinds of drugs are used and since many bacteria are zoonotic. The global livestock sector is the largest user of antibiotics and because the use of antibiotics drives the emergence of resistance it is crucial to reduce the use in the sector for the sake of animal and public health. Countries are therefore setting up regulations such as banning the use of antibiotics as feed additives for growth promotion, demanding veterinary prescription for sale of antibiotics and restrictions on use of antibiotics critical for human medicine.

However, the compliance to, and enforcement of, such regulations are sometimes limited in resource-poor settings. We have therefore identified an approach that complements these regulations and has proven to reduce the use of antibiotics with maintained animal productivity which is more appealing to farmers. The approach, about how to use antibiotics in a medically rational way, is based on effective health management routines and biosecurity and has been promoted by FAO, CGIAR and in one international on-line course.

Knowledge and awareness among farmers don't, however, always lead to changed behaviors. Therefore more economics and social science must be integrated into veterinary medicine in search for effective incentives for medically rational use of antibiotics in livestock.

References:

1. Magnusson & Nohrborg, 2018. "Effective Livestock Production with low use of Antibiotics".
2. <https://www.futurelearn.com/courses/effective-livestock-production>.
3. Magnusson, et al. 2019. FAO Animal Production and Health Manual 23. Rome. FAO.
4. <https://www.fao.org/3/ca6729en/CA6729EN.pdf>

Multi-resistance of *Rhipicephalus microplus* to amitraz, alpha-cypermethrin, and ivermectin on livestock in Ecuadorian subtropical farms

Ximena PÉREZ-OTÁÑEZ¹ (ximena.perezotanez@student.uclouvain.be), Richar RODRÍGUEZ-HIDALGO², Valeria PAUCAR-QUISHPE³, Linette JÁCOME², Lenin RON-GARRIDO², Sophie O. VANWAMBEKE¹

¹ Centre for Earth and Climate research., Université Catholique de Louvain, Ottignies-Louvain-La-Neuve, Belgium ; ² Instituto de Investigación en Zoonosis (CIZ), Universidad Central del Ecuador, Quito, Ecuador ; ³ Unit of Epidemiology and Risk Analysis applied to Veterinary Sciences, University of Liege, Liege, Belgium

Cattle ticks, primarily *Rhipicephalus microplus*, stand as the predominant overlooked ectoparasites in subtropical regions globally, significantly impacting meat and milk production and resulting in economic losses for cattle farmers. These ticks also serve as crucial vectors for pathogens like *Anaplasma* spp. and *Babesia* spp. Given Ecuador's conducive climate for tick development, acaricides have emerged as the primary method for tick control. However, their misuse has contributed to the development of resistance and multi-resistance in ticks. The effectiveness of acaricides has steadily declined in Ecuador. This study aims to assess resistance to amitraz, alpha-cypermethrin, and ivermectin. The focus is on Noroccidente de Pichincha over two years, utilizing the Larval Package Test (LPT). In the sampling conducted in 2020-2021 across 61 farms. Resistance was observed in 67.21% (41/61), 67.21% (41/61), and 57.38% (35/61) of *R. microplus* ticks to amitraz, alpha-cypermethrin and ivermectin, respectively. In the subsequent round one year later 2021-2022, resistance levels were 59.57% (28/47) for Amitraz, 68.09 (32/47) for alpha-cypermethrin, and 57.45% (27/47) for ivermectin. The percentage of multi-resistance for the first year was 67.21% (41/61), and for the second year, it was 65.96% (34/47). This study underscores the pervasive issue of tick resistance to acaricides in Ecuadorian cattle farming for the assessed products. Notably, there was no significant decrease in resistance between the two surveyed years, highlighting the urgent need to collaborate with farmers to evaluate and enhance practices, ensuring the sustained efficacy of active principles and the availability of acaricide control options.

On the current resistance situation of Triclabendazole against *Fasciola hepatica* in German sheep flocks

Alexandra KAHL¹, Jürgen KRÜCKEN¹, Christina HELM¹, Jane HODGKINSON², Diana WILLIAMS²,
Wiebke WEIHER³, Werner TERHALLE⁴, Martin GANTER⁵, Georg VON SAMSON-HIMMELSTJERNA¹,
Stephan STEUBER³ (stephan.steuber@bvl.bund.de)

¹ Institute for Parasitology and Tropical Veterinary Medicine, Freie Universität Berlin, Berlin, Germany ; ² Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, Liverpool, United Kingdom ; ³ Unit 314/Department 3 - Veterinary medicines, Federal Office of Consumer Protection and Food Safety (BVL), Berlin, Germany ; ⁴ Unit 334/Department 3 - Veterinary medicines, Federal Office of Consumer Protection and Food Safety (BVL), Berlin, Germany ; ⁵ Clinic for Swine and Small Ruminants, Forensic Medicine and Ambulatory Service, University of Veterinary Medicine, Hannover, Hannover, Germany

Introduction & Objectives:

Fasciola hepatica is a zoonotic pathogen that infects primarily sheep and cattle. Originally native to Europe it has meanwhile spread to tropical regions also in Africa. The preferred treatment option is the benzimidazole triclabendazole, which is, unlike other fasciolicides, effective against all juvenile stages of the liver fluke. Nevertheless, decades-long use of triclabendazole has led to numerous reports of resistance but efficacy data from Germany are lacking. The aim of the study was to obtain information on the current resistance situation on German sheep farms.

Materials & Methods:

Faecal samples from 71 sheep farms were coproscopically screened for the presence of *F. hepatica* eggs. Due to low egg shedding intensity in most sheep, the efficacy of triclabendazole was then evaluated in eleven flocks on D+14 post treatment with a coproantigen ELISA applied in parallel to faecal egg counting.

Results:

Out of 1673 sheep investigated, 214 animals (12.8%) from 25 farms (35.2%) tested positive for *F. hepatica* eggs in their faeces. Eggs of rumen trematodes (Paramphistominae) were found in 81 sheep (4.8%) from 11 farms (15.5%) as well. In one out of the 11 farms examined for triclabendazole efficacy, a considerable lack of efficacy (0%) was noted, leading to a high number of sudden deaths due to acute fasciolosis. Subsequent re-treatment with closantel, however, was highly effective.

Discussion & Conclusion:

Currently, triclabendazole resistance does not appear to be very widespread in German sheep farming. However, as soon as this occurs, it may have fatal consequences for animal health.

Phenotypic and genotypic characterization of pyrethroid resistant stable fly (*Stomoxys calcitrans*) populations on German dairy farms

Ricarda DAHER¹, Stefan FIEDLER², Burkhard BAUER¹, Wiebke WEIHER², Stephan STEUBER², Ard M. NIJHOF³, Jürgen KRÜCKEN¹, Peter-Henning CLAUSEN¹ (peter-henning.clausen@fu-berlin.de)

¹ Institute for Parasitology and Tropical Veterinary Medicine, Freie Universität Berlin, Berlin, Germany ; ² Federal Office of Consumer Protection and Food Safety, Berlin, Germany ; ³ Veterinary Centre for Resistance Research, Freie Universität Berlin, Berlin, Germany

Introduction:

Stable flies are biting insects that disturb the well-being of livestock and severely affect their productivity worldwide. Excessive use of pyrethroids against insects has resulted in widespread resistance. Pyrethroid resistance in stable flies has been associated with *kdr* (L1014F) and *kdr-his* (L1014H) mutations in the voltage-sensitive sodium channel (*vssc*) gene.

Objectives:

This study aimed to examine the correlation between pyrethroid resistance and the *vssc* genotype (*kdr* and *kdr-his*) in stable flies and to screen German stable fly populations for *kdr* and *kdr-his* mutations.

Materials & Methods:

Stable flies were collected from four dairy farms in Brandenburg. They were tested against deltamethrin and genotyped using PCR amplification of specific alleles (PASA). Using pooled stable fly samples collected from 65 dairy farms in Germany in 2019, deep amplicon sequencing of the *vssc* gene was used to investigate the frequency and diversity of resistance alleles.

Results:

The four tested field populations were identified as being phenotypically resistant to deltamethrin, with LD50 values of 18.3, 19.7, 40.6 and 47.4 ng deltamethrin/fly – 46.1 to 119.5-fold higher than for a susceptible laboratory strain. PASA showed the presence of *kdr* and *kdr-his* genotypes in all field populations. Deep amplicon sequencing revealed the presence of *kdr* and *kdr-his* variants on 100% of the farms with up to 55% of *kdr* and 85% of *kdr-his* alleles on individual farms.

Conclusion:

Pyrethroid resistance genotypes are widespread in stable fly populations on German dairy farms. Deep amplicon sequencing assays will allow screening for pyrethroid resistance markers on a nation-level scale.

Unravelling the socioeconomic factors linked to antibiotic use in poultry farms: a qualitative study in the Analamanga region, Madagascar

Sophie MOLIA¹ (sophie.molia@cirad.fr), Ilo TSIMOK'HAJA RAMAHATAFANDRY², Michel RAKOTOHARINOME², Alexandre HOBEIKA³, Muriel FIGUIÉ^{4, 5}, Daouda KASSIÉ^{6, 7}

¹ ASTRE, CIRAD, Montpellier, France ; ² Department of Veterinary Services, Ministry of Livestock Production, Antananarivo, Madagascar ; ³ UMR MOISA, CIRAD, Montpellier, France ; ⁴ UMR MOISA, CIRAD, Maputo, Mozambique ; ⁵ Centro de Analise das Politicas, Universidade Eduardo Mondlane, Maputo, Mozambique ; ⁶ ASTRE, CIRAD, Antananarivo, Madagascar ; ⁷ Pasteur Institute of Madagascar, Antananarivo, Madagascar

Introduction:

Antimicrobial resistance is a global public health threat mainly caused by the massive use and misuse of antimicrobials. Addressing the animal health part of this issue is challenging in low-and-middle-income countries where information is scarce regarding access and use of veterinary drugs. Our objective was therefore to investigate the socio-economic factors of antibiotic use in poultry farms of Madagascar.

Methods:

We conducted semi-structured interviews with 79 poultry farmers in the Analamanga region in April 2023. Thematic analysis was used to extract the perceptions and practices related to veterinary care, the supply and uses of veterinary medicines.

Results & Discussion:

The majority of poultry farmers had received little livestock training and raised poultry as a side job. Most farmers had very basic knowledge of diseases and treatments. They relied on varied sources of advice for how to take care of poultry: feed/chicks/drug suppliers, technicians, veterinarians, other farmers and family members in decreasing order. Access to veterinary drugs was easy, without prior clinical examination and without prescriptions. Vitamins and antibiotics were the most commonly used medication. Many constraints (food price, quality of inputs, poor selling conditions) limited the financial capacity of farmers to invest in good practices (hygiene, disinfection, vaccination...). Farmers tended to agree with the idea of using fewer antibiotics in the future but this was mainly driven by the prospect of reducing costs than of preserving public health. In conclusion, good antibiotic use should be promoted through feed/chicks/drug suppliers to maximize efficiency in contexts of poor farmers' professionalization.



ABSTRACTS POSTERS



Adoption study of a networking tool to facilitate collaborations (Too Cool)

Mamadou Alimou BARRY^{1,2} (barryalim91@gmail.com), Tagne Mouaffo STÉPHANE ROMÉO^{1,2},
Nicolas ANTOINE-MOUSSIAUX^{1,2}, Simplicie Assomption YAMEOGO¹, Jennifer PRADEL^{2,3}

¹ Faculty of Veterinary Medicine, University of Liège, Fundamental and Applied Research for Animals and Health, Liege, Belgium ; ² ASTRE, Univ Montpellier, CIRAD INRAE, Muse, Montpellier, France ; ³ CaribVET, Caribbean Animal Health and Veterinary Public Health, Petit Bourg, Guadeloupe

Introduction:

Interdisciplinary and cross-sectoral research/development networks involving wide-ranging partnerships locally and regionally have been booming under the One Health (OH) impetus. However, operationalizing OH is challenging due to many obstacles, including the lack of supporting infrastructures with shared organizational and management practices enabling more effective collaborations. The “Too Cool” tool has been designed based on a decade of experience in health in the Caribbean to facilitate networking and organizing links between projects, initiatives and regional networks.

In a context where online collaboration is becoming increasingly important for teams and organizations, understanding the factors influencing the adoption of such a tool is essential to improving collaboration practices, in health and in other agriculture/environment sector mobilising integrative approaches.

Objectives:

A study to analyse the tool’s adoption process begins in April 2024 to assess the tool’s usefulness and interest for a variety of stakeholders in various geographical and partnership settings.

Materials & Methods:

A qualitative approach based on semi-structured individual interviews will be implemented with professional animators of partner networks. The participants, volunteers wishing to improve the collaborative dimension of their work, will be trained in the use of the tool beforehand.

The Unified Theory of Acceptance and Use of Technology (UTAUT) as a conceptual framework to guide the analysis. We will use both deductive and inductive approach for the thematic analysis.

Expected results:

A thorough understanding of the motivations, perceptions and key factors influencing adoption should inform the tool’s deployment strategy and the associated capacity-building component to improve collaborative practices.

Circulation of multi-resistant bacteria in humans and animals in the urban area of Lome in Togo

Esso-tchella Madera BODOMBOSSOU (maderabodombossou@gmail.com), Andrea APOLLONI, Alexis DELABOUGLISE, Eric CARDINALE

ASTRE, CIRAD, Montferrier-sur-Lez, France

Introduction:

The circulation of Multi-Drug-Resistant Bacteria (MRB) is a growing public health concern in sub-Saharan Africa. Our study aimed at characterizing the multi-resistant bacteria strains present in the humans and domestic animals of the urban region of Lome, in Togo, and identifying their transmission pathways.

Objectives:

the study aimed to (1) estimate the prevalence of digestive carriage of Extended-Spectrum Beta-Lactamase (ESBL) and Carbapenemase-Producing Enterobacteriaceae (CPE) in patients of the University Hospitals of Lomé and in livestock farmers and pet owners and their animals living in the neighbourhood of patients identified as carriers of ESBL and CPE; (2) identify risk factors associated with the carriage of ESBL and CPE in animals.

Materials & Methods:

Faecal samples were collected from volunteer hospitalized patients. Pet owners and farmers living near the patients were contacted. Among them, those who agreed to participate were sampled and interviewed to collect data on potential risk factors associated with the carriage of ESBL and CPE. Stool samples were also collected from pets and livestock in the farms.

Results:

The study preliminary analyses reveal an overall prevalence ESBL and CPE of carriage in hospital patients of 63.9% and 8.3%, respectively, with variations between admission and patient discharge. In animals, the overall prevalence of ESBL and CPE carriage is 91.8% and 4.1%, respectively, with a higher prevalence of multi-resistant bacteria in small ruminants (51.9%) and poultry (35.2%) compared to other species. Among livestock farmers, the overall prevalence of ESBL and CPE carriage is 69.1% and 22.6%, respectively.

Do Malagasy dogs sound the epidemiological alarm bell?

Herilantonirina Solotiana RAMAROSON^{1,2,3} (herilantonirina_solotiana.ramaroson@cirad.fr), Benoît DURAND⁵, Jeff Rambinisoa FOCK², Najaina Vatosoa RABEMANANJARA², Tiana SOLOFOARILALA², Daouda KASSIE^{1,3}, Vincent LACOSTE⁴, Soa Fy ANDRIAMANDIMBY⁴, Modestine RALINIAINA², Claude Arsène RATSIMBASOA⁶, Véronique CHEVALIER^{1,3}, Laure CHEVALIER¹

¹ UMR ASTRE, CIRAD, Montpellier, France ; ² Département de Recherches Zootechniques, Vétérinaires et Piscicoles, FOFIFA, Antananarivo, Madagascar ; ³ Unité d'Epidémiologie et de Recherche Clinique, Institut Pasteur de Madagascar, Antananarivo, Madagascar ; ⁴ Unité de Virologie, Institut Pasteur de Madagascar, Antananarivo, Madagascar ; ⁵ Unité EPIMIM, ANSES-ENVA, Maisons Alfort, France ; ⁶ Centre National d'Application des Recherches Pharmaceutiques, Antananarivo, Madagascar

Introduction & Objectives:

The canine population is remarkably abundant in Malagasy communities, with the majority of dogs roaming freely without any restriction. Given the country's limited investment in the health sector, this study aims to investigate dogs as indicators of potential zoonotic pathogen circulation, contributing to the enhancement of early warning systems. Rift Valley fever virus (RVFV) and West Nile virus (WNV) were considered as first models.

Methodology:

Blood samples were collected from dogs in the Ifanadiana and Fianarantsoa I districts and analysed at the Virology Unit of the Institut Pasteur de Madagascar. ID Screen WNV ELISA Competition Multi-species kit was used for the detection of antibodies directed against Flaviviruses and ID Screen RVFV ELISA Competition Multi-species kit for the detection of antibodies directed against RVFV. A first identification of factors influencing dogs' exposure to these pathogens was then carried out using logistic regression.

Results:

These screenings revealed a flavivirus seroprevalence of 56.55%, significantly higher in rural areas (410/577) than in urban areas (56/247): $p = 2.2e-16$. RVFV seroprevalence was 3.39%, notably higher in rural areas (27/578) than in urban ones (1/247): $p = 0.001$. Dogs' exposure to these pathogens increased with age, suggesting an endemic transmission.

Further serological analysis based on Luminex technology will enable to distinguish results specific to WNV from other flaviviruses. Furthermore, calculating force of infection and comparing the results with human serological data in the same study area will enable to assess dogs' utility as sentinel animals for monitoring these zoonotic pathogens.

One Health in practice: a socio-ecological approach for the study and management of zoonotic diseases associated with free-roaming dogs in Southeast Asia (SEAdogSEA)

Michel DE GARINE-WICHATITSKY^{1, 2, 3} (degarine@cirad.fr), Anamika KRITIYAKAN^{4, 5}, Wayan Tunas ARTAMA^{6, 7}, Sowath LY⁸, Johan MICHAUX^{1, 3, 9}, Areeya KRIENGUDOM^{2, 4, 5}, Ketsarin KAMYINGKIRD¹⁰, Chuanphot THINPHOVONG^{4, 5}, Kittipong CHAISIRI⁵, Hery WIJAYANTO^{6, 7}, Dya Ayu WIDIASIH^{6, 7}, Pande Made KUTANEGARA^{11, 6}, Khesara Sastrin Prasita NEGARA^{12, 6}, Putu Cri Devischa GALLANTISWARA^{6, 7}, Mia Nur FARIDA^{6, 7}, Muhammad Nur Faiz MAHFUDZ⁶, Muhammd Najib Arung Petana RAJA BONE⁶, Woro LARAS⁶, Ni Nyoman Ayu DEWI¹³, Hélène GUISE^{1, 14, 3}, Heidi AUERSWALD¹⁵, Sopheak SORN⁸, Anan PHONPHOEM¹⁶, Chaiporn JAIKAE¹⁶, Suchaisri LI-ON¹⁶, Aphirak JANSANG¹⁶, Withawat TANGTRONGPAIROJ¹⁶, Marc CHAUMONT¹⁷, Eugenio DIAS RIBEIRO NETO¹⁷, Cyril BARRELET¹⁷, Gérard SUBSOL¹⁷, Pauline VAN LEEUWEN⁹, Thibaut LANGLOIS^{1, 18}, Serge MORAND^{4, 5}

¹ UMR ASTRE, CIRAD, Montpellier, France ; ² CIRAD, Kasetsart University, Bangkok, Thailand ; ³ ASTRE, Univ Montpellier, CIRAD, INRAE, Montpellier, France ; ⁴ Faculty of Veterinary Technology, Kasetsart University, Bangkok, Thailand ; ⁵ HealthDEEP, IRL, CNRS, Kasetsart University, Mahidol University, Bangkok, Thailand ; ⁶ One Health Collaborating Center, Universitas Gadjah Mada, Yogyakarta, Indonesia ; ⁷ Faculty of Veterinary Medicine, Universitas Gadjah Mada, Yogyakarta, Indonesia ; ⁸ Epidemiology and Public Health Unit, Institut Pasteur du Cambodge, Phnom Penh, Cambodia ; ⁹ Laboratory of Conservation genetics, Université de Liège, Liège, Belgium ; ¹⁰ Faculty of Veterinary Medicine, Kasetsart University, Bangkok, Thailand ; ¹¹ Faculty of Cultural Sciences, Universitas Gadjah Mada, Yogyakarta, Indonesia ; ¹² Faculty of Medicine, Universitas Sebelas Maret, Surakarta, Indonesia ; ¹³ Faculty of Veterinary Medicine, Udayana University, Bali, Indonesia ; ¹⁴ UMR ASTRE, CIRAD, Phnom Penh, Cambodia ; ¹⁵ Virology Unit, Institut Pasteur du Cambodge, Phnom Penh, Cambodia ; ¹⁶ Faculty of Agriculture Engineering, Kasetsart University, Bangkok, Thailand ; ¹⁷ LIRMM, Univ Montpellier, CNRS, Montpellier, France ; ¹⁸ MIVEGEC, Univ Montpellier, IRD, CNRS, Montpellier, France

Free-roaming domestic dogs are widespread in SE Asia, occurring in most biomes and interacting with human commensals in many diverse ways. Major public health threats in the region are associated with dogs, but their role in the epidemiology of numerous other zoonotic diseases is still unknown. This depends on a complex interplay between ecological drivers associated with dogs and the habitats in which they roam, and socio-anthropological parameters associated with the humans with whom they interact.

The interdisciplinary projects SEAdogSEA associated several teams from Europe and SE Asia (2019/2023), with the aim to study dog-human-environment interactions and associated epidemiological risks in four villages selected in three countries: Thailand (Nan province), Indonesia (Bali), and Cambodia (Kandal and Stung Treng provinces).

Three main interdisciplinary protocols were carried out: i) Monitoring dog movements and habitat use, mobilising ecology (GPS collars) and socio-anthropology; ii) Assessing dog contact patterns using camera-traps images analysed by Artificial Intelligence for dog re-identification; iii) Pathogen screening (arboviruses, ectoparasites and blood parasites, leptospirosis, ...) and microbiome analysis in dog/dog-owner paired samples.

We present selected results illustrating the complex interplay between dogs' ecology, owners' social characteristics and occupation, and the associated risks of zoonotic diseases (e.g. typology of dog movements/spatial behaviour). Recommendations are given for a more (than) One Health management of sanitary risks associated with domestic dogs in rural and semi-urban settings in SE Asia, including a discussion on the potential use of domestic dogs as sentinels/indicators of the infectious risks to which their owners are exposed.

The underestimated impact of dogs on public health in Southeast Asia: a lexical review

Thibaut LANGLOIS^{1,2} (thibaut.langlois@etu.umontpellier.fr), Michel DE GARINE-WICHATITSKY^{1,3},
Sylvie HURTREZ-BOUSSE^{2,4}

¹ ASTRE, Univ Montpellier, CIRAD, INRAE, Montpellier, France ; ² MiVEGEC, Univ Montpellier, IRD, CNRS, Montpellier, France ; ³ CIRAD, Kasetsart University, Bangkok, Thailand ; ⁴ Department of Biology-Ecology, Faculty of Sciences, Univ Montpellier, Montpellier, France

Introduction & Objectives:

The overall public health impact really attributable to dogs remains difficult to assess in Southeast Asia. This study aims to establish an exhaustive list of zoonotic pathogens carried by dogs in this region of the world where the canine population is primarily incriminated for its role in the spread of rabies. For each of these diseases, we will assess to what extent the dog is responsible for transmission to humans.

Materials & Methods:

For each pathogen, the 100 most cited scientific articles including the words “transmission” and “host” in their abstracts were selected using the Web Of Science data base. The number of mentions of the word «dog» in these abstracts was then compared to the number of occurrences related to other host species. Words relating to the different modes of transmission were also counted, and the public health impact of each disease was assessed using WHO criteria.

Results:

The comparison of references listing zoonotic diseases highlights 139 infectious agents carried by dogs in Southeast Asia. Dogs are particularly incriminated in infections due to bites, but their involvement in the transmission of pathogens via the fecal-oral route and through the ingestion of indirectly contaminated animal product should not be neglected.

Discussion & Conclusion:

Indeed, the dog is the preferential host of numerous emerging parasites released into the environment by the free defecation of animals within inhabited spaces and agricultural areas. Furthermore, the dog constitutes an effective maintenance reservoir which keeps vector-borne pathogens close to humans.

Occurrence of porcine cysticercosis in Burundi

Salvator MINANI^{1,2,3} (sminani@itg.be), Chiara TREVISAN¹, Emma SPIESSENS³, Anastasie GASOGO², Jean-Bosco NTIRANDEKURA⁴, Koen Peeters GRIETENS¹, Sarah GABRIËL³

¹ Department of Public Health, Institute of Tropical Medicine, Antwerp, Belgium ; ² Department of Biology, University of Burundi, Bujumbura, Burundi ; ³ Department of Translational Physiology, Infectiology and Public Health, Ghent University, Ghent, Belgium ; ⁴ Department of Animal Health and Productions, University of Burundi, Bujumbura, Burundi

Background:

Taenia solium is a zoonotic parasite leading porcine cysticercosis in pigs, taeniosis in humans, and (neuro) cysticercosis in humans, a major cause of acquired epilepsy. This study aimed to estimate and compare the prevalence of porcine cysticercosis in slaughtered pigs by meat inspection and partial carcass dissection in Burundi.

Methods:

A cross-sectional study was conducted in Bujumbura city, Kayanza and Ngozi provinces. Multisampling strategies were used to sample 576 pigs. Routine meat inspection was carried out by meat inspectors and the data was recorded. The tongue, heart and masseter of the slaughtered pigs were collected and sliced. Slices of ≤5 mm were made from each organ and muscle, and cysticerci were counted. R software was used for data analysis.

Results:

In total, 576 pigs from Bujumbura city, Kayanza and Ngozi provinces were inspected and dissected. The overall prevalence by meat inspection and partial carcass dissection was 2.4% and 11.6%, respectively. Nearly 72% of dissected pigs had light infections followed by heavy (16.4%) and moderate infections (11.9%). Most of the cysticerci counted were viable (88.3%) and the masseter muscles were the most infected by cysticerci (76.1%) compared to the tongue (18.8%) and the heart (5.1%).

Conclusion:

Partial carcass dissection showed higher sensitivity in detecting infected pigs compared to meat inspection which was only able to detect some moderate and heavy infections. Control strategies following a "One Health" approach are urgently recommended to limit the persistence and transmission of *T. solium* in Burundi.

Local distribution of cattle over Guadeloupe archipelago: an adapted method for disaggregating census dataVictor DUFLEIT¹ (victor.dufleit@cirad.fr), Laure GUERRINI², Eric ETTER¹, Valérie RODRIGUES¹¹ ASTRE, CIRAD, Petit-Bourg, France ; ² ASTRE, CIRAD, Montpellier, France

High resolution gridded livestock distribution data are produced since many years and find applications in diverse sectors such as epidemiology, livestock impact assessment or territory management. Those data are based on census conducted at national/sub-national scale downscaled using machine learning algorithm and relevant spatial predictors. Most known of livestock dataset is Gridded Livestock of the World (GLW; Da Re et al. 2020) who produce 1km resolution maps at continental scale. We propose here an adaptation of the GLW methodology at finer scale for the Guadeloupe archipelago. Cattle census data were collected from local authorities for the 32 municipalities. The Random Forest (RF) algorithm was retained from the previous methodology and Geographical Random Forest (GRF; Georganos et al. 2021) was implemented to compare the predictions of both models. Environmental factors and expert identified predictors were collected or created. A high-resolution land cover database was used to create predictors and suitability rasters. Steps were introduced to the data preparation to deal with potential bias of census data. In order to manage suitability hypothesis on possible breeding area and predictor variability within municipal area, an innovative predictor sampling method is also proposed. Cattle distribution maps were produced with a spatial resolution of 225 m for the whole archipelago of Guadeloupe. GRF algorithm does not performed significantly better than RF with higher processing time. Newly developed predictor sampling methodology also showed advantages over existing models. Importance of predictors was analyzed. The methodology needs to be further explored and possibly applied to other Caribbean islands.

Integrating the One Health perspective for the agroecological transition in a living Lab in Cambodia

Chhuon VANNY¹ (cvanny@rua.edu.kh), Myriam ADAM², Mathilde SESTER², Kimchhin SOK¹, Sophea NHEAN¹, Erwan SACHET², Raphael DUBOZ², Michel DE GARINE-WICHATITSKY²

¹ Faculty of Agricultural Economics and Rural Development, Royal University of Agriculture Cambodia, Phnom Penh, Cambodia ; ² CIRAD, Univ Montpellier, INRAE, Montpellier, France, Montpellier, France

The Santé-Territoires/Healthy-Territories project has launched six living labs in four countries in West Africa and Southeast Asia to study how the One Health concept can be a lever to favor agroecological transitions. The adoption of sustainable and environment-friendly agricultural practices can promote agroecological transition of production systems of rural areas. The One health approach recognizes the interconnectedness between the health of humans, plants, animals and ecosystems. Living Labs are opened innovations that bring together all stakeholders, including farmers, to co-learn, co-experiment, and co-construct innovative solutions.

In Cambodia/Battambang province, the living lab aims to understanding the links between Agroecological Transition and One Health and an overview of the evolution of health indicators during the agroecological transition at the living lab level. The research will discuss the approach that adopt to monitor the impact of agroecological practices implemented by farmers on their perception on One Health.

The Companion Modelling approach will be applied, using tools such as ARDI to define with all stakeholders the actors, resources, dynamics and interaction to better understand the complexity of the system and find appropriate solutions and co-design the local indicators of one health components. The research design will be structured in 3 steps: i) define with all stakeholders and farmers on the potential of solutions for adaptation within the living lab through the exchange knowledge among other farmers; ii) monitoring the field experimentations based on the local indicators; iii) evaluating with the living lab members to improve the eco-health system can be apply in the future.

Characterisation of preputial microbiome of bulls for Bovine Genital Campylobacteriosis (BGC) in association with vaccination and challenge

Mst Sogra Banu JULI¹ (m.juli@uq.edu.au), Hannah V. SIDDLE¹, Mehrnush FORUTAN¹, Ali RAZA^{1,2}, Gry B. BOE-HANSEN^{1,3}, Ala E. TABOR^{1,4}

¹ Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, Queensland, Australia ; ² Department of Veterinary and Animal Sciences, University of Copenhagen, Frederiksberg, Denmark ; ³ School of Veterinary and Animal Science, The University of Queensland, Gatton, Queensland, Australia ; ⁴ School of Chemistry and Molecular Biosciences, The University of Queensland, Brisbane, Queensland, Australia

Bovine genital campylobacteriosis (BGC) is a venereal disease of cattle caused by *Campylobacter fetus* subspecies *venerealis*. Most of the studies regarding reproductive diseases focus on female cattle while the importance of bulls in venereal transmission remains neglected. As bulls are asymptomatic lifelong carriers of BGC and responsible for venereal disease transmission, characterizing the preputial microbiome is warranted to understand the localized immune response.

A total of 23 bulls including young (<3 years) and old (>3 years) were selected and categorised into VibroVax® (Zoetis) vaccinated (V=11) and unvaccinated (UV=12) groups. Both groups were challenged with live *C. fetus venerealis* bacteria (27×10^8 CFU/bull). DNA were extracted from preputial mucus for qPCR screening and sequencing to characterise the preputial microbiome of bulls by 16S rDNA Illumina (V5-V8) and Oxford Nanopore Technology (ONT) adaptive sampling to deplete the host bovine genome.

Microbiome data indicated that Proteobacteria were identified as most abundant, followed by Actinobacteria and Fusobacteria, Firmicutes and Bacteroidetes. Vaccination did not affect the preputial microbiome while changes were observed in both groups after challenge. Adaptive sequencing identified *C. fetus venerealis* with an increased abundance in older bulls than younger following challenge in both vaccinated and unvaccinated groups while qPCR was negative. Decrease of *Pseudomonas* and increase of *Histophilus* also observed after challenge.

Overall, adaptive sequencing was more informative than microbiome analyses and able to identify species rather than only phyla or genus. Adaptive sequencing demonstrated that challenge with *C. fetus venerealis* could lead to potential BGC transmission in older bulls whether vaccinated or not.

***Brucella* driven host N-glycome remodeling controls infection**

Damien MEYER^{1, 2} (damien.meyer@cirad.fr), Qingming QIN³, Paul DE FIGUEIREDO^{3, 4}

¹ UMR ASTRE, CIRAD, Petit-Bourg, Guadeloupe, France ; ² ASTRE, Univ Montpellier, CIRAD, INRA, Montpellier, France ; ³ Department of Molecular Microbiology and Immunology, School of Medicine, The University of Missouri, Columbia, Missouri, United States ; ⁴ Department of Veterinary Pathobiology, The University of Missouri, Columbia, Missouri, United States

Over the past quarter century, powerful methods have been employed to elucidate the global transcriptomic, proteomic, or metabolic responses to infection of host cells by divergent pathogens. In contrast, the response of the host glycome to bacterial infection remains largely unexplored, and hence, our understanding of the molecular mechanisms by which bacterial pathogens manipulate the host glycome to evade or subvert host cell immune functions remains incomplete. Here, we address this gap by performing a systematic analysis of the host glycome during infection by *Brucella* spp., facultative intracellular bacterial pathogens that cause brucellosis, one of the world's most prevalent zoonotic diseases. We found, surprisingly, that a novel *Brucella* Type-IV Secretion System (T4SS) effector protein (EP) Rhg1 induced global reprogramming of the host cell N-glycome to promote bacterial intracellular parasitism. It achieved this remarkable reprogramming by interacting with components of the oligosaccharide transferase (OST) complex that control N-linked protein glycosylation. We also showed that Rhg1 regulates *Brucella* intracellular replication and tissue colonization in a mouse model of brucellosis. Taken together, these findings demonstrate that *Brucella* exploits the EP Rhg1 to reprogram the host N-glycome and promote bacterial intracellular parasitism, thereby providing a novel paradigm for bacterial control of host cell infection.

Infectious diseases management strategies in a ruminant production system: a participatory appraisal of veterinary services delivery performance, and utilization in Ghana

Francis Sena NUVEY (fsnuvey@gmail.com)

Afrique One - REACH, Centre Suisse de Recherches Scientifiques, Abidjan, Côte d'Ivoire

Introduction:

Sustainable livestock production remains crucial for attainment of global food security, climate adaptation, and for safeguarding farmers' livelihoods in developing countries. This study assessed the management strategies farmers adopt for priority infectious animals diseases, and utilization, and performance of veterinary services.

Methods:

We conducted surveys involving 350 ruminant livestock farmers and thirteen professional veterinary officers (VOs), and seven FGDs involving 65 livestock farmers in Ghana. The survey data were analyzed, and distribution of priority diseases, farmers' management strategies and performance of veterinary services described. FGD transcripts were analyzed deductively.

Results:

Almost all farmers (98%) reared small ruminants, with about 25% also rearing cattle. Farmers reported Peste des petits ruminants and mange as priority diseases affecting sheep and goats, while cattle were mainly affected by Foot-and-Mouth Disease and Contagious Bovine Pleuropneumonia. Majority (82%) of farmers used treatment, while only 20% used vaccination services. The antimicrobial medicines used for diseases are poorly controlled by the veterinary system, and mostly wrongly applied by farmers for the target diseases. Farmers primarily use services of informal providers (51%), with only 33% utilizing VOs. Farmers perceived VOs to perform highly on treatment effectiveness, medicines availability and quality, advisory services, competence and service affordability, while informal providers were better in proximity and sociability with farmers.

Conclusions:

Vaccine-preventable diseases hinder livestock production in Ghana. Despite better performance by VOs, farmers rarely utilize their services. The veterinary system's inability to control antimicrobial leads to misuse by farmers. New efforts to enhance vaccination adoption and antimicrobial stewardship are needed to achieve sustainable livestock production.

Fishery and food safety: potential smoked fish value chain in Kampong Chhnang, Tonle Sap Lake of Cambodia

Raksmey PHOEURK¹ (praksme@rua.edu.kh), Srong KEO¹, Kimchhin SOK¹, Antoine-Moussiaux NICOLAS²

¹ Faculty of Agricultural Economics and Rural Development, Royal University of Agriculture, Phnom Penh, Cambodia ; ² Tropical Veterinary Institute, Faculty of Veterinary Medicine, University of Liège, Liège, Belgium

Introduction:

Inland fish catch, main source of nutrition in tank, is the main source where is provided by Tonle Sap Lake of Cambodia. Two main forms of processing such as fermented and smoked fish. Smoked fish is practiced by smallholders' processors with traditional ways. The value added of smoked fish is still low thanks to their practice techniques and lack of market system improvement.

Objectives:

1). Understanding the dynamics of smoked fish and processing practices; 2). Identifying the value chain and key roles of actors; and 3). Analyse the perception of key actors along value chain on smoke fish.

Materials & Methods:

Kampong Chhnang province was selected, 45 samples interviewed. Mixed method was applied with interview guideline. One FGD with 7 of processors was conducted while 5 key informants interviewed.

Results:

Majority of processors process smoked fish seasonally, around 20 percent of them practice whole seasons. All of them practiced traditionally and relied on woods, mainly the freshwater mangrove (*Barringtonia acutangula*) and locally called 'Reang'. Smoked fish was identified into two groups, high value and low value smoked fish.

Discussion & Conclusion:

Wholesalers played key roles to enable fish processors expanding capacity, initial capital deposit and contracting on sold price. Processors, wholesalers and retailers shown low negative effect on consumers while addressed the negative effect on their health, especially eyes. However, consumers likely concern on negative effect from some on their health. Food safety should be disseminated to processors.

Characterization of the evolution of basic haematological and biochemical variables in relation with bovine trypanotolerance during *Trypanosoma congolense* infection

Gnohion Fabrice SOMÉ (somefabricg@gmail.com)

UMR INTERTRYP, CIRAD, Montpellier, France

Animal trypanosomosis cause major livestock losses in Africa. Abnormal haematology and biochemical parameters in infected animals were reported, however the potential relationship of these two parameters with tolerance or susceptibility to the disease remains unclear. The present study aimed to monitor the haematological and biochemical parameters and to identify the biological variability associated with tolerant versus susceptible phenotypes. For this purpose, 7 N'Damas, 9 Fulani Zebus and 8 crossbreds (Fulani Zebu X European taurine), aged between 2-3 years, were infected intradermally with *Trypanosoma congolense* IL1180. Blood samples were collected on each cow prior and during infection for parasitological analyses, and haematology and biochemical parameters assessment using respectively KHEMA4® and KBIO5® analysers (Kitvia). As expected, N'Damas showed the best anaemia control indicators compared to Fulani Zebus and crossbreds, which were sometimes anaemic. Prior infection, no significant difference in biological variables was observed between the breeds. However, after five months of infection a significant difference ($p < 0.05$) in leukocyte counts, lymphocytes and monocytes were recorded, with higher leukocytosis and lymphocytosis for N'Damas and intermediate values for crossbreds and Fulani Zebus. For biochemical the following variables: cholesterol, urea, albumin, alkaline phosphatase, calcium and glucose values were higher in Fulani Zebus and crossbreds than N'Damas. However, globulin, alamine-amino-transferase, amylase, creatinine, γ -GT and total proteins were higher in N'Damas than Fulani Zebus and crossbreds. Our study revealed major changes in haematology and biochemical variables associated with disease development. The role of each variable and how it may interact was therefore discussed in the context of trypanotolerance.

Understanding the impacts of climate change on farmers' practices and their livestock movement in Rwanda and Neighboring Countries: A Scoping Review

Karen CEBALLOS¹ (kceballos@itg.be), Soledad COLOMBE¹, Wim VAN BORTEL¹, Marie MEUDEC¹, Anselme SHYAKA²

¹ Institute of Tropical Medicine, Antwerp, Belgium ; ² University of Global Health Equity, Kigali, Rwanda

Heavy rainfall, recurrent floods, increasing temperatures, and recurrent droughts significantly affect farmers in East Africa, leading to various challenges including reduced agricultural yields, food insecurity, water scarcity, and increased pests and diseases in crops and livestock. We conducted a scoping review to explore the effects of climate change on the practices and behaviors of farmers, including the movements of their livestock, in the context of Rwanda and neighboring countries (Uganda, Democratic Republic of Congo, Burundi, Kenya, and Tanzania). We included all scientific articles and grey literature published between 2010 and 2023 whose abstracts matched a combination of the following keywords: farmers, pastoralists, climate change, farmer behaviors, animal movement. Confronted with these climate-related challenges, farmers employed various adaptation strategies including changing crop variety, diversifying into livestock rearing, reducing herd size, and seeking alternative employment. Particularly in Kenya, some pastoralists transitioned from cattle to camel herding, while some shifted livestock movement to more temperate regions. This shift may exacerbate resource scarcity and increase the likelihood of disease emergence. Studies also highlighted how adaptation strategies are influenced by various factors such as gender, wealth, education level, access and utility of climate information. Gender roles of women, associated with socioeconomic conditions, determined their lack of access to climate information which could have otherwise improved their farming decisions.

This review highlighted the vulnerability of farmers and the urgent need for adaptive strategies to ensure food security and sustainable livelihoods amidst climate change, while avoiding the emergence of new diseases and new pathways of disease transmission.

Evidence of RVFV circulation among domestic ruminants in Burundi and risk factors associated

Canesius NKUNDWANAYO^{1,2} (cnkundwanayo@yahoo.fr), Annelise TRAN^{3,4,5}, Bernard BETT⁶, Jean Bosco NTIRANDEKURA², Melance NTUNZWENIMANA², Catherine CETRE-SOSSAH⁵

¹ National Veterinary Laboratory, Bujumbura, Burundi ; ² University Of Burundi, Bujumbura, Burundi ; ³ UMR TETIS, Centre de Coopération Internationale en Recherche Agronomique pour le Développement, Montpellier, France ; ⁴ TETIS, Univ Montpellier, AgroParisTech, CIRAD, CNRS, INRAE, Centre de Coopération Internationale en Recherche Agronomique pour le Développement, Montpellier, France ; ⁵ INRAE, UMR ASTRE, Centre de Coopération Internationale en Recherche Agronomique pour le Développement, Montpellier, France ; ⁶ International Livestock Research Institute (ILRI), Nairobi, Kenya

Rift Valley fever (RVF) is a vector-borne zoonotic disease causing recurrent epidemics in Africa and Arabic Peninsula. It occurs mainly in livestock but also affects humans. In April 2022, Burundi experienced its first epidemic of RVF in different provinces. In order to better understand its geographical distribution and associated risk factors, a cross-sectional serological study was launched in Burundi (i) to assess RVF virus (RVFV) specific antibody prevalence at country level and (ii) identify risk factors associated to RVF. This study was carried out in domestic ruminants from 314 villages located in 17 provinces of Burundi, between November 2022 and September 2023. A total of 5333 serum samples was screened for RVFV antibodies by RVF specific cELISA. A structured questionnaire was used to collect information on the risk factors including animal species, age, sex, presence of water bodies, dams or irrigated rice fields. An overall RVFV specific antibody prevalence of 6.1% (95% CI: 5.4-6.8) was detected. The highest seroprevalence rates were observed in Kirundo and Makamba provinces, with 21.8% (95% CI: 17.7-26.4) and 14.4% (95% CI: 10.2-19.5) respectively, with no positive animal detected in Mwaro.

Regarding animal species, the RVFV specific highest antibody prevalence was detected in cattle (14.5%, 95% CI: 12.6-16.6), followed by goats (3.6%, 95% CI: 3.1-4.3) and sheep (1.9%, 95% CI: 0.7-4.2). Using the multiple logistic regression analysis, the survey highlighted species, access to rivers and dams as risk factors. This study evidenced for the first time RVF circulation in Burundi along with its associated risk factors.

Cost-benefit analysis of vaccination against Peste des petits ruminants and current mitigation strategies in smallholder systems of central and northeastern Nigeria

Ladi Amos CHABIRI^{1,2} (ladichabiri@yahoo.com), Victoria Isioma IFENDI³, Joshua KACHIRO^{4,5}, Mohammad Bashir BOLAJOKO¹, Matthew GAKUT³, Usman RAYYANU^{1,6}, Mayowa OLABODE¹, Nengak Gokir ISHAKU⁷, Andrea APOLLONI⁸, Abdrahmane WANE⁹, Rebecca WEKA³, Chika NWOSUH¹⁰, Thomas Duniya BIDOLI^{4,5}, Marion BORDIER¹¹, Alexis DELABOUGLISE⁸

¹ Diagnostic Services, National Veterinary Research Institute (NVRI), Vom., Jos, Plateau State, Nigeria ; ² Department of Veterinary Public Health and Preventive Medicine, University of Jos, Jos, Plateau State, Nigeria ; ³ Extension Services, National Veterinary Research Institute (NVRI), Vom., Jos, Plateau State, Nigeria ; ⁴ Agricultural Extension and Rural Development, National Agricultural Extension and Research Liaison Service, Zaria, Kaduna State, Nigeria ; ⁵ Agricultural Extension and Rural Development, Ahmadu Bello University Zaria, Zaria, Kaduna State, Nigeria ; ⁶ Department of Veterinary Public Health and Preventive Medicine, Ahmadu Bello University Zaria, Zaria, Kaduna State, Nigeria ; ⁷ Kaduna Outstation Laboratory, National Veterinary Research Institute (NVRI), Vom., Kaduna, Kaduna State, Nigeria ; ⁸ CIRAD, UMR ASTRE, CIRAD, UMR ASTRE, Montpellier, Southern France, France ; ⁹ International Livestock Research Institute, Nairobi, Nairobi, Kenya ; ¹⁰ Transboundary Animal Disease, National Veterinary Research Institute (NVRI), Vom., Jos, Plateau State, Nigeria ; ¹¹ CIRAD, UMR ASTRE, CIRAD, UMR ASTRE, Dakar-Etoile, Dakar, Senegal

Introduction:

Small ruminant farming is critical to the livelihood of millions of poor households in Nigeria, where Peste des petits ruminants (PPR) is endemic. Yet, evaluations of the economic return of vaccination against PPR are missing.

Methods:

Three parallel studies were conducted in central and northeastern regions: (1) a serological survey in 420 villages to assess PPR prevalence, (2) a questionnaire survey conducted with 420 households for characterizing livestock herd demographic structure, production and cost, and (3) 84 focus group discussions to identify costs attributable to diseases with clinical signs compatible with PPR, and risk coping strategies implemented by households. An efficiency model was implemented to predict the effect of vaccination against PPR on herd demographic structure, production level and resulting farm income.

Results:

PPR vaccination was predicted to increase the net farm income by 25 or 65 USD per adult female goat and 42 or 66 USD per adult ewe per year depending on the location. The current mitigation strategies of PPR include (1) medical treatments with conventional products, including antibiotics, or indigenous medicine, and (2) rapid sale or slaughter of animals displaying signs of sickness. Obstacles to the adoption of vaccines include (1) poor information available and (2) limited access to vaccines delivery.

Discussion:

A large fraction of the mortality of the young sheep and goats is currently attributable to PPR, which makes vaccination highly profitable at the farm level. Our study demonstrates the need to strengthen the communication and delivery of vaccines to smallholder farmers.

Bioeconomic modelling of area-specific control of foot and mouth disease (FMD) in Thailand

Thanicha CHANCHAIDECHACHAI¹ (t.chanchaidechachai@uu.nl), Egil E.A.J. FISCHER¹, Mart C.M. DE JONG², Henk HOGEVEEN³, Helmut W. SAATKAMP³

¹ Department of Population Health Sciences, Faculty of Veterinary Medicine, Utrecht University, Utrecht, the Netherlands ; ² Quantitative Veterinary Epidemiology Group, Wageningen University and Research, Wageningen, the Netherlands ; ³ Business Economics Group, Wageningen University and Research, Wageningen, the Netherlands

Introduction:

Effective foot and mouth disease (FMD) control measures require support in epidemiology and economic information, currently lacking in Thailand. This study proposes a bioeconomic model to address this gap.

Objectives:

To develop a bioeconomic model that incorporated critical factors, including spatial information, farm size, farm type, and farmers' compliance. The model was used to evaluate FMD control in two different areas in Thailand., e.g., low-farm-density and high-farm-density areas.

Materials & Methods:

Bioeconomic model consisted of two components: an epidemiological model, which is a stochastic between-farm transmission model with a spatial transmission kernel, and an economic model calculating the economic consequences and specifying the costs for each stakeholder. Four different control measures were added to simulation, including ring vaccination, animal culling, isolation of infected farms, and animal movement restrictions.

Results & Discussion:

The control measures did not yield a positive economic return in a low-farm-density area due to small outbreaks. Conversely, in a high farm-density area, the FMD outbreaks were large without control measures. The animal movement restriction was the most expensive, while the ring vaccination was the cheapest. Implementing control measures reduced costs for non-compliant farms and raised costs for compliant farms, except for ring vaccination, which benefited compliant farms. It implies that farmers might have low monetary incentives, and if more farms became free-riders, the control measures would be ineffective.

Conclusion:

The results highlighted the need for area-specific FMD control and attention to farmers' compliance when designing FMD control measures.

ASFV challenge models to understand cross-protective immunity induced by ASFV vaccines

Johanneke Dinie HEMMINK¹ (H.Hemmink@cgiar.org), Salima MUSHTAQ¹, Rose OJOUK¹, Christine MUTISYA¹, Tore TOLLERSRUD², Anna LACASTA¹

¹ Animal and human health program, ILRI, Nairobi, Kenya ; ² Animal and human health program, ILRI, ILRI, Kenya

Introduction & Objectives:

African swine fever virus (ASFV) causes an acute haemorrhagic pig disease which causes up to 100% mortality rate in infected pigs. The disease is endemic in Africa, but is rapidly becoming a global threat, with outbreaks in parts of Europe, Asia and the Caribbean. In Africa, several genotypes circulate simultaneously, which poses a challenge to the control of ASFV and the development of effective vaccines. Live attenuated vaccines are very effective in protecting pigs against homologous or genetically closely related viruses; However, there is limited information on cross-protection against other genetically more distant ASFV strains. We are developing challenge models for a panel of genetically diverse ASFV isolates, to enable us to understand cross-protective immunity induced by ASFV-vaccines.

Material & Methods:

Challenge models were established; This includes well-characterised virus stocks and standardised protocols for challenge preparation. Standardised experimental study protocols; including scoring of clinical signs and gross pathology and implementation of humane endpoint criteria. In addition, standardised laboratory protocols were developed (E.g protocols for viral titer determination).

Results:

Challenge models were developed for Benin97/1 (genotype_I), Georgia07 (genotype_II), Ken1033 (genotype_IX) and Ken05/TK (genotype_X). Challenge with all strains resulted in similar clinical scores, pathology scores, time to humane endpoint and viral titers. Development of challenge models for additional strains is in progress.

Discussion & Conclusions:

These challenge models offer the opportunity to do challenge experiments with reliable and repeatable outcomes, which allows true comparison between challenges with different genotypes/strains and thus to understand cross-protective immunity induced by ASFV-vaccines.

A structuring tool to help Caribbean veterinarians prepare and respond to natural disasters in collaboration with other sectors

Jennifer PRADEL^{1,2} (jennifer.pradel@cirad.fr), Lila KHAN³, Lorelei CORSAUT^{1,4}, Pastor ALFONSO^{2,5}, Karla GEORGES^{2,6}, Victor GONGORA^{2,7}, Coleen PHILIPPS^{8,9}, Kathian HACKSHAW^{2,8}, Candice SANT^{2,5}, Gavin PETERS^{10,2}, Maria Irian PERCEDO ABREU^{2,5}, Keri JOHNSON¹¹, Patricia D. BEDFORD^{12,13,2}

¹ UMR Astre, CIRAD, Montferrier sur Lez, France ; ² CaribVET, Caribbean Animal Health and Veterinary Public Health Network, Petit Bourg, Guadeloupe ; ³ DRM Experts, San Juan, Trinidad & Tobago ; ⁴ UMR Astre, CIRAD INRAE, Petit Bourg, Guadeloupe ; ⁵ CENSA, Centro Nacional de Sanidad Agropecuaria, Mayabeque, Cuba ; ⁶ UWI-SVM, School of Veterinary Medicine, University of the West Indies, Saint Augustine, Trinidad & Tobago ; ⁷ Belize Poultry Association, Belmopan, Belize ; ⁸ Ministry of Agriculture, Forestry, Fisheries, Rural Transformation, Industry and, Kingston, Saint Vincent and the Grenadines ; ⁹ Vincentian Society for the prevention of Cruelty to Animals, Kingston, Saint Vincent and the Grenadines ; ¹⁰ CAHFSA, Caribbean Agricultural Health and Food Safety Agency, Paramaribo, Suriname ; ¹¹ Attorney-at-law, Montego Bay, Jamaica ; ¹² Barbados Veterinary Association, Bridgetown, Barbados ; ¹³ FAO, Food and Agriculture Organisation of the United Nations, Bridgetown, Barbados

Introduction & Objectives:

In 2021, shortly before the eruption of Saint-Vincent-and-the-Grenadines (SVG) volcano, the CaribVET Network shared official information from SVG's veterinary authorities requesting network's assistance, using a GoogleSheet "2021_SVG_GS". This led to an unprecedented successful regional response, which was attributed to outstanding coordination and information sharing. To facilitate the organisation of similar emergency assistance for animals/livestock in other disasters, it was decided to develop a collaborative tool and communication rules to replace "2021_SVG_GS".

Materials & Methods:

As part of an in-depth feedback analysis organized in 2023, the SVG response organizers's core group analysed "2021_SVG_GS" to: 1/ identify key functionalities and information, 2/ define person's roles and user rights and 3/ draw-up the tool's specifications and communication guidelines that were discussed with the IT specialist before tool's development.

Results:

A first version of a secured WebApp enables users to 1/ register, declare their role and acquire associated users rights, 2/ declare an emergency (official communication from the affected country only) with priority needs, shipping procedures, animal census,... ; 2/ create a regional emergency committee (coordination and liaison roles); and 3/ document and track donations (supplies, quantities, donors...). A dashboard displays relevant up-to-date information for responses adjustment. Other functionalities include stakeholders directory, plant and animal health risks mitigation procedures, unit converter...

Discussion:

The tool should be tested and assessed to see if it could be used to improve preparedness for other, more frequent disasters, such as hurricanes. A regional disaster plan should also be formalised to describe alert phase, communication mechanisms, co-option of members and coordination.

Advancements in tracking *Ehrlichia ruminantium* infection through fluorescent mutagenesis

Laurie ROUSSET¹ (laurie.rousset@cirad.fr), Armande BELFORT², Maelle BAYET³, Naomie PATURE⁴,
Valérie RODRIGUES³, Damien MEYER³

¹ Université de Montpellier 2, CIRAD, Petit Bourg, Guadeloupe, France ; ² IUT Martinique, CIRAD, Petit Bourg, Guadeloupe, France ; ³ UMR ASTRE, CIRAD, Petit Bourg, Guadeloupe, France ; ⁴ Université des Antilles, CIRAD, Petit Bourg, Guadeloupe, France

Ehrlichia ruminantium is an obligate intracellular bacterium that causes heartwater, an acute and often fatal disease affecting wild and domestic ruminants in southern Africa and some Caribbean islands. Following transmission by *Amblyomma* spp. ticks, *E. ruminantium* primarily infects endothelial cells of the host, completing a biphasic life cycle and evading the immune response. The study of the mechanisms underlying *E. ruminantium* infection has been hampered by the challenges associated with the genetic manipulation of obligate intracellular bacteria. In this study, we applied random mutagenesis via transposon insertion to *E. ruminantium*. Bacteria were electroporated with plasmids carrying the Himar1 transposase and a transposon that expresses fluorescent proteins. These transformed bacteria were then cultured on bovine endothelial cells in a semi-agar medium. At 37°C, this system allows for the conventional maintenance of endothelial cells in liquid medium. At lower temperatures, the medium solidifies, facilitating the isolation of fluorescent mutants through subculturing. The visualization of fluorescent *E. ruminantium* at different infection stages via fluorescence microscopy marks a considerable breakthrough for pathogenesis research in the context of heartwater. These fluorescent mutants enable tracking throughout their life cycle in both mammalian hosts and tick vectors, paving the way for novel disease control strategies.

Multiple pathogen detection in small and large ruminants of Punjab, Pakistan using conventional and microfluidic PCR

Sabir HUSSAIN^{1,2} (sahussain8-c@my.cityu.edu.hk), Abrar HUSSAIN³, Muhammad Umair AZIZ⁴, Baolin SONG⁴, Jehan ZEB⁴, Sara MOUTAILLER⁵, Angélique F. SIMONIN⁵, Rebecca L. SMITH³, Alejandro C. CRUZ⁵, David GEORGE⁶, Olivier SPARAGANO⁷

¹ Department of Infectious Diseases and Public Health, City University of Hong Kong, Hong Kong, China, Hong Kong SAR China ; ² School of Biological, Environmental and Earth Sciences, University of Southern Mississippi, Hattiesburg, MS, United States ; ³ Department of Pathobiology, College of Veterinary Medicine, University of Illinois, Urbana-Champaign, Chicago, Illinois, United States ; ⁴ City University of Hong Kong, Hong Kong, Hong Kong SAR China ; ⁵ Laboratoire de Santé Animale, Maisons-Alfort, Nationale Vétérinaire d'Alfort, Maisons-Alfort, France ; ⁶ School of Natural and Environmental Sciences, Newcastle University, UK, Newcastle upon Tyne NE1 7RU, United Kingdom ; ⁷ Agricultural Sciences and Practice, Royal Agricultural University, UK, Cirencester, United Kingdom

Objective:

Pakistan faces a significant economic threat from ticks acting as vectors for various pathogens. These Tick-borne pathogens are responsible for endemic diseases that have never been studied in ticks and blood of tick-infested animals simultaneously.

Methods:

We conducted a cross-sectional study of the occurrence, diversity, and co-infection of these pathogens. We collected blood samples from 224 cattle, 224 buffalo, 69 goats, and 56 sheep from 112 farms in Punjab, Pakistan. Additionally, we collected a total of 476 ticks attached to these animals. Ticks and blood samples were processed for pathogen identification and coinfection using conventional and microfluidic PCR.

Results:

Based upon the identification of tick species and sequence analysis of the 16S rRNA and cox1 gene, we confirmed that the most commonly collected tick species were *R. microplus* (38.65%), *H. anatolicum* (31.93%) and *R. decoloratus* (8.40%). Notable pathogens detected in the collected ticks included *Theileria annulata* (18.4%), *Anaplasma ovis* (15.79%), *A. centrale* (13.16%), and *Rickettsia slovaca* (13.16%). In blood samples, the most frequently detected pathogens were *T. annulata* (n = 8), *Babesia bovis* (n = 7), *A. centrale* (n = 6), and *B. bigemina* (n = 5). In some cases, both cattle and buffaloes were found to be co-infected with *B. bovis*, *T. annulata*, and *A. centrale*.

Conclusion:

Overall, 13 TBPs were identified from ticks, and 14 TBPs were blood samples of animals. Co-infection of multiple pathogens was observed in both small and large ruminants. These findings can aid in developing effective control and prevention strategies in veterinary medicine.

S4-P01

Unravelling the epidemiology of ticks and tick-borne infections in Benue state, Nigeria

Raymond ADA¹ (r.t.ada1@edu.salford.ac.uk), Richard BIRTLES¹, Kevin BOWN², Valentina NDOLO³

¹ School of Science, Engineering & Environment, University of Salford, Salford, United Kingdom ; ² School of Biological and Environmental Sciences, Liverpool John Moores University, Liverpool, United Kingdom ; ³ Health Geography, University of Salford, Salford, United Kingdom

Introduction & Objective:

Ticks infesting cattle pose a persistent challenge to Nigeria's livestock sector, made worse by transhumance facilitating the spread of new tick species across regions. These ticks harbour pathogens such as *Anaplasma*, *Babesia*, and *Theileria*, impacting veterinary and economic aspects. Understanding tick distribution and factors influencing their populations and cattle origins through epidemiological studies is essential for devising effective control measures. This research aims to evaluate tick diversity and cattle provenance in Benue State.

Materials & Methods:

The study employed a tick survey using basic tools (compound, dissecting microscope) and identification keys, supplemented by 310 questionnaires to ascertain cattle provenance. Tick samples were collected from 281 cattle in the first survey (January-February 2022) and 310 in the second survey (August-September 2023).

Results & Discussion:

Results revealed 185 tick-infested cattle in the first survey, yielding 658 identified ticks across eight species and three genera. *Hyalomma impeltatum* was the most prevalent, followed by *Amblyomma variegatum*, *R. (B) geigy*, and *R. (Boophilus) microplus*. Notably, the presence of *Hyalomma* ticks suggests a shift in tick diversity within the North Central region, potentially influenced by climate variability. The second survey's tick identification is pending, but questionnaires completed by stakeholders indicate that most Benue cattle originate from areas further north, spending minimal time in Benue before slaughter or relocation southward.

Conclusion:

The coexistence of diverse ticks and dynamic cattle markets underscores the necessity for rigorous monitoring and surveillance to mitigate the spread of tick-borne pathogens, which carry significant implications for veterinary and public health.

Successful feeding of the *Amblyomma variegatum* tick through an *In vitro* artificial feeding system

Naomie PATURE^{1, 2, 3} (naomie.pature@cirad.fr), Mélanie DHUNE^{1, 2}, Massaro UETI⁴, Rubikah VIMONISH⁴, Susan NOH⁴, Valérie RODRIGUES^{1, 2}, Damien MEYER^{1, 2}

¹ UMR ASTRE, CIRAD, Petit-Bourg, Guadeloupe, France ; ² ASTRE, Université Montpellier, CIRAD, INRAE, Montpellier, France ; ³ Ecole Doctorale 636, Campus de Fouillole, Université des Antilles, Pointe-à-Pitre, Guadeloupe, France ; ⁴ Department of Veterinary Microbiology and Pathology, Washington State University, Pullman, Washington, United States

Heartwater is an important disease in tropical and subtropical regions, affecting ruminants and posing a serious threat to livestock health and the economy in non-endemic areas. To better comprehend the mechanisms utilized by *Ehrlichia ruminantium*, an obligatory intracellular bacterium, to infect its *Amblyomma variegatum* vector, we optimized an artificial tick feeding system.

All the *A. variegatum* instars were artificially fed in the system. The device consists of four independent feeders connected to a digital heating power source, which mimics the mammalian blood temperature through a blood heating element. Approximately 500 larvae, 50 nymphs, and 10 adult ticks were added to each feeder, respectively. To assess multiple parameters, such as tick attachment rate, engorgement rate, mortality and detachment rate, goat blood was changed twice a day every 12h. Silicone membranes, mimicking host skin, were inspected each blood changes to inspect fungal contamination.

Regardless of the instar, ticks tended to attach to the membranes within 48 hours with cement secretion visible through the silicone membrane. The artificial feeding system was successfully used to feed *A. variegatum* ticks until repletion and detachment. Furthermore, larvae and nymphs have successfully molted and adult female ticks were able to lay eggs, which hatched into larvae.

These results demonstrate that tick artificial feeding system represents an outstanding tool to study interactions between vectors and pathogens of interest and also to avoid the use of animals for feeding ticks. Further studies will be conducted to study the vector competence of *A. variegatum* for *E. ruminantium* through this system.

A systematic review of vaccine strategies against *Tritrichomonas foetus*: insights, challenges, and prospects

Harvey SANTOS¹ (johnharvey.santos@uq.edu.au), Gry BOE-HANSEN^{1,2}, Hannah SIDDLE¹, Ali RAZA¹, Loan NGUYEN¹, Michael MCGOWAN², Kieren MCCOSKER¹, Ala TABOR^{3,4}

¹ Centre for Animal Science, Queensland Alliance for Agriculture & Food Innovation, The University of Queensland, St Lucia, Queensland, Australia ; ² School of Veterinary Science, The University of Queensland, Gatton, Queensland, Australia ; ³ Centre for Animal Science, Queensland Alliance for Agriculture & Food Innovation, The University of Queensland, St Lucia, Australia ; ⁴ School of Chemistry & Molecular Biosciences, The University of Queensland, St Lucia, Queensland, Australia

Tritrichomonas foetus is a protozoan parasite that causes bovine trichomonosis resulting in substantial economic losses. The parasite colonises the reproductive tract of both male and female cattle, being asymptomatic in males but causing early reproductive failure in infected females. This systematic review aims to analyse publications about vaccine development and the associated immune responses to guide future research directions.

A systematic review was conducted using indexed sources on Scopus, PubMed, Web of Science, and Embase to search for published vaccine development studies in English utilising either experimental or commercial *T. foetus* vaccine for bovine trichomonosis. Search terms were entered (cattle, bull, heifer, vaccine, immune response, and *Tritrichomonas foetus*) into the indexed sources and no limit was set for the year of publication.

Among 373 studies imported for screening, 96 were duplicates, and 254 were excluded for irrelevancy as these studies did not meet the inclusion criteria (reports original data, vaccine tests must be done in cattle, and used either commercial or experimental vaccines that incorporated antigens from *T. foetus*). A further five studies were excluded after full-text review as either the publication described a different target pathogen or the full-text was not in English. Eighteen studies met the inclusion criteria and were subjected to data extraction using the Covidence platform. All of the studies included in the systematic review reported two vaccine strategies, including subunit and inactivated whole-cell vaccines.

Understanding the parasite's pathogenesis, host-parasite interactions, and host immune responses could lead to the development of new bovine trichomonosis vaccine strategies.

S4-P04

Occurrence, prevalence, and distribution of haemoparasites of poultry in Sub-Saharan Africa: a scoping reviewDanisile TEMBE (TembeD@ukzn.ac.za)*University of KwaZulu-Natal, Durban, South Africa*

This review collated existing data on the occurrence, distribution, and prevalence of haemoparasites of poultry in sub-Saharan Africa. A literature search was conducted on three electronic search databases using search terms and Boolean operators (AND, OR). The results recorded 16 haemoparasites, viz., *Leucocytozoon* spp., *L. marchouxi*, *L. neavei*, *L. sabrazesi*, *L. schoutedeni*, *Haemoproteus columbae*, *H. pratasi*, *Haemoproteus* spp., *Plasmodium* spp., *P. gallinaceum*, *P. circumflexum*, *P. juxtannucleare*, *Trypanosoma avium*, *T. gallinarum*, *T. numidae*, and *Hepatozoon* spp. from a wide range of poultry species distributed across Nigeria, Kenya, South Africa, Tanzania, Uganda, Botswana, Zimbabwe, Ghana, Cameroon, and Zambia. Infections due to *Haemoproteus* and *Leucocytozoon* species were the most common and documented in eight of the ten reviewed countries. The presence of mixed infections was observed in quails, pigeons, chickens, ducks, turkeys, and guinea fowls, but predominantly in chickens. Co-infections by *Plasmodium* spp. and *Haemoproteus* spp. were the most common, which may be attributed to the distribution of these species, coupled with the availability of vectors they are associated with in areas from which they were documented. The information generated in this review is essential for improving existing preventive and control measures of these parasites in sub-Saharan Africa.

S5-P01

The Tick Cell Biobank: resources for vector-borne disease research

Catherine HARTLEY (catherine.hartley@liverpool.ac.uk), Jing Jing KHOO, Alistair DARBY, Benjamin MAKEPEACE, Lesley BELL-SAKYI

Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, Liverpool, United Kingdom

Arthropod cell lines play an important role in research on control of vector-borne pathogens of veterinary, medical and agricultural importance. The Tick Cell Biobank (TCB) at the University of Liverpool is the world's only dedicated collection of cell lines derived from tick and insect vectors of viral, bacterial, protozoan and helminth pathogens. As well as storing and distributing cell lines to scientists worldwide, the TCB provides training in arthropod cell line maintenance, application and development, and ongoing advice and support to recipients. The TCB also generates new cell lines from tick and insect vectors, which can be a lengthy and challenging process. TCB Outposts in Malaysia, Kenya and Brazil assist in distribution of cell lines and training to lower- and middle-income country scientists in Asia, Africa and South America. The TCB houses over 90 cell lines derived from ixodid and argasid ticks, mosquitoes, biting midges, sand flies, tsetse flies and triatomine bugs, and a small collection of intracellular arthropod-borne bacteria including *Anaplasma* and *Ehrlichia* spp. In-house and collaborative studies include cell line and pathogen sequencing and characterisation, cell-bacteria interactions and arthropod virus discovery.

Contribution of proteomics profiling of bacterial strains to ensure quality control of production batches for multivalent vaccines against Heartwater

Philippe HOLZMULLER¹ (philippe.holzmuller@cirad.fr), Bernard FERNANDEZ¹, Nourredine DAHMANI¹, Lucile MOUNIER², Khadija EL KOULALI³, Martial SEVENO³, Oana VIGY³, Nathalie VACHIER¹, Valérie RODRIGUES⁴

¹ UMR ASTRE, CIRAD, Montpellier, France ; ² UMR ASTRE, INRAE, Montpellier, France ; ³ UMR ASTRE, CNRS, Montpellier, France ; ⁴ UMR ASTRE, CIRAD, Petit-Bourg, France

Heartwater, caused by the Rickettsiales *Ehrlichia ruminantium*, is a significant tick-borne disease affecting livestock across sub-Saharan Africa, the Caribbean, and threatening the American continent. *E. ruminantium* infects domestic and wild ruminants, infiltrating the cytoplasm of vascular endothelial cells as a small, pleomorphic, gram-negative obligate intracellular bacterium.

Strategies involving infection-antibiotic treatments of livestock have paved the way for the development of vaccination protocols against Heartwater. An inactivated vaccine, based on bacterial culture *in vitro*, has demonstrated efficacy against *E. ruminantium* infection. However, the practical application of this vaccine in the field is hindered by the significant antigenic diversity among *E. ruminantium* strains and the variable degree of cross-protection. We have recently initiated the development of multivalent inactivated vaccines, consisting of cocktails of strains isolated in different geographical areas affected by Heartwater. A unique aspect lies in the qualification of production batches using a proteomics/mass spectrometry approach. This method revealed a clustering of replicates of a given bacterial strain, despite variations in total protein concentrations across batches, affirming the robustness of the production process.

The developed bioinformatics workflow for proteome analysis of *E. ruminantium*, based on data imputation techniques tailored to the nature of missing values (missing at random or not at random), enabled a precise protein profiling of each bacterial strain used in producing inactivated multivalent vaccines against Heartwater, and provided valuable insights into their individual molecular phenotype. This advancement has opened up new avenues for capturing the diverse bacterial phenotypes representative of the geographical area intended for vaccination.

S5-P03

Characterisation of the molecular determinants involved in the replication and transmission of the West Nile virus by *Culex quinquefasciatus* mosquitoesMarie MOTOS (marie.motos@cirad.fr), Laëtitia VIRY, Lise FIACRE, Nonito PAGÈS, Sylvie LECOLLINET

ASTRE, CIRAD, Petit-Bourg, Guadeloupe

In view of current and future threats posed by arboviruses, particularly those caused by West Nile virus (WNV), the emergence and spread of new epidemics is being monitored more closely in tropical and temperate regions. This virus, which is widespread throughout the Americas, Africa, the Middle-East and Europe, is maintained in an enzootic transmission cycle between birds and mosquitoes mostly belonging to the *Culex* genus. However, infection of vertebrate hosts, such as humans or horses, can lead to severe symptoms, culminating in neurological disorders such as meningitis, encephalitis and flaccid paralysis. The severity of the disease in these hosts highlights the importance of developing new ways of effectively anticipating, characterising and controlling emerging WNV strains. In this study, 26 WNV mutants in structural as well as non structural genes (M, E, NS1, NS3, NS4A, NS4B and NS5) and in the 3' non coding region have been designed, based on relevant epidemiological and experimental infection data and have been constructed by single site mutagenesis and reverse genetics. We will study the impact of such mutations on WNV replication and tropism in the mosquito, by using mosquito cell lines as well as a *Culex quinquefasciatus* laboratory strain. The characterisation of genetic determinants involved in the modulation of mosquito-borne WNV transmission could help deciphering the cellular pathways that are key for WNV-mosquito effective interactions and drive the design of new control methods.

A new pen-side test to confirm RVF clinical suspicions in the field.

Adrien LIMOZIN¹ (adrien.limozin@innovative-diagnostics.com), Fabien DONNET¹, Aurélie PEDARRIEU², Loïc COMTET¹, Catherine CETRE-SOSSAH²

¹ INNOVATIVE DIAGNOSTICS, Grabels, France ; ² CIRAD, INRAE, UMR ASTRE, University of Montpellier, Montpellier, France

Introduction:

Rift Valley fever (RVF) is a zoonotic disease-causing acute infection in domestic ruminants, particularly impacting young animals.

To address the need for rapid confirmation of suspected cases, a new pen-side test, the ID Rapid® Rift Valley fever Antigen, was developed in collaboration with CIRAD (Cêtre-Sossah C. et al., 2019). Performance is presented here.

Materials & Methods:

Diagnostic specificity was assessed on 580 negative sera (292 cattle, 96 small ruminants and 192 camelids) and 184 heparinized whole blood (cattle) from RVF-free areas.

Analytical sensitivity was evaluated using a titrated RVFV strain (Smithburn) spiked in negative whole blood or serum (bovine and caprine).

Diagnostic sensitivity on serum of a previous similar test with the same limit of detection (LOD) was assessed with:

- 25 isolated strains from different geographical origins mimicking clinical specimens
- 10 RT-qPCR-positive clinical samples from the 2019 Mayotte outbreak (Bird et al., 2007)

Results:

Measured specificity was:

- Cattle sera: 99.7% [98.1-99.9]
- Small ruminant sera: 99.0% [94.3-99.1]
- Camelids sera: 100% [98.0-100]
- Bovine whole blood: 98.9% [96.1-99.7]

Diagnostic sensitivity was 100% [90,1-100]. Inclusivity, tested on different RVFV viral strains, is 100%. Exclusivity documented with flaviviruses and alphaviruses rules out cross-reactivity with clinically similar viruses. LOD on serum/whole blood was respectively 3.5x10³ pfu and 7.5x10⁴ pfu.

Conclusion:

The ID Rapid® Rift Valley fever antigen demonstrates excellent performance and is a reliable tool to confirm a RVF clinical suspicion and enhance virus detection during an outbreak in less than 15 minutes directly on the field, without specific lab equipment

Exploring *Galleria mellonella* as an alternative model for *Ehrlichia ruminantium* infection researchMaëlle BAYET^{1,2} (maelle.bayet@cirad.fr), Valérie RODRIGUES^{1,2}, Damien MEYER^{1,2}¹ UMR ASTRE, CIRAD, Petit-Bourg, Guadeloupe, France ; ² ASTRE, Université Montpellier, CIRAD, INRAE, Montpellier, France

Ehrlichia ruminantium is a Gram-negative, obligatory intracellular bacterium and is the causative agent of heartwater disease. The *Amblyomma variegatum* tick transmits this pathogen during blood feeding to small ruminants. Utilizing animal models is crucial for understanding bacterial virulence factors and their roles in host-pathogen interactions. However, the technical, ethical, and financial challenges associated with mammalian models in bacterial virulence research have led to the development of several insect models. Despite the lack of complexity found in the mammalian immune system, insects share key aspect of innate immunity with mammals making *Galleria mellonella*, the larvae of the greater wax moth, an increasingly used model. This study demonstrates that *Galleria mellonella* larvae are susceptible to infection with the *Ehrlichia ruminantium* Gardel strain. Following subcutaneous infection, we observed larval death within 20 days. Additionally, fluorescent staining revealed that *Ehrlichia ruminantium* resided within insect hemocytes, highlighting the potential of *Galleria mellonella* as a valuable model for studying *Ehrlichia ruminantium* infection and facilitating a deeper understanding of its pathogenesis without the ethical and financial burdens of mammalian models.

First proof of concept of CRISPR-Cas9 ribonucleoproteins genome editing of *Trypanosoma congolense* BSF

Cécile MINET^{1,2} (cecile.minet@cirad.fr), Isabelle CHANTAL^{1,2}, Sophie THÉVENON^{1,2}, David BERTHIER^{1,2}

¹ UMR 17 - INTERTRYP, CIRAD, Montpellier, France ; ² INTERTRYP, Univ. Montpellier, CIRAD, IRD, Montpellier, France

African Animal Trypanosomosis is a major vector-borne disease affecting livestock breeding in Africa. It is caused by trypanosomes, especially *Trypanosoma congolense* with major negative impacts on animal production and negative repercussions in terms of poverty. To develop new tools to fight against the disease, we need to improve knowledge of the genes involved in the pathogenicity and virulence of the parasites as well as their functions. To date, unlike for *Trypanosoma brucei* or *Trypanosoma cruzi*, genome editing tools have been used relatively little to study *T. congolense*. We present an efficient, reproducible and stable CRISPR-Cas9 genome editing system for use in *T. congolense* bloodstream forms (Tc-BSF). This plasmid-free system is based on transient expression of Cas9 protein and the use of a ribonucleoprotein formed by the Cas9 and sgRNA complex. This is the first proof of concept of genome editing using CRISPR-Cas9 ribonucleoproteins in Tc-BSF. This adapted protocol enriches the «toolbox» for the functional study of genes of interest in bloodstream forms of the *T. congolense*. This proof of concept is an important step for the scientific community working on the study of trypanosomes and opens up new perspectives for the control and fight against animal trypanosomosis.

Haematological and biochemical parameters associated with tick-borne infections in dogs from Trinidad and Tobago

Patricia POW-BROWN¹ (patricia.powbrown@my.uwi.edu), Adam BIRKENHEUER², Henry MARR², James WILSON³, Christopher OURA¹, Mervyn CAMPBELL¹, Roxanne CHARLES¹, Karla GEORGES¹

¹ The University Of the West Indies. School of Veterinary Medicine, Champs Fleurs, Trinidad & Tobago ; ² Vector Borne Diagnostic Laboratory, North Carolina State University College of Veterinary Medicine, Raleigh, N.C, USA ; ³ Galaxy Diagnostics, Inc., Durham, N.C, USA

Introduction & Objectives:

This study was conducted in dogs with symptoms of infections with tick borne pathogens (TBP) to assess the association between changes in reference haematological and biochemical parameters and the presence of TBP.

Materials & Methods:

Whole blood and serum from 363 symptomatic dogs were analysed. Real-time PCR detected TBP DNA of (*Ehrlichia/Anaplasma* spp., *Babesia* spp.). A complete blood count (CBC)-(Haematocrit, Platelet, Red Blood Cell) and serum analysis for blood urea nitrogen, creatinine, alanine aminotransferase, alkaline phosphatase and gamma-glutamyl transferase (GGT) was done. Associations between reference intervals (normal vs abnormal) and a positive PCR for any pathogen (single and co-infections) were analysed using the chi square test. Statistical significance was $p < 0.05$.

Results:

A positive PCR result for any pathogen was obtained for 246 (67.8%) dogs. Single infections occurred in 172 (47.4%) and co-infections in 74 (20.4%) dogs. Thrombocytopenia, low HCT and RBC counts were detected in 77.9%, 69.6% and 58.7% of dogs respectively. Most dogs had normal reference values for other CBC and serum biochemistry parameters.

A significant association ($p < 0.05$) was observed for thrombocytopenia, low HCT and low RBC and a positive PCR result for any pathogen. A significant association was also observed for low RBC and infection with *Babesia canis*. Elevated GGT was a sparing effect for infection with any pathogen.

Discussion & Conclusion:

The results obtained are useful in assisting veterinarians to recognise important biochemical and haematological parameters associated with TBP infections.

Dynamics of infection rates of tsetse flies fed on trypanotolerant and trypanosusceptible cattle during an experimental infection with *Trypanosoma congolense*

Sophie THEVENON¹ (sophie.thevenon@cirad.fr), Gnohion Fabrice SOMÉ^{2,3}, Modou SÉRÉ², Prudencienne AGBOHO², Bienvenu Martin SOMDA², Antoine BARREAUX⁴, Isabelle CHANTAL³, David BERTHIER³, Geoffrey GIMONNEAU⁵, Sophie RAVEL⁶, Wilfried YONI²

¹ BIOS UMR INTERTRYP, CIRAD, Montpellier, France ; ² CIRDES, Bobo Dioulasso, Burkina Faso ; ³ CIRAD, Montpellier, France ; ⁴ CIRAD, Nairobi, Kenya ; ⁵ CIRAD, Dakar, Senegal ; ⁶ IRD, Montpellier, France

Introduction & Objectives:

African cattle breeds differ in their ability to cope with trypanosomosis. While Zebu breeds present high parasitaemia and anaemia, significant production losses and high mortality, West African taurine breeds are able to mitigate infection by limiting anaemia and parasitaemia, and are known trypanotolerant breeds. However, the ability of the different breeds to transmit trypanosomes to tsetse flies remains unknown, as does the impact of trypanotolerance and trypanosusceptibility on the disease epidemiology. The objective of our study was to assess the transmission rate of trypanosomes to tsetse flies from different cattle breeds throughout infection course.

Materials & Methods:

We experimentally infected animals from three cattle breeds, trypanosusceptible Fulani Zebu, trypanotolerant N'Dama and local cross-bred animals between Fulani Zebu and European taurine with *Trypanosoma congolense*. Tsetse flies (*Glossina palpalis gambiensis*) were fed on each cattle at five time points during infection. Tsetse flies were then artificially fed with sterilized bovine blood via a silicone membrane and dissected for trypanosomes identification between 15 and 20 days after the first infected cattle blood feeding.

Results, Discussion & Conclusion:

The fraction of infected flies per cattle was 7% on average (median=10%), and the infection rate varying from 0 to 60% (estimated by cattle and time point). Interestingly, the time point that gave the maximum fraction of infected flies (mean=21%) was 54 days post-cattle infection. The inferred parameters of hosts and tsetse infection rates could be used to parametrise epidemiological models of trypanosomosis that integrate the role of cattle breeds on transmission dynamics.

Use of a tick cellular material to understand the tick-pathogen interactions in Heartwater

Mélanie DHUNE¹ (melanie.dhune@cirad.fr), Juliette FEILLET², Damien MEYER¹, Valérie RODRIGUES¹

¹ UMR ASTRE, CIRAD, Petit Bourg, Guadeloupe, France ; ² Sup'Biotech, Paris, France

Heartwater is a fatal tropical disease of ruminants, caused by the intracellular bacterium *Ehrlichia ruminantium* and transmitted by the tropical bont tick *Amblyomma variegatum*. Although this bacterium is highly virulent in mammalian hosts, it does not exhibit pathogenicity in its tick vectors. Investigating the maintenance and behavioral mechanisms within ticks is crucial for understanding this relationship. A pivotal approach involves utilizing *Amblyomma variegatum* tick cell lines to elucidate some first insights into these vector-pathogen interaction, contrasting with those in mammalian cells. In this study, we infected AVL/CTVM13 cells with the Gardel strain of *Ehrlichia ruminantium*. Cells were observed and collected each week to measure bacterial persistence or multiplication by quantitative PCR. Preliminary results indicate that *Ehrlichia ruminantium* remains detectable within the cells for at least 10 weeks, maintaining a steady bacterial load. Further analysis focusing on the expression of known virulence factors will provide valuable information into the bacterial behavior within their tick host.

S7-P01

The Peer Community In (PCI) project, PCI Infections, and the Peer Community Journal: a diamond open access way to publish research results on vector ecologyThierry DE MEEÛS¹ (thierry.demeus@ird.fr), Christine CHEVILLON², Thomas POLLET³, Jorge AMICH⁴¹ Intertryp, IRD, Montpellier, France ; ² Mivegec, CNRS, Montpellier, France ; ³ Astre, Inrae, Montpellier, France ; ⁴ National Center for Mycology, Instituto de Salud Carlos III, Madrid, Spain

Peer Community In (PCI) (<https://peercommunityin.org>) is a non-profit scientific organization consisting of communities of researchers, called recommenders, who handle the evaluation and recommendation of preprints in their scientific field, based on rigorous peer-reviews. The recommendation process by PCIs is completely free of charge. When a recommender decides to recommend a preprint, she or he writes a recommendation text that is published along with all the editorial correspondence (reviews, recommender's decisions, and authors' replies) on the PCI website. The preprint can then be published in the «Peer Community Journal» (PCJ) (<https://peercommunityjournal.org/>, launched in fall 2021). PCJ directly accepts all articles recommended by any of the existing PCIs. It is the first generalist diamond open access journal to date. Peer Community In started in 2017. There are now 17 PCIs, with more than 2000 recommenders. The initiative won the 2020 LIBER award for library innovation of the European League of Research Libraries. PCI Infections (<https://infections.peercommunityin.org/>) was launched in August 2021. It welcomes all manuscripts dealing with host-pathogen-vector systems. As published articles are free for authors and readers, it is particularly suited for low-income research fields, as researches on neglected tropical diseases. To date, the PCJ already exhibits very good citation statistics (1188 citations, i.e. 2.6 citations/year/paper). PCI Infections needs more recommenders and as many preprint submissions as possible. We hope the vector ecology community will massively join the initiative.

S8-P01

A *Theileria annulata* parasite with a single mutation, methionine 128 to isoleucine (M128I), in cytochrome B is resistant to buparvaquoneShahin TAJERI¹ (shahin.tajeri@fu-berlin.de), Debasish CHATTOPADHYAY², Gordon LANGSLEY³, Ard NIJHOF¹

¹ Freie Universität Berlin, Institute for Parasitology and Tropical Veterinary Medicine, Berlin, Brandenburg, Germany ; ² Department of Medicine, University of Alabama at Birmingham, Birmingham, Alabama, United States ; ³ Inserm U1016-CNRS UMR8104, Cochin Institute, Paris, France

The hydroxynaphtoquinone buparvaquone (BPQ) is the only available drug currently used to treat clinical theileriosis in cattle, whilst BPQ resistance is emerging and spreading in endemic areas. Here, we chronically exposed *T. annulata*-transformed macrophages *in vitro* to BPQ and monitored the emergence of drug-resistant parasites. Surviving parasites revealed a significant increase in BPQ IC50 compared to the wild type parasites. Drug resistant parasites from two independent cloned lines had an identical single mutation, M128I, in the gene coding for *T. annulata* cytochrome B (*Tacytb*). This *in vitro* generated mutation has not been reported in resistant field isolates previously, but is reminiscent of the methionine to isoleucine mutation in atovaquone-resistant *Plasmodium* and *Babesia*. The M128I mutation did not appear to exert any deleterious effect on parasite fitness (proliferation and differentiation to merozoites). To gain insight into whether drug-resistance could have resulted from altered drug binding to TaCytB we generated *in silico* a 3D-model of wild type TaCytB and docked BPQ to the predicted 3D-structure. Potential binding sites cluster in four areas of the protein structure including the Q01site. The bound drug in the Q01 site is expected to pack against an alpha helix, which included M128, suggesting that the change in amino acid in this position may alter drug-binding. The *in vitro* generated BPQ resistant *T. annulata* is a useful tool to determine the contribution of the various predicted docking sites to BPQ resistance and will also allow testing novel drugs against theileriosis for their potential to overcome BPQ resistance.



LIST OF POSTERS



S1 - One (Tropical Animal) Health / Integrated Approaches and Perspectives

Last name	First name	Title of poster	# poster
BARRY	Mamadou Alimou	Adoption study of a networking tool to facilitate collaborations (Too Cool)	S1-P01
BODOMBOSSOU	Esso-tchella Madera	Circulation of multi-resistant bacteria in humans and animals in the urban area of Lome in Togo	S1-P02
CHEVALIER	Laure	Do Malagasy dogs sound the epidemiological alarm bell?	S1-P03
DE GARINE-WICHATITSKY	Michel	One Health in practice: a socio-ecological approach for the study and management of zoonotic diseases associated with free-roaming dogs in Southeast Asia (SEAdogSEA)	S1-P04
LANGLOIS	Thibaut	The underestimated impact of dogs on public health in Southeast Asia: a lexical review	S1-P05
MINANI	Salvator	Occurrence of porcine cysticercosis in Burundi	S1-P06
RODRIGUES	Valérie	Local distribution of cattle over Guadeloupe archipelago: an adapted method for disaggregating census data	S1-P07
VANNY	Chhuon	Integrating the One Health perspective for the agroecological transition in a living Lab in Cambodia	S1-P08

S2 - Animal Health and Production

Last name	First name	Title of poster	# poster
JULI	Mst Sogra Banu	Characterisation of preputial microbiome of bulls for Bovine Genital Campylobacteriosis (BGC) in association with vaccination and challenge	S2-P01
MEYER	Damien	<i>Brucella</i> driven host N-glycome remodeling controls infection	S2-P02
NUVEY	Francis Sena	Infectious diseases management strategies in a ruminant production system: a participatory appraisal of veterinary services delivery performance, and utilization in Ghana	S2-P03
PHOEURK	Raksmey	Fishery and food safety: potential smoked fish value chain in Kampong Chhnang, Tonle Sap Lake of Cambodia	S2-P04
SOMÉ	Gnohion Fabrice	Characterization of the evolution of basic haematological and biochemical variables in relation with bovine trypanotolerance during <i>Trypanosoma congolense</i> infection	S2-P05

S3 - Transboundary Animal Diseases

Last name	First name	Title of poster	# poster
CEBALLOS	Karen	Understanding the impacts of climate change on farmers' practices and their livestock movement in Rwanda and Neighboring Countries: A Scoping Review	S3-P01
CETRE-SOSSAH	Catherine	Evidence of RVFV circulation among domestic ruminants in Burundi and risk factors associated	S3-P02
CHABIRI	Ladi Amos	Cost-benefit analysis of vaccination against Peste des petits ruminants and current mitigation strategies in smallholder systems of central and northeastern Nigeria	S3-P03
CHANCHAIDECHACHAI	Thanicha	Bioeconomic modelling of area-specific control of foot and mouth disease (FMD) in Thailand	S3-P04
HEMMINK	Johanneke Dinie	ASFV challenge models to understand cross-protective immunity induced by ASFV vaccines	S3-P05
PRADEL	Jennifer	A structuring tool to help Caribbean veterinarians prepare and respond to natural disasters in collaboration with other sectors	S3-P06
RODRIGUES	Valérie	Advancements in tracking <i>Ehrlichia ruminantium</i> infection through fluorescent mutagenesis	S3-P07
SPARAGANO	Olivier	Multiple pathogen detection in small and large ruminants of Punjab, Pakistan using conventional and microfluidic PCR	S3-P08

S4 - Veterinary Parasitology

Last name	First name	Title of poster	# poster
ADA	Raymond	Unravelling the epidemiology of ticks and tick-borne infections in Benue state, Nigeria	S4-P01
MEYER	Damien	Successful feeding of the <i>Amblyomma variegatum</i> tick through an <i>In vitro</i> artificial feeding system	S4-P02
SANTOS	Harvey	A systematic review of vaccine strategies against <i>Tritrichomonas foetus</i> : insights, challenges, and prospects	S4-P03
TEMBE	Danisile	Occurrence, prevalence, and distribution of haemoparasites of poultry in Sub-Saharan Africa: a scoping review	S4-P04

S5 - Vector-Borne Diseases

Last name	First name	Title of poster	# poste
HARTLEY	Catherine	The Tick Cell Biobank: resources for vector-borne disease research	S5-P01
HOLZMULLER	Philippe	Contribution of proteomics profiling of bacterial strains to ensure quality control of production batches for multivalent vaccines against Heartwater	S5-P02
LECOLLINET	Sylvie	Characterisation of the molecular determinants involved in the replication and transmission of the West Nile virus by <i>Culex quinquefasciatus</i> mosquitoes	S5-P03
LIMOZIN	Adrien	A new pen-side test to confirm RVF clinical suspicions in the field	S5-P04
MEYER	Damien	Exploring <i>Galleria mellonella</i> as an alternative model for <i>Ehrlichia ruminantium</i> infection research	S5-P05
MINET	Cécile	First proof of concept of CRISPR-Cas9 ribonucleoproteins genome editing of <i>Trypanosoma congolense</i> BSF	S5-P06
POW-BROWN	Patricia	Haematological and biochemical parameters associated with tick-borne infections in dogs from Trinidad and Tobago	S5-P07
THEVENON	Sophie	Dynamics of infection rates of tsetse flies fed on trypanotolerant and trypanosusceptible cattle during an experimental infection with <i>Trypanosoma congolense</i>	S5-P08
RODRIGUES	Valerie	Use of a tick cellular material to understand the tick-pathogen interactions in Heartwater	S5-P09

S7 - Teaching and continuing Education in Tropical Veterinary Medicine

Last name	First name	Title of poster	# poste
DE MEEÛS	Thierry	The Peer Community In (PCI) project, PCI Infections, and the Peer Community Journal: a diamond open access way to publish research results on vector ecology	S7-P01

S8 - Drug Resistance

Last name	First name	Title of poster	# poste
NIJHOF	Ard	A <i>Theileria annulata</i> parasite with a single mutation, methionine 128 to isoleucine (M128I), in cytochrome B is resistant to buparvaquone	S8-P01



LIST OF PARTICIPANTS



ADA Raymond

Science Engineering and Environment
University of Salford
SALFORD – UK
r.t.ada1@edu.salford.ac.uk

ALMAZÁN Consuelo

Laboratorio de Inmunología y Vacunas
Universidad Autónoma de Querétaro
QUERETARO – MEXICO
c_almazan_g@hotmail.com

AREGA Sintayehu

University of Gondar
GONDAR – ETHIOPIA
sintayehuarega@students.rossu.edu

ARSEVSKA Elena

UMR ASTRE
Cirad
MONTFERRIER-SUR-LEZ – FRANCE
elena.arsevska@cirad.fr

AUGUSTE Tennille

Clinical Veterinary Sciences
CaribVET
The University of the West Indies
CHAMPS FLEURS – TRINIDAD AND
TOBAGO
tennille.auguste@sta.uwi.edu

BARRY Mamadou Alimou

Médecine Vétérinaire - ASTRE
Université de Liège - Cirad
LIÈGE – BELGIUM
barryalim91@gmail.com

BARTHÉLEMY Amélie

Standard BioTools
PARIS – FRANCE
amelie.barthelemy@standardbio.com

BATAILLE Arnaud

UMR ASTRE
Cirad
MONTPELLIER – FRANCE
arnaud.bataille@cirad.fr

BEJO Mohd Hair

Department of Veterinary Pathology
& Microbiology
University Putra Malaysia
SERDANG – MALAYSIA
mdhair@upm.edu.my

BELL-SAKYI Lesley

Institute of Infection, Veterinary
and Ecological
University of Liverpool
LIVERPOOL – UK
l.bell-sakyi@liverpool.ac.uk

BINOT Aurélie

UMR ASTRE
Cirad
MONTPELLIER – FRANCE
binot@cirad.fr

BIRTLES Richard

School of Science, Engineering
and Environment
University of Salford
SALFORD – UK
r.j.birtles@salford.ac.uk

BODOMBOSSOU Esso-Tchella Madera

ASTRE
Cirad
MONTFERRIER-SUR-LEZ – FRANCE
maderabodombossou@gmail.com

BOISSIÈRE Anne

ASTRE
Cirad
MONTPELLIER – FRANCE
anne.boissiere@cirad.fr

BOUTAYEUR Hajar

Boehringer Ingelheim Animal Health
France
LYON – FRANCE
hajar.boutayeur@boehringer-ingelheim.com

CEBALLOS Katrina Abigail

Department of Public Health
Institute of Tropical Medicine
ANTWERP – BELGIUM
kceballos@itg.be

CÊTRE-SOSSAH Catherine

ASTRE
Cirad
MONTPELLIER – FRANCE
catherine.cetre-sossah@cirad.fr

CHABIRI Ladi Amos

Diagnostic Service Division
National Veterinary Research Institute
PLATEAU STATE – NIGERIA
ladichabiri@yahoo.com

CHANCHAIDECHACHAI Thanicha

Department Population Health Sciences
Utrecht University
UTRECHT – THE NETHERLANDS
t.chanchaidechachai@uu.nl

CHANTAL Isabelle

UMR Intertryp
Cirad
MONTPELLIER – FRANCE
isabelle.chantal@cirad.fr

CHARLES Roxanne

Basic Veterinary Sciences
University of the West Indies
MOUNT HOPE – TRINIDAD AND TOBAGO
roxanne.charles@sta.uwi.edu

CHEVALIER Laure

ASTRE
Cirad
MONTFERRIER-SUR-LEZ – FRANCE
laure.chevalier@cirad.fr

CICHON Nicole

Fressnapf Holding SE
KREFELD – GERMANY
nicole.cichon@fressnapf.com

CLAUSEN Peter-Henning

Institute for Parasitology and
Tropical Veterinary
Freie Universität Berlin
BERLIN – GERMANY
peter-henning.clausen@fu-berlin.de

COLOMBE Soledad

Unit of Emerging Infectious Diseases
Institute of Tropical Medicine
ANTWERP – BELGIUM
scolombe@itg.be

COMTET Loic

Innovative Diagnostics
GRABELS – FRANCE
loic.comtet@innovative-diagnostics.com

CONVERT Guillaume

Veterinary Public Health
Boehringer Ingelheim Animal Health
France
LYON – FRANCE
guillaume.convert@boehringer-ingelheim.com

DE GARINE-WICHATITSKY Michel

UMR ASTRE
Cirad
MONTPELLIER – FRANCE
degarine@cirad.fr

DE MEEÛS Thierry

Intertryp
IRD
MONTPELLIER – FRANCE
thierry.demeus@ird.fr

DE MIRANDA SANTOS Isabel

Faculdade de Medicina de Ribeirão Preto
University of São Paulo
RIBEIRÃO PRETO – BRAZIL
imsantos@fmrp.usp.br

DELABOUGLISE Alexis

Cirad
MONTPELLIER – FRANCE
alexis.delabouglice@cirad.fr

ELOIFLIN Roger

UMR Intertryp
IRD
MONTPELLIER – FRANCE
roger.eloiflin@ird.fr

EVANS Alec

Clinglobal
TAMARIN – MAURITIUS
alec.evans@clinglobal.com

FUANDILA Nurul Novelia

ISEM
IRD
MONTPELLIER – FRANCE
nurul.fuandila@umontpellier.fr

GARROS Claire

UMR ASTRE
Cirad
MONTPELLIER – FRANCE
claire.garros@cirad.fr

GEORGES Karla

School of Veterinary Medicine
University of the West Indies
MOUNT HOPE – TRINIDAD AND TOBAGO
karla.georges@sta.uwi.edu

GIL Patricia

BIOS
Cirad
MONTPELLIER – FRANCE
patricia.gil@cirad.fr

GUENDOUZ Samia

BIOS - ASTRE
Cirad
MONTPELLIER – FRANCE
samia.guendouz@cirad.fr

GUILLEMOT Jules

Cirad - ISTOM
MONTPELLIER – FRANCE
jules.guillemot@cirad.fr

HARTLEY Catherine

Institute of Infection, Veterinary and
Ecological
University of Liverpool
LIVERPOOL – UK
catherine.hartley@liverpool.ac.uk

HEMMINK Johanneke

Animal and Human Health Program
International Livestock Research Institute
NAIROBI – KENYA
h.hemmink@cgiar.org

HOLZMULLER Philippe

UMR CMAEE
Cirad
MONTPELLIER – FRANCE
philippe.holzmuller@cirad.fr

HOUBEN Sarah

Avia-GIS
ZOERSEL – BELGIUM
shouben@avia-gis.com

IJOMA Sandra

Veterinary Public Health and
Preventive Medicine
National Veterinary Research Institute
JOS – NIGERIA
sandraijomaifeoma@gmail.com

JACQUIET Philippe

Laboratory of Parasitology

ENVT

TOULOUSE – FRANCE
philippe.jacquet@envt.fr

JORI Ferran

UMR ASTRE
Cirad
MONTPELLIER – FRANCE
ferran.jori@cirad.fr

KEHR Dorothea

Section of Molecular and
Translational Cardiology
Heidelberg University Hospital
HEIDELBERG – GERMANY
dorotheakehr@gmx.de

KEO Srong

Faculty of Agricultural Economics and
Rural Development
Royal University of Agriculture
PHNOM PENH – CAMBODIA
keosrong@gmail.com

KWIATEK Olivier

UMR 117 ASTRE
Cirad
MONTPELLIER – FRANCE
kwiatek@cirad.fr

LANGLOIS Thibaut

MiVEGEC - ASTRE
IRD - Cirad
MONTPELLIER – FRANCE
thibaut.langlois@etu.umontpellier.fr

LE SAOUT Cécile

Alpha Visa Congrès
MONTPELLIER – FRANCE
cecile@alphavisa.com

LECOLLINET Sylvie

ASTRE
Cirad
PETIT BOURG – FRANCE
sylvie.lecollinet@cirad.fr

LIMOZIN Adrien

Innovative Diagnostics
GRABELS – FRANCE
adrien.limozin@innovative-diagnostics.com

MADDER Maxime

Clinglobal
TAMARIN – MAURITIUS
Maxime.Madder@clinglobal.com

MAGNUSSON Ulf

Clinical Sciences
Swedish University of Agricultural
Sciences
UPPSALA – SWEDEN
ulf.magnusson@slu.se

MAKGABO Sekgota Marcus

University of Pretoria
PRETORIA – SOUTH AFRICA
marcusmkgabo.mm@gmail.com

MEDOUGA Betty

UMR ASTRE
Cirad
MONTPELLIER – FRANCE
betty.medouga@cirad.fr

MÉJEAN Cathy

BIOS - UMR 117 ASTRE
Cirad
MONTPELLIER – FRANCE
cathy.mejean@cirad.fr

MEYER Damien

CRVC
Cirad
PETIT BOURG – FRANCE
damien.meyer@cirad.fr

MINANI Salvator

Department of Public Health
Institute of Tropical Medicine, Antwerp
ANTWERP – BELGIUM
sminani@itg.be

MINET Cécile

UMR 17 Intertryp
Cirad
MONTPELLIER – FRANCE
cecile.minet@cirad.fr

MOLIA Sophie

UMR ASTRE
Cirad
MONTPELLIER – FRANCE
sophie.molia@cirad.fr

MOSQUEDA Juan

Faculty of Natural Sciences
Autonomous University of Queretaro
QUERETARO – MEXICO
joel.mosqueda@uaq.mx

MST SOGRA BANU Juli

Queensland Alliance for Agriculture &
Food Innovation
University of Queensland
BRISBANE – AUSTRALIA
m.juli@uq.edu.au

NIJHOF Ard

Freie Universität Berlin
BERLIN – GERMANY
Ard.Nijhof@fu-berlin.de

NUVEY Francis Sena

Centre Suisse de Recherches
Scientifiques
ABIDJAN – CÔTE D'IVOIRE
fsnuvey@gmail.com

OWEN Rachel

The Roslin Institute
University of Edinburgh
EDINBURGH – UK
rowen2@exseed.ed.ac.uk

PÉREZ-OTÁÑEZ Ximena

Centre for Earth and Climate Research
Université Catholique de Louvain
LOUVAIN-LA-NEUVE – BELGIUM
ximena.perezotanez@student.uclouvain.be

PHOEURK Raksmei

Faculty of Agricultural Economics
and Rural Development
Royal University of Agriculture
PHNOM PENH – CAMBODIA
praksmei@rua.edu.kh

PIRO-MEGY Camille

BIOS - ASTRE
Cirad
MONTPELLIER – FRANCE
camille.piro-megy@cirad.fr

POW-BROWN Patricia

School of Veterinary Medicine
University of the West Indies
SAN JUAN – TRINIDAD AND TOBAGO
patricia.powbrown@my.uwi.edu

PRADEL Jennifer

ASTRE
Cirad
MONTFERRIER-SUR-LEZ – FRANCE
jennifer.pradel@cirad.fr

RAKOTOARIVONY Rianja

ASTRE
Cirad
ANTANANARIVO – MADAGASCAR
rianjarakotoarivony@gmail.com

RIANA Elizabeth

Parasitology Unit, Department of
Pathology
Chulalongkorn University
BANGKOK – THAILAND
elizabethriana1994@gmail.com

ROCHE Mathieu

TETIS
Cirad
MONTPELLIER – FRANCE
mathieu.roche@cirad.fr

RODRIGUES Valérie

BIOS - UMR ASTRE
Cirad
PETIT BOURG – FRANCE
valerie.rodrigues@cirad.fr

RONDEAU Alexia

Vétérinaires Sans Frontières International
BRUSSELS – BELGIUM
a.rondeau@vsf-international.org

SANTOS John Harvey

University of Queensland
ST LUCIA – AUSTRALIA
johnharvey.santos@uq.edu.au

SERVAN DE ALMEIDA Renata

BIOS - ASTRE
Cirad
MONTPELLIER – FRANCE
renata.almeida@cirad.fr

SIDDLE Hannah

QAAFI
University of Queensland
BRISBANE – AUSTRALIA
h.siddle@uq.edu.au

SOMÉ Gnohion Fabrice

BIOS
Cirad
MONTPELLIER – FRANCE
somefabricg@gmail.com

SPARAGANO Olivier

Agricultural Sciences and Practice
Royal Agricultural University
GLOUCESTERSHIRE – UK
oliver.sparagano@rau.ac.uk

SQUARZONI Cécile

ASTRE
Cirad
SAINT-DENIS – FRANCE
cecile.squarzoni@cirad.fr

STEBER Stephan

Veterinary Drugs
Efficacy and Target Animal
Federal Office Consumer Protect Food
Safety
BERLIN – GERMANY
stephan.steber@bvl.bund.de

TABOR Alicja (Ala)

Queensland Alliance for Agriculture &
Food Innovation
University of Queensland
BRISBANE – AUSTRALIA
a.tabor@uq.edu.au

TAGNE MOUAFFO Stéphane Roméo

UMR ASTRE
Cirad
LIÈGE – BELGIUM
mouaffostephane@yahoo.fr

TALLA MBA Mathias

Cirad
MONTPELLIER – FRANCE
mathias.talla_mba@cirad.fr

TEISSEIRE Maguelonne

TETIS
INRAE
MONTPELLIER – FRANCE
maguelonne.teisseire@inrae.fr

TEMBE Danisile

University of KwaZulu-Natal
DURBAN – SOUTH AFRICA
tembed@ukzn.ac.za

TESCH Maxime

Cirad
MONTFERRIER-SUR-LEZ – FRANCE
maxime.tesch@cirad.fr

THÉVENON Sophie

BIOS UMR Intertryp
Cirad
MONTPELLIER – FRANCE
sophie.thevenon@cirad.fr

THYS Eric

Institute of Tropical Medicine
ANTWERP – BELGIUM

THYS Séverine

ASTRE
Cirad
MONTPELLIER – FRANCE
severine.thys@cirad.fr

TOLNO Saa Andre

UMR ASTRE 117
Cirad
MONTPELLIER – FRANCE
saa-andre.tolno@cirad.fr

VACHIERY Nathalie

UMR ASTRE
Cirad
MONTPELLIER – FRANCE
nathalie.vachier@cirad.fr

VANNY Chhuon

Faculty of Agricultural Economics
and Rural Development
Royal University of Agriculture
PHNOM PENH – CAMBODIA
cvanny@rua.edu.kh



LIST OF SPONSORS / EXHIBITORS

Boehringer-Ingelheim Animal Health France

Transforming lives for generations.

29 avenue Tony Garnier – CS77123

69348 LYON CEDEX 7 – FRANCE

Laurence.GABANA@boehringer-ingelheim.com

www.boehringer-ingelheim.com/

Clinglobal

Clinglobal is a global, science-based, quality-driven group dedicated to accelerating innovation by providing services and solutions to the animal care industry through the ever-expanding group.

B03/04, The Tamarin Commercial Hub,

Jacaranda Avenue

90903 TAMARIN – MAURITIUS

+43 677 629 04121

enquiry@clinglobal.com

www.clinglobal.com

Innovative Diagnostics

Innovative Diagnostics develops, manufactures and markets ELISA and PCR diagnostic tests for the detection of infectious diseases in humans and animals.

310 rue Louis Pasteur

34790 GRABELS – FRANCE

naomie.vialet@innovative-diagnostics.com

www.innovative-diagnostics.com

REMVT Editor

philippe.holzmuller@cirad.fr/vincent.porphyre@cirad.fr

<https://revues.cirad.fr/index.php/remvt/>

Standard BioTools France SARL

Standard BioTools™, previously known as Fluidigm®, is the sole provider of the Biomark™ X9 System, the only genomics system on the market that can perform PCR and NGS library preparation on the same instrument. It is an open system that can be used for genotyping, gene expression, CNV experiments and more.

43-47 avenue de la Grande-Armée

75116 PARIS – FRANCE

+33 1 60 92 42 40

education.team@standardbio.com

www.standardbio.com/

LIST OF PUBLIC PARTNERS

La Région Occitanie / Pyrénées-Méditerranée

<https://www.laregion.fr/>

IRD

<https://en.ird.fr/>

INRAE

<https://www.inrae.fr/en>

