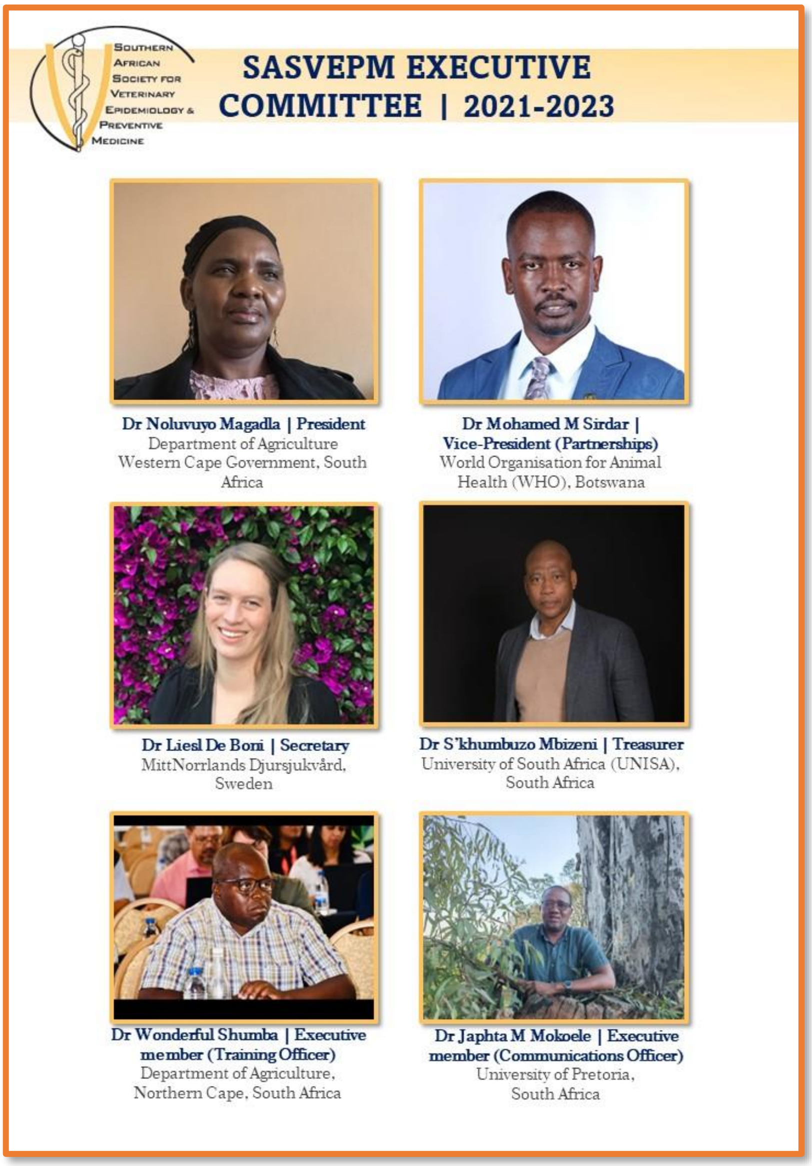
20TH ANNUAL CONGRESS

23-25 Aug. 2023 | Gaborone, Botswana

SOUTHERN
AFRICAN
SOCIETY FOR
VETERINARY
EPIDEMIOLOGY &
PREVENTIVE
MEDICINE

Programme & Abstracts

Celebrating our



Southern African Society for Veterinary Epidemiology & Preventive Medicine

SASVEPM EXECUTIVE COMMITTEE | 2021-2023

Dr Noluvuyo Magadla | President
Department of Agriculture
Western Cape Government, South Africa

Dr Mohamed M Sirdar | Vice-President (Partnerships)
World Organisation for Animal Health (WHO), Botswana

Dr Liesl De Boni | Secretary
MittNorrlands Djursjukvård, Sweden

Dr S'khumbuzo Mbizeni | Treasurer
University of South Africa (UNISA), South Africa

Dr Wonderful Shumba | Executive member (Training Officer)
Department of Agriculture, Northern Cape, South Africa

Dr Japhta M Mokoele | Executive member (Communications Officer)
University of Pretoria, South Africa

Table of Contents

Welcome

Dear SASVEPM Members

On behalf of the Southern African Society for Veterinary Epidemiology & Preventive Medicine Executive Committee (EXCO), it is with great pleasure to welcome you all to the 20th Annual SASVEPM Congress at the Avani Resort & Casino in Gaborone, Botswana from 23-25 August 2023. We are promising a platform that will continue to provide opportunities for interesting attendee engagements.

The 20th SASVEPM congress is offering a forum for authors to present research, as oral or poster presentations, to the SASVEPM audience under the theme "One Health – Without Borders" with six subthemes. SASVEPM is further looking forward to hosting some of the World's renown scientists as guest speakers to unpack the subthemes and beyond.

SASVEPM believes in healthy animals, healthy humans, and a healthy planet. The One Health perspective considers animals, people and environment and ensures that people and communities are involved in the decisions that affect their health and environment. Focussing on animals is just part of caring for the delicate balance of health that includes soil, air, water, topography, population density, markets, culture, and tradition.

A key to the approach is collaboration – across disciplines, professions, borders, and groups – that builds holistic solutions with a lens of inter-connectedness.

SASVEPM now has a multi-national membership of over 1700, including scientist, private veterinarians, state veterinarians, veterinarians in industry and members in academia and research. To date the Society has held nineteen Annual Congresses, which have been a highly successful blend of scientific papers, posters, and continuing education (CE) sessions. SASVEPM also hosted the twelfth International Symposium for Veterinary Epidemiology and Economics (ISVEE XII) during August 2009 at the ICC in Durban. We are humbled to be hosting our 20th congress and also very proud to host the next ISVEE 18 in Cape Town in 2027.

May this be a professionally productive, personally pleasant, very successful and enjoyable congress.

Dr Noluvuyo Magadla
President, SASVEPM

History of SASVEPM

How it began

SASVEPM inception was as a result of Professor Bruce Gummow's membership of the UK Epidemiology Society (SVEPM). Bruce had been a member of this society for a number of years and had been building epidemiology capacity at the Faculty of Veterinary Science, University of Pretoria since 1990. He recognised the need for a forum where veterinarians in Southern Africa could present their work and learn from others. In the late 1990's he began discussions with the SVEPM executive to see if the UK society would consider creating a branch society in South Africa. Initial discussions were positive, but the UK society was hesitant to create a branch society because financial management and control would be difficult from the UK. Permission was then obtained, by Bruce Gummow, from the UK executive to create an independent society in South Africa modelled on the UK society, who were considered as a sister society in the early years.

Equipped with his experience gained as a member of the SVEPM, Bruce Gummow then began canvassing support for a society in South Africa, which he received from colleagues such as Vincent Turner, Rick Mapham, Giel Van Aard, Adele Faul, Malcom De Bude and current or past epidemiology students of his such as Peter Thompson, Richard Emslie, and Anita Michele.

A meeting was called on the 20 October 2000 by Bruce Gummow and Peter Thompson, where the first committee was voted in and Bruce Gummow, was elected as the first Chairperson of the society, Peter Thompson the first secretary and Poncho Mokaila the first treasurer. Other committee members were Anita Michele and Rick Mapham. The meeting was well attended.

The society began with nothing and the members of the first committee had to work hard to create a viable society that would be sustainable. Bruce Gummow wrote the constitution based on the UK societies constitution. He also obtained permission from the UK society to adapt their emblem for use by the newly created SASVEPM. Quoting Bruce "*Over the first 6 months the new executive ratified an agreement of affiliation with our sister society in the UK, set up our own list server, opened our own bank account, managed, and run our first conference and produced our first set of proceedings containing papers of an international standard*". SASVEPM became internationally recognised as the regional society for epidemiologists and became instrumental in facilitating the building capacity in veterinary epidemiology through SASVEPM conference. "*We obtained sponsorship for our society from two major organisations, Bayer Animal Health and Geographical Information Systems and had the support of government through Veterinary Services, and academia, through the Faculty of Veterinary Science*". The society also opened the doors of communication between epidemiologists within Africa and beyond. A philosophy of mixing continuing education and scientific content was also introduced in the first conference and has continued since then.

The walking stick emblem of office for the chairperson of the Society was purchased and introduced by Bruce Gummow when he handed over office of chairperson to Willie Ungerer in 2003, with the aim of bringing some tradition into the society (see presidents address 2003) and as a physical reminder of where the values of the Society lay.

The symbol of office is to be passed on as a tradition from one president to the next as long as the society exists. He chose a walking stick to remind the members that the president needs all the support he can get from them, but also because our logo has a pole in it. It reminded him of Moses pole (Numbers chapter 21 vs 4-9); "*They travelled from Mount Hor along the route to the Red Sea, to go around Edom. But the people grew impatient on the way; they spoke against God and against Moses, and said, "Why have you brought us up out of Egypt to die in the desert? There is no bread! There is no water! And we detest this miserable food!*

Then the Lord sent venomous snakes amongst them; they bit the people and many Israelites died. The people came to Moses and said, "We sinned when we spoke against the Lord and against you. Pray that the Lord will take the snakes away from us." So, Moses prayed for the people.
The Lord said to Moses, "*Make a snake and put it on a pole; anyone who is bitten can look at it and live." So, Moses made a bronze snake and put it up on a pole. Then when anyone was bitten by a snake and looked at the bronze snake, he lived*."

The walking stick symbolises that pole. Epidemiology is the pole that people can look to, to provide disease prevention and control in our Land. This stick however has no bronze snake on it as Moses' pole did, rather it has a circle on it to symbolise the magnifying glass of the detective to remind us as epidemiologists that we are disease detectives. When you look at this stick you are to be reminded by the absence of snakes that are seen in our logo, that the power of Moses pole came from God himself and so the President and the society should always be under His authority as well.

A Brief Summary of SASVEPM Congresses

This section was compiled by Dr Liesl De Boni (SASVEPM Secretary 2021-2023) to summarise all the annual congresses held by SASVEPM since its inception.

Table 1. Summary of SASVEPM Annual Congresses to date, 2001 - 2023.

Congress #	Year	Congress theme	Place	Workshops
1st	2001	CE: Investigating an unknown disease in a population	Onderstepoort, GP, South Africa (SA)	Disease Outbreak Investigation
2nd	2002	CE: Theory, practice and application of surveys/ surveillance	Onderstepoort, GP SA	Risk Analysis course
3rd	2003	CE: Economics of animal disease control	Pretoria, GP SA	
4th	2004	CE: Evaluation of diagnostic tests	Pretoria, GP, SA	
5th	2005	CE: One Medicine	Irene, GP,SA	
6th	2006	CE: Epidemiology in Practice	Durban, KZN, SA	
7th	2007	CE: Wildlife epidemiology	Somerset West, WC, SA	
8th	2008	CE: Rinderpest & PPR. One disease of the past and one of the future	Kopanong, GP, SA	
-	2009	ISVEE 12 & SASVEPM	Durban, KZN, SA	
9th	2010	Animals and Man: Exploring the Expanding Interface	Pretoria, GP, SA	GIS mapping techniques
-	2011	Epidemiology Stream at World Vet Congress	Cape Town, WC, SA	Disease Outbreak Investigation course
10th	2012	Outbreak Investigation: Science and Intuition	Pretoria, GP, SA	Databases for vets
11th	2013	Preventing Disease for Better Health	Salt Rock, KZN, SA	Brucellosis
12th	2014	Innovative Epidemiology	Port Elizabeth, EC, SA	Tracing the Source Workshop
13th	2015	Wildlife-Livestock-Community Interface	Bloemfontein, FS, SA	

Congress #	Year	Congress theme	Place	Workshops
14th	2016	Epidemiology on the Edge: Economics, Trade, and Movement	Cape Town, WC, SA	
15th	2017	SASVEPM &SAVA Joint Conference	Boksburg, GP, SA	
16th	2018	SASVEPM &RuVASA Joint Conference	Boksburg, GP, SA	
17th	2019	Field Epidemiology in Action	Umhlanga, KZN, SA	Epidemiology & interdisciplinary approach
-	2020	*No congress due to COVID-19*		*African Swine Fever - online workshop* *Foot and Mouth Disease - online workshop* *Animal Health and Economics - online workshop*
18th	2021	Creative Animal Health Solutions for Sustainable Economic Growth	Bela-Bela, LP, SA	Data Management Lab Biosecurity
19th	2022	One Africa, One Health, One Welfare	Buffalo City, EC, SA	Rabies workshop
20th	2023	One Health Without Borders	Gaborone, Botswana	Disease Outbreak Investigation

ISVEE 18
Cape Town, South Africa, 2027

18th Symposium of the International Society
for Veterinary Epidemiology & Economics

SASVEPM will be hosting ISVEE XVIII in Cape Town, 2027

Table 2. List of Chairpersons/Presidents of SASVEPM, 2001 - 2023.

Period	Name
2000-2003	Bruce Gummow
2003-2004	Willie Ungerer
2004-2005	Wilna Vosloo
2005-2006	Peter Thompson
2006-2007	Marna Sinclair
2009-2010	Hannes Pienaar
2010-2011	Peter Geertsma
2011-2013	John Grewar
2013-2015	Alan Kalake
2015-2017	Lesley van Helden
2017-2019	Krpasha Govindasamy
2019-2021	Nelson Matekwe
2021-2023	Noluvuyo Magadla
2023-2025	Mohamed Sirdar

Table 3. Recipients of the Epidemiology Prize, 2001-2023

Year	Recipient
2004	Richard Emslie
2005	Gary Buhrmann
2006	Peter Thompson
2007	Bruce Gummow
2008	Marna Sinclair
2009	Willie Ungerer
2010	Anita Michel
2011	Roy Bengis
2012	Lucille Blumberg
2013	Kevin le Roux *(in 2013 it became the Willie Ungerer Memorial Epidemiology Prize)*
2014	John Grewar
2015	Grietjie de Klerk
2016	Johann Kotze
2017	Peter Geertsma
2018	Geoffrey Fosgate
2019	Cheryl McCrindle
2020	*No prize given*
2021	Michael Modisane
2022	Mpho Maja
2023	Misheck Mulumba

SASVEPM Epidemiology Prize Winners over the years

Tracing the Source Workshop, Pretoria, 2014

Databases for Veterinarians Workshop, Pretoria, 2012

SASVEPM Pre-congress Workshop on Databases for Veterinarians
30th and 31st July 2012

SASVEPM Congress 2012 attendees, Pretoria

SASVEPM Congress 2013 attendees, Port Elizabeth

Round Table Discussion at SASVEPM Congress 2022, Buffalo City

Rabies Workshop, Buffalo City, 2022

Delegates boosting at ISVEE 2022

Participant Information

Registration Information

Each participant at SASVEPM 2023 must register in person at the Registration Desk to collect a Congress kit and badge before attending any of the sessions or events.

Registration Times

Tuesday 22 August: 14h00 – 17h00
Wednesday 23 August: 07h00 – 08h00
Thursday 24 August: 07h00 – 08h00
Friday 24 August: 07h00 – 08h00

Badges

Identification badges are required for admission to all sessions, official functions, and social events of the congress. Participants who lose their badges must report to the Registration Desk, presenting proof of identity.

Presenters, Chairs & Facilitators

All speakers are required to report to the Registration Area at least 90 minutes before their presentation to ensure that we have uploaded the correct presentation onto the presentation laptop in the auditorium.

Poster Presentations

Posters will be available for viewing in the foyer for the duration of the congress. Three dedicated Poster Sessions will be hosted (one per day) and presenters are requested to present their posters during their dedicated time slots. Posters may be setup from Tuesday 14h00.

Contacts

Ms Corné Engelbrecht | +27 (0) 82 925 9241
Ms Melanie Pretorius | +27 (0) 82 410 1202
Ms Nthabiseng Letsoalo | +27 (0) 73 509 4012

On-site Congress Support

Emergency Medical assistance and Paramedic Services

For assistance with any medical emergencies, please visit the Registration area. Medical procedures and medicine will be for the attendee's own account. For any medical emergencies, please contact +27 (0) 82 925 9241 during congress hours.

Meals and Snacks

Meals and beverages will be provided to attendees as indicated in the programme, during congress times.

Safety and Security

In the interest of personal safety and security, attendees should only display their identity tags in the congress area premises and within the restricted congress areas.

Lost property can be handed in at the Registration Desk. Any losses should be reported to the Congress Secretariat. Although every effort will be made to retrieve lost personal belongings, the responsibility for securing his/her personal belongings remains that of each person attending the congress.

Accommodation and Transport

IMPORTANT: Excluding sponsored participants, all accommodation and transport arrangements will be for your own account.

Flights

Should you require any assistance with flights, please approach Nthabiseng Letsoalo at the Registration Desk area.

Dress Code

The suggested dress code for the congress is formal/business casual, but please do bring something warm along as the rooms will be air-conditioned.

Liability

Neither the Congress Secretariat nor any of its contracted service providers will be responsible for the safety of articles of any kind brought into the Congress facilities by attendees, whether registered or not, their agents, contractors, visitors and/or any other person/s whatsoever. The Congress attendee shall indemnify and not hold the organisers and associates of the organisers and their subcontractors liable in respect of any cost, claims, demands and expenses as a result of any damage, loss or injury to any person howsoever caused as a result of any act or default of the Congress Secretariat or a person representing the Congress Secretariat, its contractors, or guests. In addition, the Congress attendee shall take all necessary precautions to prevent any loss or damage to his/her property with special regard to mobile phones, carry or handbags and computing equipment.

Foreign Delegate Information

Sun **20 Aug**	☁	31 / 14 °C	Cloudy.
Mon **21 Aug**	⛅	33 / 17 °C	Broken clouds.
Tue **22 Aug**	⛅	35 / 18 °C	Morning clouds.
Wed **23 Aug**	☀	36 / 18 °C	Sunny.
Thu **24 Aug**	⛅	35 / 19 °C	Afternoon clouds.
Fri **25 Aug**	⛅	35 / 18 °C	Morning clouds.
Sat **26 Aug**	🌤	37 / 18 °C	Mostly sunny.

Climate in Gaborone

The climate of Gaborone is **sub-tropical semi-arid**, tempered by altitude, with a hot, rainy season from November to March and a long dry season from April to October, within which there is a cool period from May to August. In the latter, at night the temperature can drop a few degrees below freezing. During the day, it can get very hot from September to April. The city is the capital of Botswana and is located in the south-east of the country, near the border with South Africa and at 1,000 meters (3,300 feet) above sea level.

The **average temperature** of the coldest month (July) is of 13.5°C (56.3 °F), that of the warmest month (January) is of 26.0°C (78.7 °F).

Language

English and Tswana are the official language in Botswana. English is taught at schools and is widely spoken in all urban centres. Even in rural areas, many local villagers (especially younger ones who have received schooling) will be able to converse in English. All guides and general staff in the camps, lodges and hotel have a good command of English.

German, Italian, and French translators are available on request through your travel operator or agent. When staying at a private camp or lodge, your guide can act as interpreter if necessary, during social interactions.

Electrical Supply

Electricity is supplied at 220/240v. Both square (UK) and round (RSA) wall plugs are used.

Gratuity Guide

In Botswana, one is not under any obligation to offer gratuity (tips) for services rendered at restaurants, bars, hotels, etc. It is at the discretion of the individual whether or not to pay gratuity for services.

Emergency Numbers

Ambulance	997 (Toll Free)
Police	999 (Toll Free)
Fire Brigade	998 (Toll Free)
Medical Rescue	911 (Toll Free)
Medical Air Rescue	390-1601

Currency

The Botswana currency is the Pula (meaning ‘rain’ in Setswana).

It is divided into 100 thebe (meaning ‘shield’ in Setswana). Travellers’ cheques and foreign currency may be changed at banks, bureaux de change, and authorised hotels.

The US dollar, Euro, British Pound, and the South African Rand are the most easily convertible currencies.

Automatic teller machines accept foreign visa cards but are mostly found in larger towns and cities. Foreign cash withdrawals may be subject to additional fees.

Cultural sites and community art and craft outlets usually only accept cash; however, chip and pin and contactless payment options are becoming more common. If in doubt, inquire with your guide or upon arrival at an outlet or attraction/destination.

Exchange Rates on 13 August 2023 (these can fluctuate)
1BWP = USD 0.074
1BWP = EUR 0.067
1BWP = GBP 0.058
1BWP = ZAR 1.39

Banks

Seven main commercial banks, as well as a number of foreign exchange bureaux, operate in Botswana.

Banking hours
Monday to Friday 8:30-15:30
Saturday 8:30 to 10:45

Credit cards

Major credit cards, such as MasterCard and Visa, are accepted throughout the country, in most hotels, restaurants, retail outlets and safari companies. However, shops in remote areas and service stations may only accept cash.

Drinking Water

Tap water throughout the country is safe to drink. Bottled mineral water is readily available in most shops and supermarkets, and at camps and lodges. Tourists travelling by road are advised to carry sufficient water at all times.

Value Added Tax

To claim 14% VAT refund for total value of goods purchased, the amount spent should be more than P 5,000. In such cases, the following is required: a tax invoice stating VAT paid, your passport number and your bank account details.

It is always advisable to keep a copy of the VAT form as a record for any follow-up on the transaction. VAT claims usually can be made at all major border posts and airports.

Sponsors & Partners

With appreciation to our 2023 Congress Sponsors

DEFENSE THREAT REDUCTION AGENCY
UNITED STATES OF AMERICA

BTRP
BIOLOGICAL THREAT REDUCTION PROGRAM

OBP
ONDERSTEPOORT
BIOLOGICAL PRODUCTS

BVI
BOTSWANA VACCINE INSTITUTE

BUAN
BOTSWANA UNIVERSITY OF
AGRICULTURE AND NATURAL RESOURCES
Inspiring Sustainable Growth

MSD
Animal Health

SYLIKE
MEDICALS

With appreciation to our 2023 Congress Partners

MINISTRY OF AGRICULTURE
IMPROVING FOOD SECURITY
BOTSWANA

BOTSWANA VETERINARY ASSOCIATION
BVA

nardi
National Agricultural Research and Development Institute

Programme

Wednesday, 23 August 2023

Time	Theme	Title	Speaker
07h00	Registration opens - arrival coffee and tea / Industry Networking		
SESSION CHAIR: DR NOLOVUYO MAGADLA			
08h00	Opening session	Welcome & Opening Remarks	Noluvuyo Magadla (SASVEPM president) & Kefentse Motshegwa (Botswana Chief Veterinary Officer and Director of Veterinary Services)
08h30		**Keynote 1 - Making One Health Work: A personal journey**	**Bruce Gummow, College of Public Health, Medical and Veterinary Sciences, James Cook University**
09h30	Infectious Diseases	Investigating the epidemiology, ecology, and socio-economic impact of Rift Valley fever in southern Africa	Peter N. Thompson, University of Pretoria
09h50		Hospital-acquired and zoonotic bacterial organisms and their associated antimicrobial-susceptibility profile in veterinary hospitals: A Systematic Review	Dikeledi C. Sebola, University Of Pretoria
10h10		Cattle trade networks in the foot-and-mouth disease (FMD) Protection Zone of Limpopo Province	Kholofelo K. Malatji, University of Pretoria
10h30	Mid-morning refreshments		
SESSION CHAIR: DR WONDERFUL SHUMBA			
11h00	Infectious Diseases	The prevalence of infectious bovine keratoconjunctivitis among Western Cape dairy cattle and associated risk factors	Louis H. Maartens, Deltamune (Pty) Ltd
11h20		Evaluation of haematological parameters in cattle, detection, and confirmation of cattle *Anaplasma marginale* infection at BUAN farm in the southeast region of Botswana	Solomon S. Ramabu, Botswana University of Agriculture and Natural Resources
11h40		Parasite burden among peri-urban free-roaming pigs in Gert Sibande District Municipality of Mpumalanga Province, South Africa	Priscilla Munzhelele, University of South Africa
12h00		Botswana Vaccine Institute's contributions towards Foot and Mouth Disease control in Sub-Saharan Africa with special reference to incursion of FMD serotype O into Southern Africa	Mokganedi Mokopasetso, Botswana Vaccine Institute, WOAH Reference Laboratory for FMD
12h20	Poster Session 1		
13h00	Lunch		

SESSION CHAIR: DR MOHAMED SIRDAR			
14h00	Infectious Diseases	Evidence for a host-switch in the maintenance of canid rabies variant in the Northern Cape Province, South Africa	Ernest Ngoepe, ARC-OVR
14h20		Determination of the prevalence of bovine cysticercosis in slaughter beef cattle in Matabeleland region of Zimbabwe using B158/B60 antigen ELISA	Munyaradzi C. Marufu, University of Pretoria
14h40		Seroprevalence and factors associated with *Coxiella burnetii* exposure in goats in Moretele	Rungano Magadu, University of Pretoria
15h00		5 Bluetongue virus infection in farm dogs with exposure to an infected sheep flock in South Africa	Josef D. Hanekom, University of Pretoria
SESSION CHAIR: PROF GEOFF FOSGATE			
15h50	Infectious Diseases	Detection of Dengue Viral Infections in *Aedes aegypti* and febrile patients in Kassala City, Sudan using One Health approach	Khalid A. Enan, Department of Virology Central Laboratory - The Ministry of Higher Education and Scientific Research
16h10		Lessons from Japanese Encephalitis Virus seroposurvey in hunted wild animals from Yamaguchi prefecture in Japan	Peter Kimeli, University of Nairobi
16h30	End of Day 1		
18h30	Transport departs to dinner venue: Three Chiefs' at CBD		
19h00	DINNER SPONSORED BY BOTSWANA VACCINE INSTITUTE		

Thursday, 24 August 2023

Time	**Theme**	**Title**	**Speaker**
07h00	**Registration opens - arrival coffee and tea / Industry Networking**		
SESSION CHAIR: PROF ANITA MICHEL			
08h00	Keynote 2 - One Health as a tool for disease control		Moetapele Letshwenyo, WOAH, Sub-Regional Representative for Southern Africa
09h00	Infectious Diseases	Spatial distribution of dog rabies, rabies vaccination coverage for dog rabies and the prevalence of dog bite in three selected regions in Gauteng Province, South Africa	Oluyemisi A. Akerele, University of South Africa/ GDARDE
09h20		Molecular characterization of cattle rabies linked to cattle infections in the Northwest Province, South Africa	Onkemetse A. Khoane, North-West University
09h40	Scientific Developments & Preventative Medicine	Landscape surveillance: tagging remote collar data with risk flags in an adaptive, real-time monitoring platform	John D. Grewar, JDATA (Pty) Ltd
10h00		Exploring bovine tuberculosis vaccine efficacy in African Buffalo	Jennie M. Hewlett, Faculty of Veterinary Science, University of Pretoria
10h20	Mid-morning refreshments		
SESSION CHAIR: DR ITUMELENG MATLE			
10h50	Scientific Developments & Preventative Medicine	Evaluation of aluminium hydroxide nanoparticles as efficient adjuvants to potentiate the immune response against botulinum C and D toxoid vaccine	Ziphezinhle Mbhele, Onderstepoort Biological Products
11h10		The role of smallholder pig farmers in the biosecurity of pig diseases in the Eastern Cape Province of South Africa using ASF as a model	Vincent Simbizi, Department of Production Animal Studies, University of Pretoria
11h30		Efficacy of *Aloe Vera* and *Curcuma Longa* in managing Porcine Staphylococcal Infections	Joshua Ngwisha, University of Zambia, School of Veterinary Medicine

Thursday, 24 August 2023

Time	Theme	Title	Speaker
11h50	Scientific Developments & Preventative Medicine	Safety and immunogenicity of inactivated Rift Valley Fever Smithburn viral vaccine in sheep	Matome S. Matsiela, Onderstepoort Biological Products
12h10		Production of recombinant Lumpy skin disease virus A27L and L1R proteins for application in diagnostics and vaccine development	Nomfundo P. Ntombela, University of KwaZulu-Natal
12h30	Poster Session 2		
13h00	Lunch		
SESSION CHAIR: DR JOHN GREWAR			
14h00	Onderstepoort Biological Products Presentation		Onderstepoort Biological Products
14h20	Public Health & Environmental Health	The hippopotamus and One Health - What's the link?	Anita L. Michel, University of Pretoria
14h40		Antimicrobial resistance in fish and poultry: Public health implications for animal source food production in Nigeria, Egypt, and South Africa	Ekemini M. Okon, Ghent University
15h00		Serological evidence and co-exposure of selected infections among livestock slaughtered at Eastern Cape abattoirs in South Africa	Koketso D. Mazwi, University of Pretoria
15h20	Mid-afternoon refreshments		
16h00	SASVEPM AGM – Download Agenda and documents for meeting <click here> Online Link: ZOOM - Passcode: 774900		
18h00	End of Day 2		

OFFICIAL CONGRESS DINNER & AWARDS

Dress code: Semi-formal or Traditional

18h30	Buses depart from Avani to Botswanacraft
19h00	Congress Dinner & Awards
22:00	First bus leaves back to Avani
24:00	Last bus leaves back to Avani

Friday, 25 August 2023

Time	Theme	Title	Speaker
07h00	Registration opens - arrival coffee and tea / Industry Networking		
SESSION CHAIR: DR SKHUMBUZO MBIZENI			
08h00	**Keynote 3 - One Welfare – research and development for holistic and transformative interventions in livestock production**		**Julius R. Atlhopheng, National Agricultural Research and Development Institute, Botswana**
09h00	Public Health & Environmental Health	Seroprevalence of *Taenia saginata* cysts in cattle, human hospital cases and Risk Factors for human taeniasis in Kajiado County, Kenya	Ruphline M. Anyango, University of Pretoria
09h20		Molecular characterization and antimicrobial resistance profiles of *Staphylococcus aureus* isolated from meat and meat products in South Africa	Emmanuel M. Seakamela, Limpopo Department of Agriculture and Rural Development
09h40		Occurrence, antimicrobial resistance, and genetic diversity of *Klebsiella pneumoniae* from broiler chicken carcasses in Gauteng Province, South Africa	Itumeleng Matle, ARC: OVR
10h00		Occupational health and safety knowledge, awareness and practices to prevent zoonotic diseases among veterinary services fieldworkers in the North-West Province, South Africa	Sboniso Mhlongo, North-west Department of Agriculture
10h20	Mid-morning refreshments		
SESSION CHAIR: DR TANDILE NDOBENI			
11h00	Public Health & Environmental Health	Strategies used by locals in Lephalale Municipality, Limpopo, South Africa, to cope with inadequate water supply	Nthabiseng A. Modimola, Tshwane University of Technology
11h20		Africa One Health Network	Misheck Mulumba, Africa One Health Network
11h40		Molecular epidemiology and risk assessment of non-typhoid Salmonella isolates from poultry in South Africa	Elly Masitha, University of Pretoria
12h00	Socioeconomic/ Cultural Dynamics	Village Livestock Auction facilities as catalyst for socioeconomic development and control of infectious diseases: The case of North-West Province in South Africa	Mothusiotsile P. Setlhabi, Department of Agriculture and Rural Development
12h20	Poster Session 3		
13h00	Lunch		
SESSION CHAIR: PROF CHRIS MARUFU			
14h00	Socioeconomic/ Cultural Dynamics	Economic and social burdens of Non-Typhoidal Salmonella infections in Nigeria	Abdullahi S. Ozomata, University of Pretoria
14h20		Communal farmer's knowledge, attitudes and perceptions of foot-and-mouth disease (FMD) in the FMD control zone of South Africa	Kibambe D. Kiayima, University of Pretoria
14h40		An Exploration of Knowledge and Attitudes Toward Homeless Dogs in Gaborone	Abdelkareem A. Abdallah, Botswana University of Agriculture and Natural Resources
15h00		Drivers and indicators of dairy cow welfare from Midlands Province, Zimbabwe large scale dairy sector indicators	Zivanayi Matore, University of Zimbabwe
15h20		Animal Welfare Challenges in Africa: A focus on Animals Used in Research in Nigeria	Dauda Bwala, National Veterinary Research Institute, Vom- Nigeria
15h40	Closing Ceremony		
16h00	End of Congress		

POSTERS

Wednesday, 23 August 2023

POSTER SESSION 1: 12h20-13h00

Description		Speaker
Infectious Diseases	1. Modelling African Horse Sickness emergence and transmission in the South African control zone using a deterministic metapopulation approach	Joanna de Klerk, University of Warwick
	2. Biosecurity issues related to ASF and FMD in the Ekurhuleni Local Municipality in Gauteng, South Africa	Rorisang P. Malatji, University of Pretoria
	3. Knowledge, attitude, practice (KAP) and the risk of exposure of abattoir workers to *Mycobacterium* spp. in Gauteng Province, South Africa	Tiny Hlokwe, Agricultural Research Council
	4. Molecular characterization of resistant *Brucella* spp isolated from livestock in the Eastern Cape, South Africa	Thierry Y. Fonkui, University of Johannesburg
	5. Prevalence and risk assessment of *Coxiella burnetii* in sheep and goats of North-West and Free State province	Katleho N. Mosikidi, Agricultural Research Council, North-West University
	6. Molecular epidemiology of *Brucella* spp. among cattle presented for slaughter at selected abattoirs in Gauteng.	Simangaliso P. Mkhatshwa, University of South Africa
	7. Genetic and genomic characterization of *Coxiella burnetii* isolates from South African livestock	Vhahangwele Sadiki, University of Pretoria
	8. Differential antibody staining of Nigerian dog rabies viruses using a southern African monoclonal antibody panel.	Mmantshuruge J. Miyen, ARC-OVR
	9. Molecular characterization of lyssavirus rabies from domestic and African wild cats confirmed between 2010-2020 and newly identified *Lyssavirus mokola* (MOKV)	Ernest Ngoepe, Agricultural Research Council-Onderstepoort Veterinary Research (ARC-OVR)
	10. Contamination of beef and beef products by *Listeria* spp. and molecular characterization of *L. monocytogenes* in Mpumalanga, South Africa	Khomotso C. Moabelo, University of Pretoria
	11. Carp Edema Disease: An emerging global concern	Ekemini M. Okon, Ghent University
	12. Morphological identification of ticks and molecular detection of tick-borne pathogens from small ruminants in Matlwang, Potchefstroom	Mpho Tawana, North-West University (Potchefstroom campus)
	13. Comparison of the immunogenicity of two locally formulated inactivated LEP flurry adjuvanted rabies vaccines and a standard modified live LEP flurry rabies vaccine	Dauda Bwala, Viral Vaccine Production Department, National Veterinary Research Institute, Vom
	14. Seroprevalence of brucellosis among communal cattle in Sekhukhune District Municipality, Limpopo Province. A retrospective study	Makgethoa B. Kgwete, University of South Africa

Thursday, 24 August 2023

POSTER SESSION 2: 12h30-13h00

Description		Speaker
Regional education in animal disease control	15. Effects of supplementary diet protein on growth performance and reproductive health of Tswana goats	Mpho S. Tsheole, North-West University
	16. Awareness and practices of biosecurity measures in smallholder pig production in South Africa: Case of Buffalo City Metro in the Eastern Cape Province	Nwabisa Nogauza, Department of Agriculture

Description		Speaker
Scientific Developments & preventative medicine	17. Seroprevalence of Brucellosis in communal and smallholder cattle farming in North-West Province, South Africa	Bontsi Marumo, Agricultural Research Council
	18. Movement patterns of equines into the African Horse Sickness controlled area of South Africa	John D. Grewar, South African Equine Health and Protocols NPC
	19. Reverse genetics as a platform for manufacturing of Bluetongue Vaccine	Tendai A.M. Mlingo, Onderstepoort Biological Products
	20. Ethnoveterinary use of plants to treat livestock diseases in the Eastern Cape Province, South Africa	Siza Mthi, Department 0Of Agriculture
Public Health & Environmental Health	21. Cost implications for coping with inadequate water supply in locals of Lephalale Municipality, Limpopo, South Africa	Nthabiseng A. Modimola, Tshwane University of Technology
	22. Comparative genomics of Listeria species recovered from meat and food processing facilities	Itumeleng Matle, ARC: OVR
	23. Comprehensive analysis of Staphylococcus aureus isolates from subclinical mastitis dairy cows in Free state Province, South Africa using whole genome sequencing	Ntelekwane G. Khasapane, Central University of Technology
	24. Exploration of the use of moringa oleifera in aquaculture: A Review	Zimasa B. Dubeni, University of Fort Hare
	25. A descriptive epidemiological study of food-borne diseases in Mhlontlo Local municipality, O.R. Tambo District, Eastern Cape Province, South Africa: A One health approach	Nandisa N. Ndlame, University of South Africa

Friday, 25 August 2023

POSTER SESSION 3: 12h20-13h00

Description		Speaker
Public Health & Environmental Health	26. Virulence characterisation and antimicrobial resistance profiles of Shiga toxin-producing *Escherichia coli* and Enteropathogenic *Escherichia coli* isolates from dairy cattle in South Africa	Alaba S. Olawole, University of Pretoria
	27. Prevalence and antimicrobial resistance of *Staphylococcus* spp. isolated from human specimens submitted to diagnostic laboratories in South Africa, 2012–2017	Themba T. Sigudu, University of South Africa
	28. Antibiotic resistance and virulence profiles of *P. mirabilis* isolated from broiler chickens in North-West Province, South Africa	Kealeboga Mileng, North-West University
	29. Occurrence, serotypes and virulence characteristics of Shiga-Toxin-Producing Escherichia coli isolates from goats on communal rangeland in South Africa	Mogaugedi N. Malahlela, University of Pretoria
	30. Seroprevalence of *Toxoplasma gondii* in free-range pigs within Ngaka Molema District Municipality, North-West Province	Naomi Masango, North-West University
	31. Trend-analysis of generic *E. coli, Salmonella* spp., total bacterial count detected in imported poultry meat into South Africa (2016 - 2018)	Maleho E. Machedi, Border Management Authority
Socioeconomic/ cultural dynamics	32. Use of remedies by illiterate small-scale farmers for treatment of livestock diseases in Lubala Village of the Eastern Cape Province in South Africa	Tandile N. Ndobeni, Gauteng Department of Agriculture Rural Development and Environment
	33. Socio-economic dynamics influencing livestock farmers to apply primary animal health care practices in Gauteng Province	Xolisiwe Y. Potelwa, Gauteng Department of Agriculture, Rural Development and Environment
	34. The socio-economic profile of communal cattle farmers and tick infestation levels among communal cattle in Sinthumule - Kutama area	Makhado P. Sedina, University of South Africa

Description		Speaker
Socioeconomic/ cultural dynamics	35. Are socio-economic dynamics a threat to infectious diseases prevention and control? The narratives of animal health practitioners and smallholder farmers in South Africa.	Zimbini Mdlulwa, North-West Department of Agriculture and Rural Development
	36. Reflections on ancient veterinary practices in Africa and contextual relevance to primary animal health care	Alfred T. Kgasi, University of Pretoria
One Welfare	37. Socio-economic and welfare aspects of working equines in the peri-urban areas around Mogalakwena Municipality in Limpopo Province, South Africa	Dimakatso B. Molapo, University of South Africa
	38. A review and meta-analysis on the identification of *Klebsiella pneumoniae* from various sources	Katlego L. Ndlovu, North-West University
Ethnoveterinary medicine (indigenous knowledge)	39. Documentation and promotion of ethnoveterinary medicine used by amaNdebele in Nkangala District Municipality	Fikile M. Maseko, North-West University

Keynote Presentations

Making One Health Work: A personal journey

Professor Bruce Gummow[1,2]

[1]Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Onderstepoort 0110, South Africa - bruce.gummow@jcu.edu.au
[2]Discipline of Veterinary Sciences, College of Public Health, Medical and Veterinary Sciences, James Cook University, Townsville 4811, Australia

Background: The concept of One Medicine can be traced back to ancient times. Yet, despite the long history of the concept, it is still not widely practiced. Arising from the notion of One Medicine the principles of One Health emerged, and its definition and application continues to evolve. Yet, despite many philosophical papers expounding the merits of One Health, there remains little published on the outcomes of a One Health approach to complex problems. The question remains as to what makes a One Health approach successful or not?
Our world continues to be faced with complex challenges and the recent Covid pandemic and increase in climate related problems has focused attention on the need for regional resilience to cope with the increasing frequency of such events. Little has been published on the role One Health plays in addressing resilience in health.

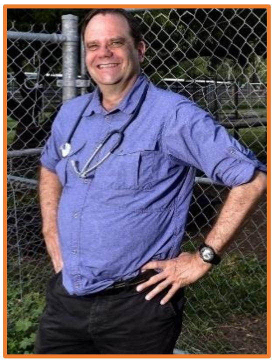
Objectives: This paper addresses the question as to what makes a One Health approach successful and can it be used to create resilience within the region.

Materials and methods: Professor Gummow is a specialist veterinary epidemiologist that has dealt with multiple disease outbreaks in his 40-year career as a veterinarian and has had to deal with complex problems involving human, environmental and animal health. He has extensive experience in applying a One Health approach to addressing complex problems. A review of five of these case studies was undertaken to highlight the One Health methodology used in these studies and the factors that determined their success or failure from a One Health perspective.

Results: Experience has shown that a successful One Health outcome requires an integrated driver and funding, a well-defined common focus that affects all stake holders, working in a transdisciplinary fashion as required, identifying the right stakeholders at the right times, and common training to set a strong foundation and build trust.

Discussion and recommendations: The role of One Health and SASVEPM in creating a foundation for regional resilience is discussed in the light of the results.

Conclusions: One Health outcomes are difficult to achieve if the approach does not have certain key elements. SASVEPM can play a key role in creating regional health resilience.



Biography: Professor Bruce Gummow is a registered specialist in Veterinary Preventative Medicine (Epidemiology) and a Diplomat of the European College of Veterinary Public Health with European certification as a specialist in population medicine. He is also recognised as a Fellow of the Australasian College of Tropical Medicine (ACTM) due to his interest in One Health and zoonotic diseases and chairs the steering committee on One Health in the ACTM. He is currently Associate Head of Research and Postgraduate training in the Discipline of Veterinary Science and is head of the section of Veterinary Preventative Medicine at James Cook University.

He holds a dual appointment with the University of Pretoria in South Africa where he is an Extraordinary Professor and has taught for many years at their Faculty of Veterinary Science. He is recognised as a leading scientist in South Africa by the National Research Foundation and is one of their top-rated scientists. He is also a registered specialist with the South African Veterinary Council and Member of the Royal College of Veterinary Surgeons.

In addition, he Chairs the research and postgraduate committee in the Discipline of Veterinary Science, College of Public Health, Medical and Veterinary Sciences and is their Academic Advisor for Veterinary Postgraduate Studies. He also serves on several other JCU committees and is a senior staff member at JCU and a member of the Veterinary Science Executive management team.

His other activities include being an external examiner for the epidemiology Fellowship exams of the Australian and New Zealand College of Veterinary Scientists and an examiner for the VPH chapter membership exams of the ANZCVS.

WEDNESDAY 23 AUGUST: 08h30

One Health as a tool for disease control

Moetapele Letshwenyo
WOAH, Sub-Regional Representative for Southern Africa

In Africa, livestock play a crucial role in the economy and social wellbeing of communities, where they are used as a protein (food), draught power, wealth (social status), source of raw material for industry, etc. However, one of the major impediments to livestock production is diseases, some which are shared between animals and humans (zoonosis). Zoonosis are worse in that they affect both livestock and humans, with devastating socio-economic impact. This compromises efforts to reduce poverty thereby disrupting the realisation of the UN SDGs. Sixty (60) percent of infectious diseases affecting humans, have their origins in animals. Seventy-five (75) percent of animal diseases can be transmitted to humans, eighty (80) percent of bioterrorism agents are pathogens of animal origin. Given this situation, One Health approach consider interactions at the human-animal-environment interface as integral to positive health outcomes.

In recent years the international community, led by the Quadripartite organizations, made up of the Food and Agriculture Organization of the United Nations (FAO), United Nations Environment Programme (UNEP), World Health Organization (WHO), and the World Organisation for Animal Health (WOAH), have advocated more for the concept of One Health. "One Health" approach is a concept that has been known for more than a century; that human, animal and plant health are interdependent and bound to the health of the ecosystems in which they exist. The Quadripartite, leveraging on individual strengths, implements One Health as a collaborative, whole of society, whole of government approach to understanding, anticipating and addressing risks to global health. They have developed the One Health Joint Plan of Action (2022-2026) to drive the implementation of this initiative. One-health approach is critical for the control of priority zoonotic diseases such as rabies, avian flu or viral haemorrhagic fevers like Ebola, as well as cross-cutting issues, like antimicrobial resistance (AMR) and food safety.

The World Organisation for Animal Health, throughout its work, promotes the One Health approach, recognising the interdependence of animal, human and environmental health. The health of animals and of the environment strongly depend on human activities, hence the health of animals and the environment also determine human health.

Biography: Dr Letshwenyo is a national of Botswana, veterinarian (BVMS), graduated from the Veterinary School of the University of Edinburgh (United Kingdom), followed by a Masters' degree (MSc) in Preventative Veterinary Medicine (MPVM) awarded by the University of California, Davis, USA.

A former Delegate to the OIE from 2008 to 2009, and former Director of the Botswana Department of Veterinary Services, Dr Letshwenyo was also Deputy Permanent Secretary at the Ministry of Agriculture of Botswana.

He was a Member of the OIE Ad-Hoc Group on Commodities (2008 to 2013) and Member of the OIE Ad-Hoc group on FMD (2009 to 2013). For his outstanding services to veterinary science, he was the recipient of the 2013 OIE Meritorious Award. He currently serves as the SADC Sub-Regional Representative for the World Organisation for Animal Health.

THURSDAY 24 AUGUST: 08h00

One Welfare – research and development for holistic and transformative interventions in livestock production

Julius R. Atlhopheng
National Agricultural Research and Development Institute, Botswana

Agriculture, when transformed, is commercially viable and offers economic competitiveness, generates revenue and export earnings. The livestock sector continues to be pivotal to livelihoods, food, and nutrition security, and, as a driver of economic and scientific advances. The cultural norms, especially in African settings, are tied to livestock – going beyond meat and related products, but also central to social norms and celebratory undertakings. Yet, the continued livestock production systems are perturbed by animal diseases, one health challenges, climate change, data driven interventions and inclusion mechanisms.

This presentation will thus give an overview of advances in key areas of economic impact of the livestock sector to developing countries economically. The sector must demonstrate economic diversification, enable clusters, and value chains which enable growth at local levels, such as enterprises contributing significantly, through productivity frameworks. For improved economic benefits, there is need for better national coordination mechanisms, including compliances to legal and regulatory measures. There is, additionally, need for the economic and social interventions to be measured. For this to be realized, there is need for accessible and impact data to investors, farmers, and analysts to plan effectively. A commercially viable livestock sector needs the balance of diseases control, climate proofing livestock production systems through nutrition, management, and technological advances, which include value innovation. Livestock sector needs to prove its worth in the national systems of innovation, inclusion, and gross domestic product, and to transform futures. Thus, the keynote presentation addresses building blocks of transformative agricultural sector (livestock) in terms of how it integrates with other sectors of the economy. The astute beneficiations, including enterprises and value chains, competitiveness, and the right portfolio investments, promoted under ease-of-doing business. The rigors of climate change, diseases prevalence and limited coordination, remain opportunities to be explored, to achieve empowered agriculture with co-creations and enterprises.

Biography: Professor Atlhopheng is the Chief Executive Officer of the Botswana National Agricultural Research and Development Institute (NARDI). The Institute drives innovations, high impact engagements, service delivery and improved research agenda – to build transformed futures. As a biophysical environmental scientist, Prof Atlhopheng has experience as academic for 30 years at the University of Botswana (served as Head of Department and Dean of Science; as well as Chairperson of the university SDGs). He has chaired several committees such as the Vaccine-able Botswana, Botswana Open Data Open Science, National Mirror Committee on developing international land degradation and desertification standards and case studies, under ISO. He has participated in climate change initiatives, the SDGs and national projects such as transformation, and digital innovation strategies to enable knowledge economy. The key intervention areas, which continue to be pursued are digital and data transformations, agricultural productivity, commercialization, the co-creations through collaborations, to enhance the benefits of coordination in the agricultural sector.

FRIDAY 25 AUGUST: 08h00

Lifetime Achievement Award

The Southern African Society for Veterinary Epidemiology and Preventative Medicine would like to honour **Prof. Bruce Gummow**, one of the founding fathers of SASVEPM, for his continued support to SASVEPM, which as a result became internationally recognised as the regional society for epidemiologists, for being instrumental in facilitating the building capacity in veterinary epidemiology and for his contribution to disease control.

Prof. Gummow's Experience & Achievements

- 119 refereed research papers in quality non-predatory research Journals
- 4 books/book chapters
- 32 posters
- 6 non-referred scientific papers
- 107 presentations at local and international conferences
- 20 invited lectures or congress presentations
- 22 major contract reports for industry
- 22 interactive veterinary epidemiology workshops / courses
- 5 television interviews
- 44 completed dissertations or thesis as supervisor/co-supervisor

Willie Ungerer Award

The Southern African Society for Veterinary Epidemiology and Preventative Medicine are honoured to announce the recipient for the 2023 Willie Ungerer Award:

Dr Misheck Mulumba

Dr Misheck Mulumba is a qualified veterinarian with Thirty-one (31) years' experience in agriculture (animal health) extension, animal disease control work in the field, laboratory diagnostics and research, animal vaccines production and agriculture trade related issues. He has intimate knowledge of government and African Union structures and how they operate having worked as Head of Veterinary Services in Zambia before joining the AU-IBAR Centre for Ticks and Tickborne diseases (CTTBD) as Director of the CTTBD, Southern African Development Community (SADC) where he worked as the Regional Project Coordinator and Network Surveillance expert for the African Development Bank (AfDB) funded Transboundary Animal Disease Surveillance project.

Since 2014, Dr Mulumba has been the Director of Onderstepoort Veterinary Research Institute, the reference animal health institute for South Africa and designated regional and continental reference centres of WOAH and UN-FAO for nine animal health areas. Dr Mulumba is a founding member of SASVEPM and has been actively engaged in all the Society's activities.

Dr Mulumba have been associated with the World Organisation for Animal Health (WOAH) for more than 10 years through its Ad hoc groups on PPR for which he was appointed Chair in December 2017. He is also a member of the WOAH Scientific Commission for Animal Diseases (SCAD). In February 2019, he was elected the Chairperson of the newly formed African One Health Network (AfOHNet).
Dr Mulumba was also appointed in 2020 as a founding member of and continues to serve on the WOAH Ad hoc Advisory Group on COVID19. He also served as an expert for AU-IBAR on a number of occasions and currently he serves on the AU-IBAR list of experts on animal control.
Dr Mulumba is the current Editor in Chief of the renowned Onderstepoort Journal for Veterinary Research (OJVR).

Since January 2002, Dr. Misheck Mulumba has been the Director for the African Union/Centre for Ticks and Tick-borne Diseases (AU/CTTBD). His primary duties include production of tick-borne disease (TBD) vaccines for livestock; training (epidemiology and diagnostics); supervision of postgraduate students; coordination of regional livestock disease work; and participation in policy formation at the livestock/wildlife interface.

Between June 2000 and December 2001, Dr Mulumba held the position of Deputy Director at AU/CTTBD. He was Chief Veterinary Officer and Subprogram Manager, Animal Production and Health, for the Ministry of Agriculture, Food and Fisheries in Zambia from September 1997 to May 2000. Dr Mulumba was the Senior Veterinary Officer for the Ministry of Agriculture in Zambia between May 1995 and August 1997, and helped oversee the translocation of more than 2,000 game animals within the country. From December 1993 to December 1999, he was the Counterpart Project Manager and later Project Manager for ASVEZA, a Belgium-funded animal health project. Between October 1989 and November 1993, Dr Mulumba was a Government Veterinary Officer for Zambia.

Dr Mulumba is a founding member of the African Chapter of the Wildlife Disease Association (WDA) and a member of the African Association of Insect Scientists (AAIS), the IUCN Veterinary Specialist Group, the Veterinary Association of Zambia (VAZ), and the African Tick Group.

Oral Presentations

in order of appearance as on the programme

THEME: INFECTIOUS DISEASES

Investigating the epidemiology, ecology, and socio-economic impact of Rift Valley fever in southern Africa

Peter N. Thompson

Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Onderstepoort, 0110 - peter.thompson@up.ac.za

Rift Valley fever (RVF) virus (RVFV) (Bunyavirales, Phenuiviridae) is a mosquito-transmitted, zoonotic arbovirus of global concern, having shown its ability to spread over long distances and become established in areas beyond its historical mainland sub-Saharan African range. The virus is maintained in nature by a combination of circulation between its mosquito vectors (mainly *Aedes* and *Culex* spp.) and domestic and wild ruminants, and by transovarial transmission in floodwater-breeding *Aedes* spp. Outbreaks are precipitated by a combination of high rainfall and associated flooding, the presence of susceptible hosts, and the introduction of the virus via either emergence of infected *Aedes* spp. or introduction of viraemic hosts.

In South Africa, RVF is best known as the cause of large outbreaks amongst domestic ruminants, particularly sheep, associated with high abortion and neonatal mortality rates. These occur on the relatively arid interior plateau and at very long, irregular intervals of up to 30 years, but have severe economic impact and associated human morbidity and mortality. Less well known is the fact that RVFV circulates endemically, sometimes at high levels, in more tropical eastern areas of southern Africa, where associated clinical disease is likely undiagnosed and socio-economic impact is unknown. In contrast to East Africa, where a single RVFV lineage tends to predominate, isolations in southern Africa show that outbreaks have been caused by a wide variety of different virus lineages, and that other lineages likely continue to circulate largely undetected.

The reasons for the wide variation in epidemiological manifestations of RVF across southern Africa remain poorly understood, but recent studies have started to shed light on the factors that determine the occurrence and timing of RVFV circulation and RVF outbreaks. Phylogenetic studies have also provided clues to the likely patterns of RVFV movements across the region and the continent. This paper will provide an update on our current state of knowledge regarding the epidemiology of RVF in southern Africa, based on the results of both historical and recent studies. Important gaps in our knowledge of this high impact zoonosis will also be highlighted.

WEDNESDAY, 09h30

Hospital-acquired and zoonotic bacterial organisms and their associated antimicrobial-susceptibility profile in veterinary hospitals: A Systematic Review

Dikeledi C. Sebola[1], James W. Oguttu[2], Marleen M. Kock[3,4] & Daniel N. Qekwana[1]

[1]Section Veterinary Public Health, Department of Paraclinical Sciences, Faculty of Veterinary Science, University of Pretoria, Pretoria, South Africa - dc.sebola@gmail.com
[2]Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, University of South Africa, Johannesburg, South Africa
[3]Department of Medical Microbiology, University of Pretoria, Pretoria, South Africa
[4]Tshwane Academic Division, National Health Laboratory Service, Pretoria, South Africa

Background: Hospital-acquired infections (HAIs) are associated with increased mortality, morbidity, and an economic burden due to costs associated with extended hospital stays. Furthermore, most pathogens associated with HAIs in veterinary medicine are zoonotic. This study used published data to identify organisms associated with HAIs and zoonosis in veterinary medicine. Furthermore, the study also investigated the antimicrobial-susceptibility profile of these bacterial organisms.

Methods: A systematic literature review was conducted in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-analyses (PRISMA) guidelines. Search terms and five electronic databases were used to identify studies published over 20 years (2000–2020). The risk of bias was assessed using the "Strengthening the Reporting of Observational Studies in Epidemiology-Vet" (STROBE-Vet) checklist.

Results: Out of the identified 628 papers, 27 met the inclusion criteria for this study. Most studies (63%, 17/27) included were either from small animal or companion animal clinics/hospitals, while 5% (4/27) were from large animal clinics/hospitals inclusive of bovine and equine hospitals. Hospital-acquired bacteria were reported from environmental surfaces (33%, 9/27), animal clinical cases (29.6%, 8/27), and fomites such as cell phones, clippers, stethoscopes, and computers (14.8%, 4/27). *Staphylococcus* spp. was the most (63%; 17/27) reported organism, followed by *Escherichia coli* (19%; 5/27), Enterococcus spp. (15%, 4/27), Salmonella spp. (15%; 4/27), *Acinetobacter baumannii* (15%, 4/27), *Clostridioides difficile* (4%, 1/27), and *Pseudomonas aeruginosa* (4%; 1/27). Multidrug-resistant (MDR) organisms were reported in 71% (12/17) of studies linked to Methicillin-resistant *Staphylococcus aureus* (MRSA), Methicillin-resistant *Staphylococcus pseudintermedius* (MRSP), *Enterococcus* spp., *Salmonella* Typhimurium, *Acinetobacter baumannii*, and *Escherichia coli*. The *mecA* gene was identified in both MRSA and MRSP, the *bla*CMY-2 gene in *E. coli* and *Salmonella* spp., and the *van*A gene in *E. faecium* isolate. Six studies reported organisms from animals with similar clonal lineage to those reported in human isolates.

Conclusion: Organisms associated with hospital-acquired infections and zoonosis have been reported from clinical cases, environmental surfaces, and items used during patient treatment and care. *Staphylococcus* species is the most reported organism in cases of HAIs and some isolates shared similar clonal lineage to those reported in humans. Some organisms associated with HAIs exhibit a high level of resistance and contain genes associated with antibiotic resistance.

WEDNESDAY, 09h50

Cattle trade networks in the foot-and-mouth disease (FMD) Protection Zone of Limpopo Province

Malatji Kenneth[1], Fosgate Geoffrey[2], Sirdar Mohamed[3] & Heath Livio[4]

[1]*Department of Production Animal Studies, Faculty of Veterinary Sciences, University of Pretoria, Onderstepoort, 0110, South Africa* - malatjikk@gmail.com
[2]*Onderstepoort Veterinary Research, Agricultural Research Council, Onderstepoort, 0110, South Africa*
[3]*World Organisation for Animal Health, WOAH Representation for Southern Africa, Gaborone, Botswana*
[4]*Onderstepoort Veterinary Research, Agricultural Research Council, Onderstepoort, 0110, South Africa*

Foot and mouth disease is a viral disease that affects cloven-hoofed animals and is caused by FMD virus. The virus is extremely contagious; animals can be infected by close or direct contact with other infected animals, contaminated people, vehicles and equipment. The main economic impact of the disease comes from trade bans and the inability to move or sell animals and animal products from affected areas. The objective of this study is to describe the trade network of livestock farmers in the FMD Protection Zone of Limpopo Province, which will be useful for the development of a strategic surveillance system within the livestock movement network. All 55 dip tanks within the FMD Protection Zone with vaccination of Limpopo Province were selected for study. Participants were interviewed at dip-tanks concerning the management and movement of their livestock. The questionnaire included four sections: owner demographics, livestock marketing, enterprise economics and the impact of FMD. 480 questionnaires have been administered, the participants were most males 77% (23% females). Most participants have no formal education (45%) while 32% a had primary educational level and 23% had secondary level. Of those interviewed, 85% were over 40 years of age and 15% were less than or equal to 39 years. Fifty-five dip-tanks have been sampled with current respondents reporting that 86% of livestock movements are within the FMD Protection Zone. Most livestock movement is due to trade (for income), while weddings and funerals are playing a major role of these movements. The remaining 14% are movements outside the FMD Protection Zone mostly representing trade to obtain better pricing. Prices within the FMD protection zone are very low and not competitive which leads to farmers seeking other alternative means to sell their livestock at satisfying price. Livestock movements outside of the FMD Protection Zone put the country at risk of continuing outbreaks. It is therefore recommended that marketing opportunities with better prices be created within the FMD Protection Zone in effort to limit these movements.

WEDNESDAY, 10h10

The prevalence of infectious bovine keratoconjunctivitis among Western Cape dairy cattle and associated risk factors

Louis H. Maartens[1], John D. Grewar[2], Jacqueline A. Picard[3], Peter N. Thompson[2] & Bruce Gummow[3]

[1]*Research & Development Section, Deltamune (Pty) Ltd, Pretoria, South Africa - louism@deltamune.co.za*
[2]*Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, South Africa*
[3]*College of Public Health, Medical and Veterinary Sciences, James Cook University, Townsville 4811, QLD*

Infectious bovine keratoconjunctivitis (IBK), or pinkeye, occurs globally in domestic cattle with detrimental effects on production and animal welfare. The epidemiology of IBK involves complex interactions between the hosts' ocular tissues, several microbial agents and numerous environmental factors. Although well studied in beef cattle, there is a paucity of epidemiological information about IBK in dairy herds.

A survey was conducted on dairy farms in the Western Cape Province (WCP) of South Africa to estimate IBK prevalence among dairy cattle in this area. Farms were selected based on location in the WCP and the farmers' willingness to participate in the study. A total of 28 dairy farms were included in the study and 60 cattle were examined on each farm for clinical signs of IBK. The farm managers were asked to complete a questionnaire on management, demographics and potential risk factors relevant to their farms. Conjunctival swabs were screened by real-time PCR for the presence of IBK-associated bacterial agents. The role of vaccination as control measure was also gauged by comparing disease prevalence on vaccinated versus unvaccinated farms. Keratoconjunctivitis was recorded in 5.91% (CI: 4.05 – 6.20%) of the 1,676 head of cattle examined. Both IBK-associated *Moraxella* species (*M. bovis* and *M. bovoculi*) were demonstrated among healthy and diseased individuals within the sampled population (15.45%, CI: 13.80 -17.26% and 8.23%, CI: 7.01 – 9.65%, respectively). *Mycoplasma bovoculi* was present in an unusually high proportion (80.73%, CI: 78.77 – 82.55%) of cattle; while *Mycoplasma bovis* was infrequently encountered (0.36%, CI: 0.16 – 0.78%). Statistically significant associations could not be demonstrated between clinical IBK and the presence of these microbes (OR = 1.45, CI: 0.99 – 2.02), or between disease prevalence in vaccinated versus unvaccinated herds (OR = 0.99, CI: 0.79 – 1.24).

The inability to demonstrate associations between the presence of IBK-associated microbes and keratoconjunctivitis, or between vaccination status and disease prevalence, parallels findings in similar beef cattle studies. The unusually high prevalence of *Mycoplasma bovoculi* in dairy cattle eyes warrants further investigation into the epidemiological role of this agent. These findings are discussed further in this paper.

WEDNESDAY, 11h00

Evaluation of haematological parameters in cattle, detection, and confirmation of cattle *Anaplasma marginale* infection at BUAN farm in the southeast region of Botswana

Solomon S. Ramabu[1], Monkgogi Motladiile[1], Motheo Ramotshubi[1], Sumbikane, Gasebonwe[1] & Abdelkareem A. Ahmed[1]

[1]*Department of Veterinary Sciences, Faculty of Animal and Veterinary Sciences, Botswana University of Agriculture and Natural Resources, Department of Veterinary Sciences. Private Bag 0027, Gaborone, Botswana* - ssramabu@buan.ac.bw

Anaplasmosis is a tick-borne disease caused by obligate intercellular gram-negative bacteria, *Anaplasma spp*. The present study evaluates dairy and beef cattle blood parameters at Botswana University of Agriculture and Natural Resources to determine *Anaplasma* infection in the herds. Thirty (30) dairy animals and 30 beef animals were randomly selected and tested for blood parameters using a haematology analyser and microscopic examination of Giemsa-stained blood smears was used to identify blood parasites. Subsequently, 48 dairy and 48 beef animals were randomly selected and tested for *Anaplasma* infection using competitive inhibition enzyme-linked immunosorbent assay (ci-ELSA). To confirm *Anaplasma* infection 43 dairy animals were tested using polymerase chain reaction (PCR). Nine PCR-positive animals were tested again with a PCR that is specific for *Anaplasma marginale*. Except for mean cell haemoglobin concentration (MCHC), blood parameters while within normal ranges, were higher in beef as compared to dairy cattle. There was a statistically significant difference in white blood cell count (WBC) (P = 0.0162) and granulocyte counts (P = 0.0265) with beef having higher counts compared to dairy cattle. The only blood parasite detected in both breeds was *Anaplasma marginale*. The study found a high level of *Anaplasma* infection with 98% (47/48) and 100% (48/48 of dairy and beef cattle testing positive by ci-ELISA receptively. PCR confirmed that 34.9% (15/43) of dairy cattle were positive for *Anaplasma spp* infection and *Anaplasma marginale* specific PCR confirmed the infection in 78% (7/9) of the animals tested. We conclude that cattle blood parameters at BUAN farm fall within normal ranges but that immune response cells were significantly lower in dairy compared to beef cattle. Also, a high-level endemic infection exists in the herd caused by *Anaplasma marginale*. The findings are discussed in the context of the utility of evaluating cattle health using diagnostic tests.

WEDNESDAY, 11h20

Parasite burden among peri-urban free-roaming pigs in Gert Sibande District Municipality of Mpumalanga Province, South Africa

Priscilla Munzhelele[1,3], Nqubeko Prosperity Stewart Sibeko[2], James Wabwire Oguttu[3], Christian Anayochukwu Mbajiorgu[3] & Folorunso Oludayo Fasina[4,5]

[1]*Department of Agriculture, Rural Development, Land and Environmental Affairs, Nooitgedacht Research Farm, Animal Research, Non-Ruminant sub-directorate, Ermelo, 2350* - priscilla.munzhelele@gmail.com
[2]*Department of Agriculture, Rural Development, Land and Environmental Affairs, Mpumalanga Provincial Veterinary Laboratory, Parasitology unit, Ermelo, 2350*
[3]*Department of Agriculture and Animal Health, College of Agriculture and Environmental Science, University of South Africa,*
[4]*Emergency Centre for Transboundary Animal Diseases, Food and Agriculture Organization of United Nations (FAO-ECTAD), Dar es Salaam, 14111, United Republic of Tanzania*
[5]*Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, Onderstepoort, 0110, South Africa*

Background: Parasite infections, unlike regulated animal diseases do not receive much veterinary attention. Meanwhile, ecto- and endo-parasites are major sources of financial losses in pig enterprises, particularly in subsistence and small-scale pig production systems.

Aim: The purpose of this study was to identify and quantify the prevalence of ecto- and endo-parasites among peri-urban free roaming pigs in Gert Sibande District Municipality (GSDM), Mpumalanga.

Material and methods: Pig owners were identified using the snowball sampling method since no sampling frame for free roaming pig farmers exists. However, stratified sampling was used to select pigs for sampling for ecto- and endo-parasites. A total of 283 samples were collected from 132 peri-urban free roaming pig farmers in GSDM. Pairwise correlation analysis and Chi-square Test (X^2) were performed using Stata 15.0 and SPSS V28.0 respectively. Statistical significant was set at $\alpha = 0.05$.

Results: Over 90% (91.2%) of the pigs examined were infested with at least one parasite, including *Haematopinus suis, Sarcoptes scabiei*, *Ascaris suum*, *Fasciola hepatica*, *Trichuris suis*, *Strongylids*, *Coccidia* spp, *Moniezia expansa*, and *Siphonaptera* spp. *Sarcoptes scabiei* was the most frequently isolated parasite in all age groups, especially among pigs ≤4 months (75.8%), and those that were ≥12 months (74.7%). The correlation between *Ascaris suum* and body condition was slightly correlated ($r = 0.24$; $p<0.05$).

Implications: Free roaming pigs carry a variety of ecto and endo parasites in the peri-urban areas of Gert Sibande District Municipality, Mpumalanga Province with implications on animal and human health. This may directly negatively affect pig performance and productivity. In addition, *Ascaris suum* has zoonotic potential and may have serious public health consequences.

Conclusion: Policy makers and extension services must focus on developing policies and risk communication and community engagement (RCCE) materials, which targets pig farmers in peri-urban areas like Gert Sibande District Municipality, Mpumalanga Province to reduce disease burdens in humans and animals.

WEDNESDAY, 11h40

Sponsor Talk: Botswana Vaccine Institute's contributions towards Foot and Mouth Disease control in Sub-Saharan Africa with special reference to incursion of FMD serotype O into Southern Africa

Mokganedi Mokopasetso[1], Joseph Hyera[1], Mbaakanyi Mazwiduma[1], Andrew Madeswi[1], Latoya Seoke[1] & Elliot Fana[1]

[1]*Botswana Vaccine Institute, WOAH Reference Laboratory for FMD - mmokopasetso@bvi.co.bw*

Botswana Vaccine Institute (BVI) Limited is a public company wholly owned by the Government of Botswana. BVI was formed in 1978 as a result of widespread and protracted outbreaks of foot and mouth disease (FMD) in the northern parts of Botswana. The first vaccine produced at BVI was therefore the FMD vaccine that ensured sustainable control of the disease thus safeguarding Botswana's beef exports industry. Through continuous technological improvements over the years, BVI has been able to increase its product portfolio from FMD vaccine (1978) to include other high quality livestock vaccines targeting diseases of social and economic importance such as Rinderpest vaccine (1985), Anthrax vaccine (1992), Black leg vaccine (1992), Contagious Bovine Pleuropneumonia (1993), Thermostable rinderpest vaccine (1994), Peste des petit ruminants vaccine (1998) and the purified FMD vaccine (2010).

Since 1985 the Institute has hosted the World Organisation for Animal Health (WOAH) FMD Regional Reference Laboratory for Sub-Saharan Africa. The WOAH laboratory provides technical and laboratory diagnostic support to all countries in sub-Saharan Africa through collection and characterisation of FMD field isolates. This has provided countries within the African continent with an early warning system in the surveillance, prevention and control of FMD. Early disease detection enables prompt and efficient control of disease outbreaks thereby reducing the negative impact of the disease on national economies.

Foot and Mouth Disease (FMD) is endemic to most parts of Africa. Out of the seven known Foot and Mouth Disease virus (FMDv) serotypes (O, A, C, SAT 1, SAT 2, SAT 3 & Asia 1), five serotypes (O, A, SAT 1, Sat 2 & SAT

3) are present in Africa, but their distribution varies within and between the different sub regions of the continent.

FMD outbreak data obtained from the WOAH FMD regional reference laboratory, hosted at BVI has indicated a resurgence of FMD outbreaks within Southern Africa. Between 2014 and 2018, the most predominant serotype has been SAT 2, however, since 2018 there has been a resurgence of serotype O. Initial serotype O outbreaks were reported in the central province of Zambia and eventually spilled to all provinces. In 2021, FMDv with 99.8% nucleotide similarity to that isolated in the western province of Zambia was detected in cattle in the Zambezi region of Namibia. This signalled the first incursion of FMDv serotype O outside Zambia in recent years. The virus has since spread to Malawi (MAL/03/22) and Mozambique (MOZ/04/2022), both outbreaks occurring in 2022 within two months of each other.

WEDNESDAY, 12h00

Evidence for a host-switch in the maintenance of canid rabies variant in the Northern Cape Province, South Africa

Ernest Ngoepe[1], Wonderful Shumba[2] & Claude Sabeta[1,3]

[1]WOAH Rabies Reference Laboratory, Agricultural Research Council (Onderstepoort Veterinary Institute), Onderstepoort, 0110, Pretoria, South Africa - ngoepee@arc.agric.za
[2]Epidemiology and Laboratory Services, Northern Cape Department of Agriculture, Land Reform and Rural Development, Kimberley, South Africa
[3]University of Pretoria, Department of Veterinary Tropical Diseases, Private Bag 04, Onderstepoort, 0110, Pretoria, South Africa

Rabies is a zoonotic infectious disease that causes at least 59 000 human deaths worldwide annually, with 95% of the cases occurring in the developing countries of Asia and Africa (1). There are two *Lyssavirus rabies* (RABV) variants circulating in South Africa notably the canid and mongoose RABV biotypes (2). The canid RABV biotype is maintained in the domestic dog and two wild carnivore species, the black-backed jackal (*Canis mesomelas*) and bat-eared fox (*Otocyon megalotis*) (2). The mongoose RABV biotype is well maintained by the member species of the *Herpestidae* family especially the yellow mongoose (*Cynictis penicillata*) (2). The rabies positive cases trends showed an increase in rabies positive cases between 2011 and 2016 in aardwolves surpassing the bat-eared fox as the most rabies affected wild carnivore in the Northern Cape Province of South Africa. The aim of the study was to establish the genetic relationships amongst rabies viruses recovered from both the aardwolves and bat-eared foxes. A partial region of the glycoprotein gene and the variable G-L intergenic region of the viral genome was analysed using nucleotide sequences generated from PCR amplicons. The phylogenetic reconstruction demonstrated that the rabies viruses obtained from the two wild carnivore species from the Northern Cape Province clustered independently of each other with 96% nucleotide sequence identity, suggesting that the aardwolf were be able to maintain and transmit the canid RABV variant in this geographical area. Furthermore, the rabies viruses recovered from the aardwolves between the year 2015-2017 had 100% nucleotide sequence identical, suggesting a single or common source of infection and possible evidence for a host switch. Understanding the role of different species in the transmission of multi-host pathogens, such as rabies virus, is vital for effective control strategies.

REFERENCES

1. Hampson, K., Coudeville, L., Lembo, T., Sambo, M., Kieffer, A., Attlan, M., Barrat, J., Blanton, J. D., Briggs, D. J., Cleaveland, S., et al. (2015). Estimating the global burden of endemic canine rabies. PLOS Neglected Tropical Disease, 9: e0003709.
2. Von Teichman, B.F., Thomson, G.R., Meredith, C.D., Nel, L.H. (1995). Molecular epidemiology of rabies virus in South Africa: evidence of two distinct virus groups. Journal of General Virology 76, 73-82.

WEDNESDAY, 14h00

Determination of the prevalence of bovine cysticercosis in slaughter beef cattle in Matabeleland region of Zimbabwe using B158/B60 antigen ELISA

Munyaradzi Christopher Marufu[1], Zolile Kwakhiwe Ncube[2], Takula Tshuma[2], Charles Byaruhanga[2], Sunday O. Ochai[2], Veronique Dermauw[3], Pierre Dorny[3]

[1]*Department of Veterinary Tropical Diseases, Faculty of Veterinary Sciences, University of Pretoria, Onderstepoort, Pretoria, South Africa - chris.marufu@up.ac.za*
[2]*Department of Production Animal Studies, Faculty of Veterinary Sciences, University of Pretoria, Onderstepoort, Pretoria, South Africa*
[3]*Department of Biomedical Sciences, Institute of Tropical Medicine, Antwerp, Belgium*

Taenia saginata is a zoonotic tapeworm of public health and economic importance. Its prevalence in cattle in Zimbabwe is thought to be grossly underestimated, because it is only reported based on the less sensitive meat inspection method. We estimated the prevalence of bovine cysticercosis in 381 cattle slaughtered in three abattoirs in the Matabeleland region of Zimbabwe. Serum samples were analysed using the monoclonal antibody-based B158/B60 antigen enzyme-linked immunosorbent assay (Ag ELISA), indicating the presence of viable cysticerci. *Taenia saginata* cysticerci that were detected on meat inspection were confirmed using polymerase chain reaction (PCR) and characterised by cloning and Sanger sequencing of the 12s rDNA amplicons. The Ag-ELISA determined an apparent prevalence of bovine cysticercosis of 37.9 %, whereas the true prevalence, calculated using Bayesian methods, was estimated at 92.1 % for Matabeleland South, followed by Matabeleland North (89.3 %) and Bulawayo (83.2 %). Seven of the 381 cattle (1.90 %) were positive for bovine cysticercosis by meat inspection. All the detected cysts, found in the masseter muscles were confirmed to be *T. saginata* cysticerci on PCR. Sequence alignment to reference sequences from the GenBank showed 99.75 % to 99.87 % similarity to a *T. saginata* reference sequence from South Africa. The present study confirmed that Ag ELISA gives a more sensitive estimate of bovine cysticercosis prevalence than meat inspection. The high prevalence of bovine cysticercosis and the presence of viable cysticerci observed in this study suggest that humans could be frequently exposed to *T. saginata* cysticerci warranting further investigation of taeniasis prevalence in the human population.

WEDNESDAY, 14h20

Seroprevalence and factors associated with *Coxiella burnetii* exposure in goats in Moretele

Rungano Magadu[1] & Peter N. Thompson[1]

[1]*Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Pretoria, South Africa - rungano.magadu@up.ac.za*

Q fever is a zoonotic disease caused by *Coxiella burnetii* which infects humans and a wide birds, mammals, ticks, fish and reptiles. Domestic ruminants (cattle, goats and sheep) are the reservoirs for human infection. Infection with *C. burnetii* causes significant economic impact and poses zoonotic risk to people exposed to livestock. Despite the economic and public health risks associated with this emerging zoonosis, there is little detailed knowledge of the distribution and prevalence of *C. burnetii* in South Africa and no information is available for goats. Scant information is available regarding risk factors and outcomes of infection in South African livestock systems, especially in peri-urban farming areas where risk of human exposure is greatest.

The aim of this study was to estimate the prevalence of *C. burnetii* antibodies in goats in Moretele municipality, close to Hammanskraal, and to identify factors associated with seropositivity. Multi-stage random sampling was conducted and sera collected from 216 goats in 32 goat herds. A questionnaire was completed for each participating goat owner to collect information on potential animal, management and environmental risk factors, and potential animal health consequences of infection. *C. burnetii* antibody testing was done by LSIVET™ Ruminant Q Fever- Serum/Milk ELISA.

Thirty two of 216 goats tested positive for *C. burnetii* antibodies and overall seroprevalence, adjusted for sampling weights and clustering, was 18.4% (95% confidence interval [CI]: 12.2% - 23.5%). The intraclass correlation coefficient was 0.06, indicating low-to-moderate clustering. Multiple logistic regression showed age was significantly associated with seropositivity, with higher seroprevalence in animals $\geq$ 19 months old (26%) than animals $\leq$ 6 months old (6%) (odds ratio [OR]: 6.6; $p = 0.010$). There was an association between seropositivity for *C. burnetii* and the number of abortions experienced in a herd over the previous year (OR: 2.5; $p = 0.071$). We concluded that *C. burnetii* infection is common in goats in Moretele and a potential cause of abortion in goats, and also poses a zoonotic disease risk. *Coxiella burnetii* should therefore be considered when investigating abortions and should also be considered a potential cause of human disease in the study area.

WEDNESDAY, 14h40

---

5 Bluetongue virus infection in farm dogs with exposure to an infected sheep flock in South Africa

Josef Hanekom[1], Karen Ebersohn[1], Andrew Leisewitz[2], Lisa Penzhorn[1], Melvyn Quan[1], Alan Guthrie[1] &
Geoffrey T. Fosgate[1]

[1]*Faculty of Veterinary Science, University of Pretoria, South Africa* - *joe.hanekom@up.ac.za*
[2]*College of Veterinary Medicine, Auburn University, Auburn, USA*

In 2021, a pregnant Rottweiler dog living on a sheep farm was diagnosed with clinical bluetongue disease (BT). This study reports the investigation where this dog lived to better understand the context of this atypical bluetongue virus (BTV) infection.

Samples were collected during farm visits at 14, 28, 60 and 89 days after the onset of clinical signs in the pregnant Rottweiler dog. Blood was collected from all farm dogs (n=6) including the original dog and tested for BTV RNA using a reverse-transcriptase quantitative PCR (RT-qPCR) assay and for BTV-specific antibodies using a competitive blocking ELISA (cELISA). The BTV serotype of dogs that tested positive by RT-qPCR also was determined by serum virus neutralisation (VNT).

On the day 14 farm visit, blood was also collected from sick sheep (n=16/400) on the farm and evaluated using RT-qPCR, and midges were trapped using an Onderstepoort UV light trap placed above a sheep pen. A portion of trapped midges (1/24th) were evaluated individually using visual identification keys and categorised by species, sex, and parity. Parous/gravid midges were tested using BTV RT-qPCR in batches of up to 200 midges. Blood-fed midges (n=308) were tested for blood meal analysis using a PCR species probe.

Three dogs (50%) tested positive for BTV RNA with the RT-qPCR assay and had high antibody VNT titres (>1:112) to BTV serotype 5. All RT-qPCR positive dogs and one additional dog tested cELISA seropositive (n=4/6). Only the original case dog developed clinical signs of BT and BTV RNA was detected in 5/16 sheep.
The most abundant midge species was *Culicoides imicola* (99.3%) and BTV was only detected in this species (n= 3/4 batches of 200 parous midges). Blood meal analysis identified sheep (90.3%), human (20.9%), horse (1.6%) and unidentified (4.6%) DNA. Dog blood was not detected in any blood-fed midges tested.

A high proportion of farm dogs had been exposed to BTV and developed detectable viraemia, including two subclinically infected dogs. The occurrence of natural BTV viraemia especially in subclinically infected dogs creates a potential risk of BTV entry into BT-free areas through dog importation.

WEDNESDAY, 15h00

Detection of Dengue Viral Infections in *Aedes aegypti* and febrile patients in Kassala City, Sudan using One Health approach

Khalid A Enan[1], Abdel Rahim M. El Hussein[1] , RBab M. Haj. Ahmed[1] & Shawgi M. Hassan[3]

[1]*Department of Virology, Central Laboratory-The Ministry of Higher Education and Scientific Research, Sudan - khalid.enan@gmail.com*
[2]*Department of Community Medicine Faculty of Medicine and Health Sciences University of Kassala, Sudan*
[3]*Department of Parasitology, Faculty of Veterinary Medicine University of Khartoum, Sudan*

Background: One Health is increasingly recognized as an optimal approach to address the global risk of health threats originating at the human, animal, and ecosystem interface, and their impact. Dengue burden has been rising in the recent years in Sudan and became a public health problem of significant importance in especially in Kassala City, in Eastern region of the country.

Materials and Methods: This study was conducted in Kassala City, Sudan, during 2014 and 2016, to determine Dengue virus IgG and IgM antibodies in malaria negative febrile patients using ELISA and to Correlate these results to our earlier published data (Rabab *et al,* 2019) obtained on the detection of dengue virus in mosquitoes during the same period in Kassala city.

A. aegypti samples were collected from 20 sites of Kassala City in summer, winter and autumn seasons. Indoor and outdoor resting *Ae. aegypti* adults were collected from residential houses using knockdown technique, light traps and mouth aspirators. The randomly captured females were pooled in five pools (ten females per pool). Mosquitoes in each pool was crushed, centrifuged, and RNA extracted from the supernatant that was then tested for viral genome using Reverse Transcription Polymerase Chain Reaction[RT-PCR] test.

100 sera samples were collected from malaria negative febrile patients (age between 35 to 65 years). The patients were 50 males and 50 females. The sera were tested for dengue IgM and IgG antibodies using ELISA (Euro-immune, Germany).

Results: The results showed that supernatant that was then tested for viral genome using Reverse Transcription Polymerase Chain Reaction[RT-PCR] test. 68% samples of females Ae. aegypti were positive using NS1 primer. Dengue positive mosquito pools were found highest positivity in winter (72.2%), followed by autumn season (64.7%), and the lowest in summer season (66.7%). The total positivity of dengue virus was the highest in pools of BantAlmsna, BantNorth and BantSouth localities (78.6%), followed by pools of Alkrmota, Gharb Algash2, and Gharb Algash 3 (70%) localities, compared with other pools.

Dengue virus IgG were present in 78.5% while Dengue virus IgM antibodies were demonstrable in 4.3% of patients.

Conclusions: The current approach of testing multiple hosts at different sites used in this study could enable advancement and sustainment of One Health activities to control and prevent dengue virus transmission at the humans-mosquitoes-ecosystem niches interface.

From the results of this study, it is concluded that dengue virus infection is endemic in Kassala City of Eastern Sudan. Control of *Ae. aegypti* is recommended targeting water holding containers and to increase people's awareness of the ways dengue infections is transmitted.

WEDNESDAY, 15h50

Lessons from Japanese Encephalitis Virus seroposurvey in hunted wild animals from Yamaguchi prefecture in Japan

Peter Kimeli[1], Waga Elvis Madara[2], Hiroshi Shimoda[2] & Daisuke Hayasaka[2]

[1]Department of Clinical Studies, Faculty of Veterinary Medicine, University of Nairobi, P.O. Box 29053- 00625 Nairobi, Kenya - kimeli08@uonbi.ac.ke
[2]Department of Public Health, Pharmacology & Toxicology, Faculty of Veterinary Medicine, University of Nairobi, P.O. Box 29053- 00625 Nairobi, Kenya
[2]Laboratory of Veterinary Microbiology, Joint Faculty Veterinary Medicine, Yamaguchi University, 1677–1 Yoshida, Yamaguchi 753–8515, Japan

Introduction: Japanese encephalitis virus (JEV) is a zoonotic, vector-borne virus spread primarily by Culex mosquitoes, and it causes acute encephalitis in horses and humans. JEV is widely endemic to Southeast Asia and the Western Pacific region but has been reported in Angola. Continuous serosurvey for JEV antibodies in wildlife is important in determining disease distribution and the potential amplifiers. The study determined the factors associated with JEV seropositivity in hunted wildlife from Yamaguchi prefecture.

Methodology: Blood samples were collected from 476 wild animals captured by licensed hunters to detect JEV antibodies using indirect enzyme-linked immunosorbent assay (ELISA). Data on the sampling date, city area, sex, weight and animal species were captured. Descriptive statistics and logistic regression were used to evaluate the association between predictors and seropositivity.

Results: Serum antibodies against JEV were detected in wild boars (92.2%, 189/227), sika deers (7.3%, 15/158) and Nutria (0.5%, 1/61). All the badgers (n=9) and Japanese macaques (n=21) tested negative. In the final multivariable logistic regression model, the odds of testing seropositive were higher for wild boars (OR=365.39, 95%CI 41.63- 3205.49) and Sika deers (OR=2.27. 95%CI 0.22, 23.29) when compared to Badger, Nutria and Japanese macaque. Compared with Mine city, the odds of testing seropositive were lower for Sanyo-Onoda city (OR= 0.27, 95% CI 0.11, 0.69) but similar to that of Ube city (OR= 0.29, 95%CI 0.08, 1.05) and Yamaguchi city (OR= 0.40, 95% CI 0.10, 1.59). Also, the odds of testing seropositive were higher for samples collected in the years 2021 (OR= 5.72, 95%CI 2.52, 12.97) and ≥ 2022 (OR=2.32, 95%CI 1.07, 5.03) compared with ≤2020.

Conclusion: We conclude that the wild boars and Sika deers play an important role in the transmission and/or amplification of JEV.

WEDNESDAY, 16h10

Spatial distribution of dog rabies, rabies vaccination coverage for dog rabies and the prevalence of dog bite in three selected regions in Gauteng Province, South Africa

Oluyemisi A. Akerele[1,2], J. Ncayiyana[3], C. Mbajiorgu[2] & J.W. Oguttu[2]

[1]Gauteng Department of Agriculture, Rural Development and Environment - yemi.akerele@gauteng.gov.za
[2]Department of Agriculture and Animal Health, Florida Campus, UNISA, South Africa
[3]University of KwazuluNatal

Background: Gauteng province has always had the least number of rabies cases in South Africa (SA). However, there was a re-emergence of the virus pre and post 2010. The spatial distribution of rabies in Gauteng Province (GP) is unknown. This study will investigate the spatial distribution of rabies, vaccination coverage and the prevalence of dog bites in the province.

Methods: Although GP is the smallest province, its human population constitutes about a quarter of the population of the country. Secondary data from the Gauteng Department of Agriculture, Rural Development and Environment (GDARDE) will be used to investigate the spatial distribution of dog rabies, using the average nearest neighbour (ANN).

Gridded human and dog population density online municipal maps will be used to estimate the number of vaccinated dogs per kilometre grid cell and then extrapolated to a 20 by 20 km grid cells to determine the vaccination coverage. The number of dogs vaccinated annually during GDARDE rabies campaigns and by the private sector, will serve as reference dog populations for each grid cell.

Retrospective data on dog bite cases reported pre and post 2010 will be used to estimate the proportion of dog bites by the sociodemographic characteristics of the victims using the Chi-square test of proportions. Statistical significance will be set at $\alpha < 0.05$.

Discussion and conclusion: The distribution of rabies based on the average ANN method will be described for the first time in Gauteng. Investigation of the predictors of dog bites will shed light on the risk of exposure to rabies. Findings of this study will help to establish the progress made towards achieving the 70% vaccination coverage recommended by World Health Organization. This study will serve to further strengthen recommendations to the political and economic establishments with respect to the control strategies for rabies disease.

THURSDAY, 09h00

Molecular characterization of cattle rabies linked to cattle infections in the Northwest Province, South Africa

Antoinette O. Khoane[1], N Mphuthi[1], C Sabeta[2] &M Syakalima[1]

[1]*Department of Animal Health, School of Agricultural Sciences, North-West University, Private Bag X2046, Mmabatho 2735, South Africa - okhoane@gmail.com*
[2]*Agricultural Research Council—Onderstepoort Veterinary Institute, World Organisation for Animal Health (OIE) Rabies Reference Laboratory, Onderstepoort, Pretoria 0110, South Africa*

Rabies is a zoonotic disease that poses a public and occupational health risk in the African continent, responsible for an increased annual fatality in the human population. Rabies infection is a potential hazard in cattle extensive production systems where dogs and cattle interact. The aim of this study was to determine rabies virus strains in infected cattle samples in the North-West province of South Africa using conventional PCR.

Brain-infected tissue samples from cattle collected during the period between 2008 and 2018 in the North-West province was used to undertake a retrospective study. A total of 50 samples that were positive on immunohistochemistry were subjected to PCR targeting the G-L intergenic region. Of these, only 16 samples successfully amplified and were sent for sequencing. The sequences were then blasted on the NCBI database to determine the similarities with other gene sequences. Additional previously isolated gene sequences from cattle, dogs, and jackals deposited on the GenBank were used with our sequences to construct a phylogenetic tree to establish their genetic relatedness. Out of 16 analysed samples, 87.5% (14/16) were related to the gene sequences isolated from dogs originating from Kwa-Zulu Natal province, while 12.5% (2/16) were related to the ones isolated from cattle in the Northwest province. The analysis delineated two dominating clades consisting of wildlife and bovine rabies virus (representing canid rabies cycle), and the third one comprising exclusively bovine viruses of mongoose origin (mongoose rabies biotype). The data obtained in this study showed that the spillover of the rabies virus infections was mainly from canine host.

THURSDAY, 09h20

THEME: SCIENTIFIC DEVELOPMENTS & PREVENTATIVE MEDICINE

Landscape surveillance: tagging remote collar data with risk flags in an adaptive, real-time monitoring platform

John Duncan Grewar[4], Louis van Schalkwyk[1,2] & Grant Beverley[3]

[1] *Department of Agriculture, Land Reform and Rural Development, State Veterinarian: Skukuza, South Africa, 1350*
[2] *Contemplate Wild, Lynwood Park, Gauteng, South Africa, 0081*
[3] *Endangered Wildlife Trust, Carnivore conservation program, Hoedspruit, South Africa, 1380,*
[4] *JDATA (Pty) Ltd, 28 Tambali Village, Sandbaai, 7200, South Africa - info@jdata.co.za*

Background and Objective: Wildlife tracking, using collar-based remote sensing, generates space-time data that is generally retrospectively evaluated. Risk analysis in the wildlife sector involves identifying hazards such as disease risks and human-wildlife interface risks (e.g., snaring, persecution). This pilot study focuses on African Wild Dog (AWD), an endangered wildlife species, in the greater Kruger National Park conservation area (KNPCA), demonstrating landscape surveillance by tagging remote collar data with risk flags in an adaptive, real-time monitoring platform that integrates epidemiologic risk processes with tracking data. The platform utilizes freely available software and integrates with existing conservation management platforms.

Results: Figure 1 shows, as an example, the space-time depiction of an AWD pack moving into a high-snare risk region (B), with alerts sent when the threshold is breached (A). To date ~ 40 AWD have been saved through the snaring program of which the described system is a component.

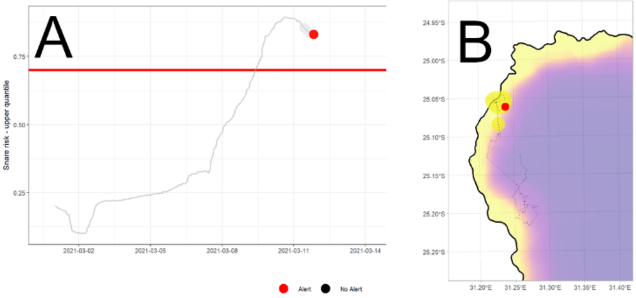


Figure 1

Method and Materials: To monitor 30 AWD packs in the KNPCA, the study aimed to collar one non-alpha female per pack. Tracking data was retrieved from collar-specific APIs or existing data repositories (Movebank). Amazon Web Services' (AWS) Lambda system was used to insert the data into a PostgreSQL cloud (RDS) database. Risk allocation was performed differently depending on the process. For example, persecution risk was attributed through a series of PostGIS spatial queries within the RDS infrastructure, while the snare and domestic dog interaction risk utilized a maximum entropy modeling approach, requiring the use of an R-enabled AWS EC2 server. Data was pushed to various endpoints, including WhatsApp, using AWS Lambda.

Discussion and Recommendations

This study describes a use-case example of landscape surveillance using risk-event tagging of wildlife tracking data to facilitate risk mitigation. The availability of cloud-based resources allows for near-real-time allocation of risk status onto tracking data. This integration of landscape surveillance with tracking activity enhances the ability to intervene when risk thresholds are reached. Moreover, the types of risks that can be addressed are limited only by their potential for automation, as open-source databases and processing infrastructure, such as AWS, PostgreSQL, R, and Python, facilitate automation.

THURSDAY, 09h40

Exploring bovine tuberculosis vaccine efficacy in African Buffalo

J. Hewlett[1], E. Mitchell[2], LM de Klerk Loris[3], V. Rutten[4] & A. Michel[5]

[1]*Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, South Africa - jennie.hewlett@up.ac.za*
[2]*Paraclinical Department, Faculty of Veterinary Science, University of Pretoria, South Africa*
[3]*Department of Agriculture, Land Reform and Rural Development, Skukuza, , South Africa*
[4]*Infectious Diseases and Immunology, Faculty of Veterinary Medicine, Utrecht University, Netherlands*
[4]*Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, South Africa*

African buffalo (*Syncerus caffer*) are the primary wildlife reservoir host for bovine tuberculosis (BTB) in Africa. Infected buffalo populations spread this disease to numerous coexisting species in conservation areas as well as to cattle at park boundaries. This results in increased mortalities in many threatened wildlife species and ensuing quarantine requirements complicates metapopulation management.

The test and slaughter method of controlling BTB is difficult and costly to implement in extensive conservation areas with complex species composition. In recent years, considerable interest has arisen in the vaccination of cattle and indigenous wildlife species against BTB as an additional control strategy.

In this vaccination trial, 21 sub-adult African buffalo (6-12 months) were divided four treatment groups, and received BCG intramuscularly (10^6 CFU), a heat inactivated *M. bovis* vaccine either intramuscularly (HIM) (10^7 CFUs) or orally (HIO) (10^7-10^8 CFU), a control group received 1ml phosphate buffered saline. After 7 months all animals were challenged with *M. bovis* (10^6 CFU) via the intra-tracheal route and the study was terminated 5 months later.

Post mortal analysis showed that HIM had the lowest average macroscopic lesion scores across lung and lymph node tissues, whereas HIO had the highest average scores. *M. bovis* culture and enumeration (CFU/g) revealed that while HIM had the lowest number of positive cultures of lymph node and standardised lung samples, while HIO had the lowest bacterial burden in lung and lymph node tubercles. These results indicate that the heat inactivated vaccine had a protective effect, compared to the control and BCG groups. In particular, HIM appeared to prevent tuberculous lesion formation while HIO was able to reduce bacterial viability within advanced lesions.

THURSDAY, 10h00

Evaluation of aluminium hydroxide nanoparticles as efficient adjuvants to potentiate the immune response against botulinum C and D toxoid vaccine

Ziphezinhle Mbhele[1,2], Lungile Thwala[3], Thandeka Khoza[2] & Faranani Ramagoma[1]

[1]*Onderstepoort Biological Products, 100 Old Soutpan Road, Onderstepoort,0110, Pretoria, South Africa-Ziphezinhle@obpvaccines.co.za*
[2]*Biochemistry, School of Life Sciences, University of KwaZulu Natal (Pietermaritzburg Campus), Private bag X01, Scottsville, 3209, South Africa*
[3]*Current address; Council for Scientific and Industrial Research, National Laser Centre, P O BOX 395, Pretoria, 0001, South Africa*

Clostridium botulinum serotypes C and D cause botulism in livestock, a neuroparalytic disease that results in substantial economic losses. The spread of botulism is controlled by vaccination with the botulinum toxoid (Bot C and D) vaccine. The toxoid vaccines are often adjuvanted with aluminium based salts. Aluminium based adjuvants have been widely used in veterinary prophylactic immunizations owing to their apparent stimulation of the immune responses to toxoid vaccines and superior tolerability when compared to other adjuvants. The aim of our study was to evaluate nanoalum as a potential substitute for alhydrogel in the botulism bivalent vaccine. The botulism bivalent vaccines were formulated with either alhydrogel or nanoalum and comparative efficacy of the two formulations was conducted by measuring the immune response in vaccinated guinea pigs. A significant difference in immunological parameters was observed, with the antibody titer higher (20 IU/ml anti-Bot C/D) in serum of guinea pigs injected with nanoalum-containing vaccine than guinea pigs injected with standard alhydrogel-containing vaccine (8.7 IU/ml and 10 IU/ml anti-Bot C and anti-Bot D, respectively). Additionally, the nanoalum-containing vaccine-maintained potency in a multivalent vaccine (20 IU/ml anti-Bot C/D), while the standard alhydrogel-containing vaccine showed a decline in anti-Bot C (5 IU/ml) antibody titres.

THURSDAY, 10h50

The role of smallholder pig farmers in the biosecurity of pig diseases in the Eastern Cape Province of South Africa using ASF as a model

V. Simbizi [1,2,4], R. Moerane [2], J. van Heerden[3] & B. Gummow[2,4]

[1]State Veterinary Services, Department of Rural Development and Agrarian Reform, Lady Frere 5410, South Africa - vsimbizi@gmail.com
[2]Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Onderstepoort 0110, South Africa
[3]Transboundary Animal Diseases, Onderstepoort Veterinary Research, Agricultural Research Council, Onderstepoort 0110, South Africa
[4]Discipline of Veterinary Sciences, College of Public Health, Medical and Veterinary Sciences, James Cook University, Townsville 4811, Australia

Background: African swine fever (ASF) is an important disease and a threat to the global pig industry. The Eastern Cape Province (ECP) of South Africa has experienced outbreaks of ASF from May 2020 but data on the demographics and practices of smallholder pig farmers are scant, and little is published on the biosecurity related to these farms. Similarly, there is little published on its prevalence in smallholder pig farms.

Objectives: To understand the role of smallholder pig farmers in biosecurity and prevention of pig diseases using ASF as model. To conduct a pig serological survey (from August 2019 to May 2020) to estimate the seroprevalence of ASF at the provincial level.

Materials and methods: A questionnaire survey describing the demographics and practices of 214 smallholder pig farmers was carried out from February 2019 to June 2019. In parallel, a serological survey of pigs was conducted to estimate the seroprevalence of ASF at provincial level (from August 2019 to May 2020).

Results: Females represented 52% of pig farmers and reflect the cultural importance of pig farming in Xhosa culture. All the farmers interviewed had low biosecurity measures on their farms. A low level of education, lack of training and reliance on the use of remedies to treat and prevent pig diseases for many farmers were a key finding that could explain the poor implementation of biosecurity measures. Furthermore, a poor knowledge of antibiotic use could contribute to anti-microbial resistance (AMR) in these pigs. Our findings show that smallholder pig farming could therefore be a high risk for disease incursion and spread. A total of 1000 pig sera were collected. The seroprevalence of ASF was found to be 0.01% (95% CI-0.003-0.015).

Discussion and recommendations: Smallholder farms were frequently involving free-ranging pigs, swill feeding and informal trading; practices known to contribute to the spread of ASF and other communicable pig diseases. Cost-effective biosecurity measures and marketing opportunities will help to prevent pig diseases while a continuing education programme will modernise the rural pig industry and reduce the impact of AMR.

THURSDAY, 11h10

Efficacy of *Aloe Vera* and *Curcuma Longa* in managing Porcine Staphylococcal Infections

Joshua Ngwisha[1], Mulemba Samutela[1,2], Bernard Hang'ombe[1] & Kennedy Choongo[3]

[1]*University of Zambia, School of Veterinary Medicine, Paraclinical Studies Department, Lusaka, Zambia - drjoshuangwisha@gmail.com*
[2]*University of Zambia, School of Health Sciences, Biomedical Sciences Department, Lusaka, Zambia*
[3]*University of Zambia, School of Veterinary Medicine, Biomedical Sciences Department, Lusaka, Zambia*

Introduction: Antimicrobial resistance (AMR) has become a global public health concern, and the livestock sector is not immune to this problem. In Southern Africa, little research has been conducted on alternative ethno-remedies that could potentially curb AMR in pigs. This study aimed to evaluate the efficacy of locally accessible herbs in managing *Staphylococcus aureus* infections in pigs, specifically *Aloe vera* and *Curcuma longa.*

Materials and Methods: The study was conducted using an experimental design. The herbs were collected from Zambia using a non-participatory rapid appraisal approach, and the *S. aureus* strain was sourced from a porcine nasal swab from another cross-sectional study. Crude extracts were prepared using ethanol, ethyl acetate, and aqueous solvents. Three groups were prepared: *Aloe vera* only, *Curcuma longa* only, and a combination of *Aloe vera* and *Curcuma longa* (5:1). The agar dilution method was used to assess the efficacy of the herbal extracts against the bacterial isolate at 0.5 McFarland. A cephalexin, neomycin, and kanamycin formulation served as the positive control, while Dimethylsulfoxide (DMSO) was used as the negative control.

Results: The Clinical and Laboratory Standards Institute (CLSI) guide was used to grade the sensitivity of the isolates to the drugs as Susceptible (S), Intermediately Susceptible (I), and Resistant (R). The highest susceptibility was recorded for *Curcuma longa* (S=75%, I=25%), followed by *Aloe vera* (S=56%, I=19%, R=25%). The combined formulation yielded S=48%, I=26%, and R=26%. The positive control produced S=63% and R=37%, while the negative control had R=100%. The results were analyzed using frequency graphs and charts in MS Excel 2010 and interpreted descriptively.

Discussion: The highest susceptibility of *S. aureus* was observed in *Curcuma longa* (100% S+I) and *Aloe vera* (75% S+I). Despite previous studies showing susceptibility of *S. aureus* to Aloe and Curcumin, there is still a lack of data on their application in swine upper respiratory tract infections. This study could potentially pave way for further *in vitro* and *in vivo* assessments to find cost-effective solutions to Methicillin-Resistant S. aureus (MRSA) and multidrug-resistant (MDR) Staphylococcal infections.

Conclusion: The results suggest that *Curcuma longa* and *Aloe vera* have potential for managing porcine upper respiratory tract infections caused by *S. aureus* in Zambia. Further safety and clinical tests are necessary to validate their use, determine the minimum inhibitory concentration, and establish suitable dosages.

THURSDAY, 11h30

Safety and immunogenicity of inactivated Rift Valley Fever Smithburn viral vaccine in sheep

Matome Matsiela[1], Leeann Naicker[1], Thandeka Khoza[2] & Nobalanda Mokoena[1]

[1]*Onderstepoort Biological Products (Pty. Ltd), 100 Old Soutpan Road, Onderstepoort 0110, Pretoria South Africa - matome@obpvaccines.co.za*
[2]*Department of Biochemistry, School of Life Sciences, University of KwaZulu-Natal (Pietermaritzburg campus), Scottsville, 3209, KwaZulu-Natal, South Africa*

The live attenuated Rift Valley Fever Smithburn (SB) vaccine is one of the oldest products used for controlling the spread of RVF disease in ruminants. Vaccinations with RVF Smithburn result in residual pathogenic effect and is limited for use in non-pregnant animals. Commercially available RVFV inactivated vaccines are considered safer options to control the disease. These products are prepared from virulent RVFV isolates and present occupational safety concerns.

This research study evaluates the ability of an inactivated SB vaccine strain to elicit neutralising antibody response in sheep. The RVF Smithburn vaccine was inactivated with BEI at 37 °C. Inactivated RVFV cultures were adjuvanted with MontanideTM Gel-01 and aluminium hydroxide (Al(OH)3) gel for immunogenicity and safety determination in sheep. The study was conducted in a total number of twenty sheep, which were subdivided into five per group. The commercial RVF inactivated vaccine and a placebo were included as positive and negative control groups, respectively. Vaccine formulations were safe with animals in vaccinated groups showing no clinical signs of RVFV infection and temperature reactions following prime-boost injections. The aluminium hydroxide formulated vaccine induced an immune response as early as 14 days post primary vaccination with neutralising antibody titre of 1:20 and a peak antibody titre of 1:83 was reached on day 56. A similar trend was observed in the animal group vaccinated with the commercial inactivated RVF vaccine obtaining the antibody titre of 1:128 on day 56. The neutralizing antibody levels remained within a threshold for the duration of the study. Merino sheep vaccinated with MontanideTM Gel-01-Smithburn were characterised with overall lower immune response when compared to aluminium hydroxide vaccine emulsions. These finding suggests that the aluminium-hydroxide based Smithburn can be used for protection of ruminants against RVF disease, and the vaccine can further be evaluated for safety in pregnant ewes. The RVF SB can be used as an alternative to the current commercial inactivated RVFV vaccines.

THURSDAY, 11h50

Production of recombinant Lumpy skin disease virus A27L and L1R proteins for application in diagnostics and vaccine development

Nomfundo Ntombela[1], Nobalanda Mokoena[2] & Thandeka Khoza[1]

[1]Department of Biochemistry, School of Life Sciences, University of KwaZulu-Natal (Pietermaritzburg Campus), Scottsville 3209, KwaZulu-Natal, South Africa - ntombelanp12@gmail.com
[2]Onderstepoort Biological Products (SOC. Ltd), 100 Old Soutpan Road, Onderstepoort, 0110, Pretoria, South Africa

Live attenuated vaccines (LAVs) are considered the most effective vaccines for control of lumpy skin disease (LSD). However, the application of LAVs globally is limited by safety concerns, with reports of adverse reactions following vaccination. Hence, this study focused on the development of recombinant sub-unit vaccines against LSD as safer and efficacious alternatives. Proteins A27L and L1R essential for virus attachment and membrane fusion were investigated as possible candidates for vaccine development. The proteins were recombinantly expressed in Escherichia coli and purified to homogeneity using His-tagged affinity chromatography. Purified protein yields of 6 and 8,5 mg/mL were obtained for A27L and L1R, respectively. Proteins were formulated individually with 10% (w/w) Montanide™ Gel 01 PR adjuvant at a final antigen dose of 20 µg. The adjuvanted proteins were also formulated as a combination of both proteins containing the same vaccine dosage. The safety and immunogenicity of these vaccines were evaluated in rabbits in a 42-day trial conducted with two vaccinations administered on days 0 and 21. No clinical signs and deaths were recorded in vaccinated animals for all three vaccine formulations. The highest neutralizing antibody response was detected with individual vaccines (A27L/ L1R) and the combination vaccine on day 42 post-primary vaccination, and results were correlated with antibody titres quantified using ELISA. The application of A27L and L1R and the combination of both proteins as potential diagnostic reagents was assessed through indirect ELISA using LSDV-positive serum. Reagents containing the combination proteins showed the best serum detection with all six coating concentrations. While reagents containing individual proteins could only detect LSD with five out of six coating concentrations. To our knowledge, this is the first report on the immunogenicity of the combination of recombinant LSDV A27L and LSDV L1R and the potential of this combination in diagnostics and vaccine development research.

THURSDAY, 12h10

THEME: PUBLIC HEALTH & ENVIRONMENTAL HEALTH

Sponsor Talk - Onderstepoort Biological Products

THURSDAY, 14h00

The Hippopotamus and One Health – What's the link?

Anita L. Michel[1], M. Engelbrecht[1], A. Jonker[1], J. Wentzel[1] & A. Michel[1]

[1]*Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, Private Bag X04, Onderstepoort, 0110, South Africa -* anita.michel@up.ac.za

Background and objective: Hippopotamus-human conflict occurs when humans threaten the territories of hippopotami, both inside and outside the water. It is estimated that the hippopotamus is responsible for approximately 10% of all injuries recorded in humans as a result of wildlife-human conflicts and for 500- 3000 human deaths per year worldwide. Complications of the severe injuries include chronic osteomyelitis and deep wound infections, often necessitating limb amputation and other complicated surgeries (Haddara et al, 2020).

This study aimed to identify the normal flora in the oral cavity of the hippopotamus (*Hippopotamus amphibious)* and perform antibiotic sensitivity testing of the most abundant bacterial species. For this purpose, oral swabs were collected from 34 hippopotami in the Greater Kruger National Park Complex and cultured for aerobic and anaerobic bacteria.

Findings: A total of 112 aerobic isolates were obtained from the 34 hippopotami. The most frequently isolated aerobic bacterial species included *Aeromonas hydrophila*, *Shewanella putrefaciens*, *Aeromonas sobria* and *Vibrio parahaemolyticus* while there were only 11 anaerobic isolates representing two bacterial species, namely *Prevotella melaninogenica* and *Clostridium* spp.

All aerobic isolates were subjected to disc diffusion antibiograms to determine their sensitivity/resistance to a panel of 17 antibiotics. Antibiotic resistance was mainly observed against Ampicillin, Amoxicillin/clavulanic acid and cephalosporins. One *A. hydrophila* isolate was resistant against the full panel of antibiotics.

Conclusion: The study showed that treatment of patients who sustained wounds inflicted by hippopotami can be severely compromised by the antibiotic resistance of the oral bacteria common in these animals and should be strictly guided by antimicrobial sensitivity testing. Especially *A. hydrophila* and *S. putrefaciens* are highly pathogenic and have the ability to cause severe wound infections and may also cause bacteraemia.

Reference

Haddara, M. M. et al., 2020. Hippopotamus Bite Morbidity: a report of 11 cases from Burundi. *Oxford Medical Case Reports,* 2020(8), pp. 271-274.

THURSDAY, 14h20

Antimicrobial resistance in fish and poultry: Public health implications for animal source food production in Nigeria, Egypt, and South Africa

Ekemini Okon[1], Reuben Okocha[2], B. T. Adesina[2], J. O. Ehigie[3], O. O. Alabi[2], A. M. Bolanle[2], Nelson Matekwe[4], Babatunde Falana[2], Adebisi M. Tiamiyu[5], Isaac O. Olatoye[6] & Olufemi B. Adedeji[6]

[1]*Faculty of Bioscience Engineering, Ghent University, Ghent, Belgium -* okon.ekeminimoses@gmail.com
[2]*Department of Agriculture, College of Agricultural Sciences, Landmark University, Omu-Aran, Kwara State, Nigeria*
[3]*Faculty of Sciences, University of Porto, Porto, Portugal*

[4]*Department of Agriculture Environmental Affairs, Rural Development and Land Reform, Veterinary Services, Northern Cape Province, South Africa*
[5]*University of Medical Sciences, Ondo City, Ondo State, Nigeria*
[6]*University of Ibadan, Ibadan, Nigeria*

Antimicrobial resistance (AMR) is a significant threat to global public health. Specifically, excessive usage of antimicrobials in food animal production is one significant reason for AMR development in humans. Therefore, it is essential to identify the trends of AMR in fish and poultry and develop better surveillance strategies for the future. Despite this imperative need, such information is not well documented, especially in Africa. This study used a systematic review to assess AMR trend, spatial distribution, and incidence in fish and poultry research in Nigeria, Egypt, and South Africa. A literature assessment was conducted for published studies on AMR between 1989 and 2021 using the Scopus and Web of Science databases. One hundred and seventy-three relevant articles were obtained from the database search. Egypt was the leading exponent of antimicrobial resistance research (43.35%, 75 studies), followed by Nigeria (39.31%, 68 studies), then South Africa (17.34%, 30 studies). The majority of the antimicrobial resistance studies were on poultry in Egypt (81%, 61 studies), Nigeria (87%, 59 studies), and South Africa (80%, 24 studies). Studies on fish were 17% (13 studies), 9% (6 studies), and 10% (3 studies) in Egypt, Nigeria, and South Africa, respectively. Antimicrobial resistance patterns showed multiple drug resistance and variations in resistant genes. AMR research focused on sulfamethoxazole groups, chloramphenicol, trimethoprim, tetracycline, erythromycin, and ampicillin. Most studies employed the disk diffusion method for antimicrobial susceptibility tests. Among the four mechanisms of AMR, limiting drug uptake was the most reported in this study (both in fish and poultry). The findings reveal public and environmental health threats and suggest that it would be useful to promote and advance AMR research, particularly for countries on the global hotspot for antimicrobial use.

THURSDAY, 14h40

Serological evidence and co-exposure of selected infections among livestock slaughtered at Eastern Cape abattoirs in South Africa

K.D. Mazwi[1], F.B. Kolo[1,] I.F. Jaja[3,4], R.P. Bokaba[1], Y.B. Ngoshe[2], A. Hassim[1], L. Neves[1,5] & H. van Heerden[1]

[1]*Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, Onderstepoort, South Africa - Desireemazwi@gmail.com*
[2]*Epidemiology Section, Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Onderstepoort, South Africa*
[3]*Department of Livestock and Pasture Science, Faculty of Science and Agriculture, University of Fort Hare, South Africa*
[4]*Department of Agriculture and Animal Health, University of South Africa, Roodepoort Johannesburg, South Africa*
[5]*Centro de Biotecnologia, Universidade Eduardo Mondlane, Maputo, Mozambique*

Selected zoonotic diseases such as brucellosis, coxiellosis and toxoplasmosis all have a public health impact. The infections were investigated on apparently healthy livestock slaughtered in abattoirs in the Eastern Cape Province. Antibodies against *Brucella* spp., *Coxiella burnetti* and *Toxoplasma gondii,* as well as the co-exposure were investigated using serological tests. A total of 565 animals were screened using RBT followed by confirmation for *Brucella* using iELISA and CFT. The Mast® Toxoreagent test and iELISA were used for the detection of antibodies against *T. gondii* and *C. burnetti*, respectively.

The overall *Brucella* seropositivity using RBT, CFT and iELISA was 5.4%, 2.0% and 1.2% in cattle, sheep, and pigs, respectively. *T. gondii* seropositivity of 37.9%, 1.5% and 7.1% was observed in cattle, sheep, and pigs, respectively. *Coxiella burnetti* seropositivity of 26.4%, 15% and 2.4% was observed in cattle, sheep, and pigs, respectively. Co-exposure was detected in cattle for antibodies against *C. burnetti* and *T. gondii* (40.54%), *Brucella* spp. and *T. gondii* (4.05%), and *Brucella* spp. and *Coxiella burnetti* (4.05%). Co-exposure for *Brucella*

spp., *Coxiella burnetti* and *Toxoplasma gondii* (4.05%) was detected in cattle. Co-exposure of *Brucella* spp. and *Coxiella burnetti* (13.33%) was detected in sheep.

To our knowledge co-infection of *Brucella* spp., *T. gondii* and *C. burnetti* in cattle has not been reported in literature. Although more than one third of the serum samples were *T. gondii* positive in cattle, this result should be considered with caution due to the frequent lack of evidence of viable *T. gondii* infections in seropositive cattle. Co-infection of *Brucella* and *C. burnetii* in both cattle and sheep is significant as it results in reproductive losses, and both constitute an infection risk to humans in contact with these livestock. The detection of antibodies against multiple zoonotic infections in livestock from abattoirs has implications for public health and poses a risk of exposure for humans. It is thus, essential to raise awareness among the public on the presence of pathogens in slaughtered animals. The results of this study will facilitate the development of effective strategic measures regarding the diagnosis and control of zoonotic infection in SA.

THURSDAY, 15h00

Seroprevalence of *Taenia saginata* cysts in cattle, human hospital cases and Risk Factors for human taeniasis in Kajiado County, Kenya

Ruphline M. Anyango[1], Timothy M. Wachira[1], Gerald M. Muchemi[1]

[1]*Department of Public Health, Pharmacology and Toxicology, University of Nairobi, Kenya - ruphlinemargaret@students.uonbi.ac.ke*

Taenia saginata is a zoonotic tapeworm of major economic importance that causes disease in cattle and humans. A cross-sectional survey was conducted between June and July 2021 in Kajiado County, Kenya to (i) estimate the seroprevalence of *Taenia saginata* cysts in cattle presented for slaughter in Kitengela, Kiserian and Keekonyokie slaughterhouses, (ii) to determine the annual hospital reported cases of *T. saginata* in humans that visited all level 4 hospitals in Kajiado county between 2015 and 2021 and (iii) to assess the risk factors for *T. saginata* in humans. Analyzed data in this study revealed that the seroprevalence of *T. saginata* cysts in cattle in the selected slaughterhouses was 2.67% (4/150). The meat inspectors recorded no cysts during the study period, confirming that Antibody ELISA is three times as sensitive as meat inspection. Data from hospital records showed that a total of 1,487,687 patients visited different facilities in Kajiado County between 2015 and 2021. During the same period, 29 patients were diagnosed with human taeniasis. The highest proportion of reported cases (0.006%) was encountered in 2015 and the least proportion (0.004%) in 2020. From the risk factors assessed, uninspected home slaughter (75%), consumption of raw/improperly cooked beef (100%) and open defecation by herders (11%) still pose a risk to humans getting infected by *T. saginata* while the presence and use of latrines (89%) and availability, accessibility and use of taenicides (89%) seem to have significantly contributed to the reduction of *T. saginata* prevalence in this region. Considering the cultural practices of the local (Maasai) community, who are the main residents of Kajiado County, and since humans are the only definitive hosts of *T. saginata*, it is recommended that control of the infection should be centred towards continuous focused education coupled with regular deworming of humans and especially the herders and school going children. This will gradually result in behavior and culture change that will ultimately reduce the prevalence and lead to the elimination of the disease.

FRIDAY, 09h00

Molecular characterization and antimicrobial resistance profiles of *Staphylococcus aureus* isolated from meat and meat products in South Africa

Emmanuel Seakamela[1], Frank Mtshali[2,3], Bohani Mtileni[2] & Itumeleng Matle[3]

[1]*Lephalale Veterinary Laboratory, Veterinary Services, Department of Agriculture and Rural Development, Limpopo, South Africa - bio4slim@gmail.com*
[2]*Tshwane University of Technology (TUT), Faculty of Science, Department of Animal Sciences, Pretoria, South Africa*

[3]*Bacteriology Division, Agricultural Research Council: Onderstepoort Veterinary Research, Onderstepoort, Pretoria, South Africa*

The objective of this study was to analyse *Staphylococcus aureus* isolates obtained from meat and meat products for the presence of enterotoxin genes and antibiotic resistance profiles. A total of 148 isolates were collected from different sources, including game, chicken, cattle, and pig samples. Polymerase chain reaction (PCR) was used to screen the isolates for the presence of 19 Staphylococcal enterotoxin (SE) genes, as well as the *eta*, *tst*, *femA*, and *femB* genes. The antibiotic resistance profile of the isolates was determined using both the disc diffusion method (for 12 antibiotics) and PCR.

Out of the 148 S. aureus isolates tested, 97 (65.5%) were found to harbor SE gene regions. The most prevalent SE genes detected in the S. aureus strains were sec (60.1%), followed by sea (21.0%), seb (20.3%), and sed (18.8%). The tst gene, which is associated with toxic shock syndrome, was found in 42.6% of the isolates. The *femB*, *eta*, and *femA* genes were found in 19.6%, 16.2%, and 7.4% of the isolates, respectively.
Regarding antibiotic resistance, the study found that amoxicillin-clavulanic acid, oxytetracycline, and chloramphenicol were ineffective against a significant number (60-90%) of the isolates. The most frequently detected antimicrobial gene was *BlaZ* (41.9%), followed by *mecA* (39.2%), *ermA* (16.2%), *ermB* (12.8%), *ermC* (27.7%), *tetA* (11.5%), *tetM* (22.3%), and *aacA-aphD* (26.4%).

These findings indicate a high prevalence of sea and tst genes in the S. aureus strains, which raises serious concerns for public health and poses challenges to food safety. Additionally, the high levels of *BlaZ* and *mecA* genes observed in this study have implications for therapy, suggesting potential difficulties in treating infections caused by these isolates.

Overall, this study highlights the importance of monitoring enterotoxin genes and antibiotic resistance in S. aureus isolates from meat and meat products to ensure food safety and effective treatment of related infections.

FRIDAY, 09h20

Occurrence, antimicrobial resistance, and genetic diversity of *Klebsiella pneumoniae* from broiler chicken carcasses in Gauteng Province, South Africa

Itumeleng Matle[1], Emmanuel Radebe[1], Lavhelesani Makhado[1] & Magdeline Magoro[2]

[1]*Bacteriology Division, Agricultural Research Council, Onderstepoort Veterinary Research, Onderstepoort, South Africa - Matlel@arc.agric.za*
[2]*Food Science and Technology, Agricultural Research Council: Animal Production, Irene, Pretoria, South Africa*

Klebsiella pneumoniae is a well-studied human pathogen due to its ability to acquire genetic elements that confer antimicrobial resistance traits, leading to the emergence of multidrug-resistant and hypervirulent clones globally. *K. pneumoniae* is also present in diverse environmental niches; however, there is a dearth of information on its occurrence and characteristics from non-human sources in South Africa. This study aimed to assess the prevalence of *K. pneumoniae* in broiler chicken carcasses and to detect antibiotic resistance phenotypes, antimicrobial resistance genes, and the molecular subtypes of the recovered isolates. A total of 404 carcass samples from informal (unregistered) and registered abattoirs were collected across Gauteng provinces. The samples for K. pneumoniae were isolated using microbiological techniques, and all positive isolates were studied for capsular serotypes and antibiotic genes using various molecular method. The occurrence of *K. pneumoniae* in carcasses from informal abattoirs (68%; 28/41) was significantly ($p < 0.01$) higher than in registered abattoirs (31%; 13/41). High resistance was observed against aztreonam (92.7%), amoxicillin/clavulanic acid (73.2%), and ampicillin (70.7%), and multidrug resistance to ≥ 3 classes of antimicrobials was found in 20.4% of isolates. All typeable isolates were typed into K2, K5, K20, and K54 serotypes, and among them, K54 was observed to be predominant. Of the 18 tested antimicrobial resistance genes, *blaTEM* was the most predominant (39%), followed by *Qnr* (29.5%) and *DrfXII* (24.4%). Two sequence types, ST45 and ST29, from *K. pneumoniae* were the most common. The results of this study indicate that informal abattoirs might be an important zoonotic reservoir for *K. pneumoniae* compared to registered abattoirs. Furthermore, our results show a highly diverse *K. pneumoniae* population, high levels of antimicrobial resistance, and a hypervirulent K54/ST45 clone circulating in broiler carcasses.

FRIDAY, 09h40

Occupational health and safety knowledge, awareness and practices to prevent zoonotic diseases among veterinary services fieldworkers in the North-West Province, South Africa

Sboniso Mhlongo[1,2], Nisha Naicker [2,3] & Tanusha Singh [2,3]

[1]*Veterinary Services Directorate, North-West Department of Agriculture, South Africa* - sboniso@yahoo.com
[2]*Department of Environmental Health, Faculty of Health Sciences, University of Johannesburg, South Africa*
[3]*National Institute for Occupational Health, National Health Laboratory Service, Johannesburg, South Africa*

Background: Zoonotic diseases account for 60% of infectious diseases worldwide. The lack of effective control of the human-animal interface increases the risk of infection. This warrants an assessment of occupational health and safety (OHS) knowledge, awareness and practices related to preventing zoonotic diseases.

Objectives: To assess veterinary fieldworkers' knowledge, awareness and common OHS practices related to handling infected animals and their biological products to help identify zoonotic disease risk factors and exposure.

Methods: A self-administered questionnaire on OHS knowledge, awareness and practices, and zoonotic disease risk factors was distributed to 137 veterinary fieldworkers in the North-West Department of Agriculture-Veterinary Service. Collected data were analysed using descriptive analyses and the chi-square statistic to assess differences with a p-value of 0.05, significant at a 95% confidence interval.

Results: Eighty animal health technicians, 13 public health officers and 12 veterinarians participated in the study. Most participants had not received any OHS/biosecurity/biosafety training (n=91, 86.7%). There was a statistically significant difference between occupations for departmental biosecurity/biosafety training (p=0.008), other OHS-related training (p=0.005); knowledge for the description of Rabies (p=0.040) and awareness on reporting accidents (p=0.007).

Most participants had good practices of always using overalls (n=91, 86.7%) and safety boots (n=80, 76.2%) during fieldwork. The participants were most often exposed to Brucellosis (69.5%, n=73), other potentially infectious material (82.9%, n=87) and sharps injuries (74.3%, n=78), with statistically significant ($p<0.001$) differences between occupations in all these factors, and their zoonotic diseases vaccination status ($p<0.001$). Only 38.1% (n=40) of participants were vaccinated against a type of zoonotic disease.

Conclusion: This study showed that most participants had good OHS knowledge, awareness and practices but required improvements in OHS training and the provision of personnel protective equipment. Other risk factors included exposure to animals/material with Brucellosis and other potentially infectious diseases and inadequate employee vaccination against zoonotic infections.

FRIDAY, 10h00

Strategies used by locals in Lephalale Municipality, Limpopo, South Africa, to cope with inadequate water supply

N. A. Modimola[1], L.S. Mudau[1], & M.M. Mokoena[1]

[1]*Department of Environmental Health, Tshwane University of Technology, P/Bag X680, Pretoria, 0001, SA* - nthabiseng.modimola@yahoo.com

Most settlements in South Africa have the persistent challenge of water supply that comes with a cost. The research sought to evaluate the coping mechanisms used by communities to cope with inadequate water supplies. A survey was carried out in the Local Municipality of Lephalale using an online questionnaire. A total number of two hundred participants responded to the online questionnaires. The results showed that the majority (69%) of communities depend on municipal water as their main water supply. However, participants confirmed that the water supply in the area is inadequate. These have forced the communities to improvise by resorting to several solutions for using as secondary water sources. These contributed to 20% of the participants purchasing water from their neighbours and local businesses; hence, 11% drilled private boreholes, and 20% obtained water from rivers and rainwater collection systems. Despite of developing secondary water sources to deal with the inadequate water supply, it has been reported that these strategies were not enough. Hence, they adopted additional strategies which include fetching water at a distant water source, re-using water and resort to illegal water connections. However, these strategies have a negative financial impact on the population. On the other hand, communities reported highest reasons of water scarcity as failure of the water delivery system (22%), population growth (31%), and inefficient water use (15%). The study concluded that a lack of continuous water supply contributed to communities making unsafe decisions, which had some financial ramification.

FRIDAY, 11h00

Africa One Health Network

Misheck Mulumba, Chair-AfOHNET Steering Committee
https://afohnet.org/

Recent global disease events highlight the significant impact of zoonotic diseases on human and animal health. Changes in the environment, such as human encroachment, climate change, population growth, and agriculture intensification are factors contributing to zoonotic disease emergence. The One Health approach to detection, diagnosis, and reporting of disease events employs multi-disciplinary approaches to address the interactions among human, animal, and environmental health risks and threats. This strategy has been recognized as a major component to global health security by international organizations and further promoted by targets within the Global Health Security Agenda and UN Development Sustainability Goals.

Across the African continent, there are multiple effective national, regional, and sub-regional networks that are centered around One Health initiatives. These networks work to mobilize policy makers and One Health professionals to improve disease surveillance, outbreak preparedness and response, and information sharing. While many of these groups are aware of each other's efforts and priorities, there is significant opportunity for better coordination and integration to share best practices, lessons learned, and resources to promote the next generation of pan-African One Health leadership.

About AfOHNet

The Africa One Health Network was formed in 2019, following the first Africa One Health Congress, with the support of the Defense Threat Reduction Agency, Biological Threat Reduction Program to connect existing One Health initiatives and networks across the African continent and formalize cross-border collaboration and information-sharing. Under a mechanism for regular communication exchange, the AfOHNet shall facilitate sharing of best practices and lessons learned of One Health initiatives and discuss national and regional One Health engagement strategies, policies, and gaps related to operational biosurveillance, biosecurity, biosafety, and sustainability.

Provisions of the AfOHNet Charter aims to formalize membership, obligations, and authorities; as well as the long- and short-term goals and objectives of its activities.

Network Mission

AOHN aims to improve coordination and communication between One Health networks with the mission of strengthening disease detection, diagnoses, and reporting. We aim to strengthen One Health implementation across the African Continent by sharing best practices and lessons learned from established initiatives.

Network objectives and Scope

The objectives and scope of the Africa One Health Network workshop is to convene various One Health leaders in their respective networks, creating a network of networks, institutions and individuals in their respective OH fields, with the following objectives:

1) Developing Thought Leaders in One Health
2) Stimulating Science linkages between Policy and Community practice. In the process discuss the integration of One Health science, policy, advocacy and action on the continent.
3) Developing effective Science leadership capability to generate competent and confident African scientists that can lead OH partnerships.
4) Exploring technologies that promote effective One Health surveillance, affordable pathogen detection & identification, and stimulate prompt response and disease containment and create a platform to share One Health surveillance research findings and practices.
5) Cultivate a supportive community of OH scientists, bound together in the promotion of collaborative African-led research initiatives.
6) 6). Improve coordination and communication between existing One Health networks to strengthen disease detection, diagnosis, and reporting.
7) 7). Strengthen One Health implementation by sharing best practices and lessons learned from established One Health initiatives.
8) 8). Link with World One Health Platform as a partner in organizing OH events on the continent (AfOHNet together with University of Pretoria will be co-hosting the next WOHC in Cape Town in September 2024).

FRIDAY, 11h20

Molecular epidemiology and risk assessment of non-typhoid *Salmonella* isolates from poultry in South Africa

E. Masitha[1] & M. Karama[1]

[1]*Veterinary Public Health Section, Department of Paraclinical Sciences, Faculty of Veterinary Science, University of Pretoria, Onderstepoort 0110, South Africa - u20805536@tuks.co.za*

Salmonella species are commonly associated with foodborne disease characterised by gastroenteritis, bacteraemia, and focal infections. Virulence factors, host susceptibility and serovar fitness contribute to the severity and outcome of Salmonellosis. Virulence factors facilitate attachment, invasion, survival replication in macrophages and systemic dissemination of *Salmonella* in animal and human hosts. In this study a total of 200 *Salmonella* serovars Muenchen (26%), Senftenberg (21%), Isangi (15.5%), Schwarzengrund (14.5%), Riggil (7.5%), Typhimurium (7%), Kisii (6.5%) and Heidelberg (2%) from diseased birds organs and farm environments were obtained from 30 poultry farms throughout South Africa. The isolates were characterised by PCR for a total of 44 chromosomal, bacteriophage, plasmid, and *Salmonella* pathogenicity Islands (SPIs)-encoded virulence genes. Virulence genes *sopB*, *tolC*, *msgA*, *sseL* essential for *Salmonella* invasion, survival in macrophages and replication were present in all isolates 100% (200/200). Bacteriophages-encoded virulence genes *sopE* 11% (22/200), *gipA* 3% (6/200) (colonisation and invasion), *sspH1* 33% (66/200), *sspH2* 28.5% (57/200) (immune modulation), *gtgB* 1.5% (3/200) and, *sodC1* 8% (16/200) (survival and replication in macrophages) were sporadically distributed across *Salmonella* serotypes. Virulence plasmid-encoded genes *rck* 4.5% (9/200), *srgA* 4.5% (9/200), *mig 5* 4.5% (9/200) which are essential for resistance of *Salmonella* to the host complement system were present in *Salmonella* serovar Typhimurium only. The genetic markers encoded by SPIs 1-5,6,7,8,9,16,18,19, 24 were diversly distributed among most of *Salmonella* isolates indicating that

these serotypes are possibly more virulent. In conclusion, poultry are a reservoir of NTS serovars that carry virulence genes essential for causing foodborne gastroenteritis and invasive disease in animals and humans. Further *Salmonella* surveillance and characterisation will be needed to identify highly virulent strains circulating in poultry in South Africa to prevent their entry in the food chain.

FRIDAY, 11h40

THEME: SOCIOECONOMIC/CULTURAL DYNAMICS

Village Livestock Auction facilities as catalyst for socioeconomic development and control of infectious diseases: The case of Nort- West Province in South Africa

Mothosietlile P. Setlhabi[1], Zimbini Mdlulwa[1], Kenneth Lepedi[1], Ntshipi Maeco[1] & Aleta Mothupi[1]

[1]*Agricultural Economics Services, North-West Department of Agriculture and Rural Development - msetlhabi@nwpg.gov.za*

Generally, live animal sales are characterised as hotspots for the spread of infectious diseases. However, localised village livestock auction sales can work as catalysts for traceability of animals and minimisation of the spread of infectious diseases. Since 2010 the North-West Department of Agriculture and Rural Development initiated development of village livestock auction facilities (VLAFs) to facilitate access of communal farmers to livestock markets. To date a total of 5VLAFs have been implemented in three district municipalities across the province. An evaluation of the impact of the village livestock auction facilities on communal farmers has been initiated and is on-going. The purpose of the evaluation is to assess the impact of VLA sales in relation to accessibility of VLAFs and the associated impacts. The evaluation was carried through administration of household interviews. Preliminary results indicate that the improved earnings from VLA sales have influenced communal farmers ‘behaviour and decision making with regards to the general welfare of animals, reduced economic losses and animal health and diseases management procedures. Farmers have also reported reduced transaction costs due to proximity of the VLAFs, improved income, reduced animal movement, traceability of animals and reduced livestock theft as auctions are held locally. The VLAFs have proved to be stimulants for livestock marketing, attracting buyers from other provinces, collective efforts in breeding improvement initiatives, primary animal health care as suppliers for veterinary and feed supplies also come to sell during the auctions. With high market related prices that farmers realise from the auction sales, they have prioritized buying of veterinary supplies to improve the animal health to have their livestock market ready, and in good body condition. Overall, the implementation of VLAFs in North-West province have improves household food security, increased livestock earnings and economic activities. With increased circulation of money within the community, one of the commercial banks has installed an automated teller machine (ATM) on the request of VLA committee, village leadership and the community in general. Continuous assessment for the need of village marketing infrastructure for livestock and other agricultural commodities is recommended.

FRIDAY, 12h00

Economic and social burdens of Non-Typhoidal *Salmonella* infections in Nigeria

Abdullahi S. Ozomata[1], Annelize Jonker[1] & Folorunso O. Fasina[1]

[1]*Department of Veterinary Tropical Diseases, University of Pretoria - drsao.epidemi@gmail.com*

Background: Estimating economic burdens of diseases is important to inform investment decisions and empirical interventions but are challenging where data are scarce. In Nigeria, economic estimates of some animal diseases have been made and such costs include direct losses through morbidity and mortality, treatment and intervention costs, effects on production and productivity, and human health related costs

(livelihoods, psychosocial and zoonotic impacts). The non-typhoidal *Salmonella* (NTS) is prevalent in Nigeria but its costs have not been evaluated.

Objectives: The aim of this work was to determine the economic and social costs and consequences of NTS in human and poultry in Nigeria, using the year 2020 as a reference point.

Materials and Methods: Background data on prevalence of NTS in Nigeria were obtained from previous works. Key informant, experienced stakeholders and value chain actors in the poultry industry, and medical and veterinary professionals were interviewed using the snowballing sampling. All experts' opinions were triangulated with field surveys, literature search and official statistics. Additional data briefs on humans and poultry, industry, populations, economics and NTS were collected using Google Form. The semi-automated Microsoft Excel® costing tool developed under the FAO's Africa Sustainable Livestock 2050 was used for all calculations.

Results: Using the year 2020 reference point, the overall economic losses associated with NTS was US$ 930,887,379, with the losses in humans (social costs) and animals (poultry sector) being 50.9% (US$ 473,982,068) and 49.1% (US$ 456,905,311) respectively. Approximately 325,731 human cases and 1,043 human deaths, at a disability-adjusted life year (DALYs) of 37,321 occurred. The losses in poultry included the direct value of animal loss, US$ 224,236,769, loss from salvage slaughter and culling, US$ 220,386,556, and value of foregone production, US$ 12,281,987.

Discussion and Conclusion: The losses were significant as a proportion of the national GDP. Findings highlighted the underestimated burden of NTS in Nigeria, especially in the human population. This should stimulate discussions on the effort at control and eradication of poultry salmonellosis, to reduce the burden of NTS in humans in Nigeria. This study bridges the existing knowledge gaps on salmonellosis in Nigeria and provides empiricism to inform policy on bacteria zoonosis reduction.

FRIDAY, 14h00

Communal farmer's knowledge, attitudes and perceptions of foot-and-mouth disease (FMD) in the FMD control zone of South Africa

Kibambe Daddy[1], Eric Etter[1,2], Petronella Chaminuka[3], Alexis Delabouglise[4], & Geoffrey Fosgate[1]

[1]Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Ondersterpoort South Africa - daddykibambe@yahoo.fr
[2]Animal health Territories Risks Ecosystems ASTRE, CIRAD, CRVC- Centre for Research and surveillance on Vector-borne diseases in the Caribbean Domaine Duclos-Prise d'Eau, 97170-Petit Bourg, Guadeloupe, France
[3]Economic analysis Agricultural Research Council ARC, South Africa
[4]Animal health Territories Risks Ecosystems ASTRE, CIRAD - Campus international de Baillarguet Montpellier, France

Background: Cattle in the FMD protection zone are not simply means of social and cultural relations among farmers, but they are also marketable commodities that can play a critical role in poverty reduction. However, farmers in this zone are typically smallholder, communal farmers who do not have access to lucrative markets within the FMD-free zone.

Methods: A cross-sectional study was performed to assess the level of knowledge, attitudes, and perceptions of FMD among small-scale, communal cattle producers using a structured questionnaire and a two-stage interview process. A total of 44 diptanks of which 12 were randomly selected in Vhembe and Mopane districts in Limpopo Province and 32 in the Bushbuckridge and Ehlanzeni districts in Mpumalanga Province.

Results: A total of 630 interviews were conducted at dip-tanks and 310 at homesteads. Sixty-nine percent of interviewed farmers were from Mpumalanga. Most (80%) interviewed farmers were male and the majority

(65%) were 60 years of age or older. Sixty-eight percent of interviewed farmers were involved in livestock farming as the main activity and 39% did not have a formal education. Sixty-six percent of interviewed farmers knew the name of FMD in the local language and 46% reported that buffalo was associated with the disease. Respondents described the clinical signs of FMD in their animals as including lameness (38%), excessive salivation (38%), weight loss (8%), and death of calves (1%). According to interviewed farmers, co-grazing with infected cattle (27%), contaminated feed (21%) and contact with buffalo (15%) were among the main causes of FMD spread. Sixty-seven percent of farmers believed that the injection of antibiotics such as oxytetracycline is an effective treatment for FMD in cattle. Also, most farmers (52%) believed that FMD can be prevented though vaccination and 80% percent of farmers strongly agreed that the currently used FMD vaccine is effective in preventing outbreaks in cattle.

Conclusion: Collecting information from farmers can help identify practices at the local farm/household level that potentially cause FMD spread and is an important step towards FMD control.

FRIDAY, 14h20

THEME: ONE WELFARE

An exploration of knowledge and attitudes toward homeless dogs in Gaborone

O. Mokgethi [1], S.Y. Adam[2] & A.A. Ahmed [1,3]

[1]*Department of Veterinary Sciences Faculty of Animal and Veterinary Sciences, Botswana University of Agriculture and Natural Resources, Gaborone, Botswana - aabdallah@buan.ac.bw*
[2]*Animal Welfare Centre, Nyala, South Darfur, Sudan*
[3] *Biomedical Research Institute, Darfur University College, Nyala, South Darfur, Sudan*

Stray dogs are part of the scene in many cities, including Gaborone, where they gather on public streets and spaces. with limited to no direct human contact. If left free to roam, they may present a public safety problem, since they can facilitate the spread of zoonotic diseases and resort to aggressive Behaviors towards humans. If captured, their chance of rehoming into human families is low because of their low sociability towards humans. To understand the relationship people, have with stray dogs in Botswana, 160 individuals Young 93.75 % (150) and old 6.25 % (10) participated in this study. 92.5 % (148) of correspondents were university while 7.5 % (8) of correspondents were secondary school level. Provide food Over 69.4 % (111) of correspondents reported that they don't care about homeless dogs when they see them around their areas whereas 30.6 % (49) reported that they avoid meeting homeless dogs. Over 63.1 % (101) of correspondents showed their willingness to provide food to homeless dogs while 36.9 % (59) don't care about the homeless dogs. In addition, 81.3 % (130) of correspondents showed their willingness to provide shelter to homeless dogs but 18.7 % (30) did not. On the other hand, 53.7 % (86) of correspondents showed their willingness to help save the homeless dog, 38.7 % (62) may be, and 7.6 % (12) refused. 64.4 % (103) of correspondents showed that they will report when they found among their dogs, 20 % (32) chase it away and 15.6 % (25) will keep it. These results indicate that people are willing to find solutions to the stray dog issue in Botswana.

However, there is a need for extension programs that target awareness of homeless dogs to improve their knowledge of homeless dogs' welfare.

FRIDAY, 14h40

Drivers and indicators of dairy cow welfare from Midlands Province, Zimbabwe large scale dairy sector indicators

Zivanayi Matore[1], Pamela Woods[1] & Tonderai Mutibvu[1]

[1]*University of Zimbabwe, Department of Livestock Sciences and applied ecology, Harare, Zimbabwe - zetmatore@gmail.com*

Globally consumers of animal products are becoming increasingly aware of the need to consume purchase and consume animal products that are produced in an animal friendly environment. In Zimbabwe a lot of studies have been done on nutrition, breeding, physiology and healthy of farm animals but with little or no consideration of the impacts of these studies on animal welfare. For this, 728 dairy cows from all the 31 large scale dairy farms in Midlands Province, Zimbabwe and were selected for the study and indicators observed during both the dry and rainy season. Avoidance distance test results revealed that 81% of the cows were touched by the approaching stockpeople, whereas 19% could not be touched, and this was significantly associated with breed of the cow ((χ^2=115, DF=9, P<0.0005). From the study 95% of the cows examined were not lame (score1) and for those that were lame only 0.6 % (n=4) of the cows were extremely lame (score 5). 30 % of the cows of the cows observed during the rainy season were heavily soiled with manure (score 4), whereas from the dry season study 1 only 1% of the cows were heavily soiled (score 4). Cleanliness scores were significantly associated with manure accumulation in housing and handling facilities in both study 1 (χ^2=18, DF=6, P=0.006) and study 2 (χ^2=47, DF=6, P<0.001) i.e., higher cleanliness scores were recorded among cattle housed in facilities with visibly high manure accumulation. The average body condition score of observed dairy cows from both study1 and study 2 was fair (BC=3) and body condition was signficantly associated with the breed of animal in both study 1 (χ^2=22, DF=12, P=0.039), and study 2(χ^2=38, DF=12, P<0.005). Exotic breeds like the Holstein generally faired low when compared to cross breeds locally adapted breeds like the Aryshire. of feeding troughs (χ2=153, =P=4, P<0.001) and adequacy of shading facilities (χ^2=24, P=2 , P<001). Prevalence of cows with teat lesions and hair loss patches was slightly high, being 11 % (n=79) and 8% (n=58) in observed cows.

FRIDAY, 15h00

Animal Welfare Challenges in Africa: A focus on Animals Used in Research in Nigeria

Dauda Bwala[1], Clement Meseko[1], Ruben Ocholi[1] & Maryam Muhammad[1]

[1]*National Veterinary Research Institute, Vom- Nigeria – dgbwala@yahoo.com*

Domestic livestock/wild animals offer ample investment opportunities and growth for the economy, guarantees food security, and provides sustainable employment [1, 2. 3. 5]. In addition, animals are commonly used for scientific purposes/research in most parts of the world, including Africa. This calls for some obligation and commitment to cater for the welfare of these animals which according to the American Veterinary Medical Association, includes proper housing, nutrition, disease prevention and treatment, responsible care, humane handling and, when necessary, humane euthanasia [2]. However, the humane care/welfare of animals used for scientific purposes in Africa and the Middle East is generally poor, and more often inadequately regulated [4]. This is due largely to number of issues including the lack of standards/regulations, poor enforcement of laws; and lack of appropriate education and training of relevant stakeholders [4]. Despite these challenges, significant progress has been made in some African countries (North African region, Kenya, and South Africa) in establishing standards and policies for animal care and use, while in other education and training are being pursued and implemented. In the West African sub-region, there is the general perception until recently, that animals are for humans to use or as objects to serve human selfish interest alone, and therefore, relatively few ethical limits to animal use exists [4].

Although Nigerian legislation contains several provisions for the protection of animal rights, such as: the Endangered Species (Control of International Trade and Traffic) Act; the Animal Diseases (Control) Act;

Criminal Code Act, etc., they are poorly implemented. There is a general lack of political will to implement and enforce this provision. In addition, persisting mind-set within the society which did not view laboratory animals as being sentient, capable of pleasures and suffering is largely being propelled by lack of proper training, religious backgrounds, poverty and poor resources for research. Some scientists question why they should spend significant funds on animals which can be easily sacrificed when humans are starving or battling with poverty.

This article will provide an overview of the governance and challenges of the care and use of animals for scientific purposes in Nigeria.

1. M. Herrero, D. Grace, J. Njuki, N. Johnson, D. Enahoro, S. Silvestri, and M.C. Rufino. "The roles of livestock in developing countries". *Animal*, 7(Suppl 1), 2013: 3-18.

2. G.E. Ifenkwe. "Animal Rights and Welfare Advocacy for Enhanced Food Security in Nigeria". *Journal of Agriculture and Social Research*, 10(2), 2010: 113-121.
3. J.J. McDermott, S.J. Staal, H.A. Freeman, M. Herrero, and J.A. Van de Steeg. "Sustaining intensification of smallholder livestock systems in the tropics". *Livestock Science*, 130 (1-3), 2010: 95-109.
4. B.J. Mohr, F.A. Fakoya, J. Hau, O. Souilem, and L. Anestidou. "The Governance of Animal Care and Use for Scientific Purposes in Africa and the Middle East". *ILAR Journal*, 57(3), 2016: 333–346.
5. OECD/FAO "Agriculture in Sub-Saharan Africa: Prospects and challenges for the next decade". In: OECD-FAO Agricultural Outlook 2016-2025. Paris, France: OECD Publishing, 2016: 59-95.

FRIDAY, 15h20

- - END ORAL PRESENTATIONS - -

Poster Presentations

in order of appearance as on the programme

POSTER SESSION 1 – WEDNESDAY 23 AUGUST 2023, 12h20

THEME: INFECTIOUS DISEASES

Modelling African Horse Sickness emergence and transmission in the South African control zone using a deterministic metapopulation approach

Joanna N. de Klerk[1], Erin E. Gorsich[1], John D. Grewer[2], Benjamin D. Atkins[1], Warren S.D. Tennant[1], Karien Labuschagne[3] & Michael J. Tildesley[1]

[1]*The Zeeman Institute for Systems Biology and Infectious Disease Epidemiology Research, School of Life Sciences and Mathematics Institute, University of Warwick, Coventry CV4 7AL, UK -* jo.de-klerk@warwick.ac.uk
[2]*South African Equine Health and Protocols NPC, Baker Square, Paardevlei, Cape Town, 7110, South Africa*
[3]*Epidemiology, Parasites and Vectors, Agricultural Research Council, Onderstepoort Veterinary Research, Onderstepoort, 0110, South Africa*

African horse sickness is a devastating orbiviral disease which has been recorded across Africa, Europe, the Far and Middle East and South-East Asia. It is transmitted by *Culicoides* Latreille midges which feed on susceptible equine populations, among other livestock. In South Africa, the disease is endemic and therefore the safe exportation of horses to non-endemic countries is frequently prohibited. However, a unique solution has been developed in the Western Cape. A "control area" has been implemented where increased surveillance and control measures are undertaken. This area therefore provides an area of decreased risk for exportation purposes.

A previously published deterministic model was further developed using a metapopulation approach to explore how outbreak dynamics might spatiotemporally vary across the study area if an infected horse were to be accidentally imported. The ordinary differential equation model presented in this research was the first to include a vaccinated population which was age-stratified to capture differences in vaccination protection.

The warmer months experienced longer lasting outbreaks which were slow to develop to the peak, however overall had a larger total outbreak size and more horses infected at the peak than colder months. R_0 appeared to be a poor predictor of outbreak dynamics, agreeing with previously published data that alternative measurements are better in heterogenous populations with spatial relationships.

A univariate sensitivity analysis exploring the control measures indicated that vector control and vaccination may be impactful control measures. Also, the model highlighted that a shorter vaccination window of July to September may help mitigate vaccine-associated outbreaks.

Biosecurity issues related to ASF and FMD in the Ekurhuleni Local Municipality in Gauteng, South Africa

Rorisang Malatji[1] & G.T. Fosgate[2]

[1]Department of Production Animal studies, Faculty of Veterinary Science, University of Pretoria, Onderstepoort, 0110, South Africa - :thebyanerorisang@gmail.com
[2]Onderstepoort Veterinary Research, Agricultural Research Counsel, Onderstepoort, 0110, South Africa

For both the welfare of the animals and their economic output, it is essential to keep pigs healthy by preventing infectious diseases. When it comes to zoonotic pathogens, prevention is also crucial for food safety and public health. The prevention of pathogens entering and spreading within a group of animals is all a part of biosecurity. As of late, with the rise and reappearance of hard to-control diseases, for example, African swine fever or Swine dysentery, the view of the basic significance of pig wellbeing and its relationship with biosecurity has expanded as of late. Some animal pathogens, including ASF and FMD, have the potential to cause an epidemic. The risk of new pathogens entering farms and spreading within farms is minimized when biosecurity measures are implemented throughout the production chain. However, many pig farms still face difficulties in implementing and maintaining sustainable biosecurity programs. The significance of the proposed study is to improve the control of African swine fever and foot–and-mouth disease by identifying the drivers of the outbreaks of these diseases. Biosecurity plays a vital role in the prevention of the spread of diseases. Ensuring that backyard and emerging farmers adhere to strict biosecurity measures will assist in lowering or preventing the spread of ASF and FMD. This can be achieved by assessing the knowledge of the farmers and management practices occurring in their facilities. A questionnaire is developed to target biosecurity issues and assess the knowledge of each farmer related to ASF and FMD epidemiology. The total of 115 pig farmers will participate in the study, informed consent will be obtained prior to enrolling participants into the study for questionnaire administration (via in-person interview). The questionnaire will be pilot tested within pig farmers in a different location of the Ekurhuleni municipality prior to the administration in this study. The questionnaire will include a combination of open and closed questions. Farmers will be asked about pig movement on their facility and the disinfection for vehicles, equipment's, and boots.

Knowledge, attitude, practice (KAP) and the risk of exposure of abattoir workers to Mycobacterium spp. in Gauteng Province, South Africa

Vuyokazi Mareledwane[1,2], Tiny M. Hlokwe[3], Yusuf B. Ngoshe[1] Abiodun A. Adesiyun[1,4]
[1]Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Private Bag X04, Onderstepoort, 0110, South Africa - MareledwaneV@arc.agric.za

[2]*Vaccines and Diagnostic and Development Programme, Agricultural Research Council-Onderstepoort Veterinary Research, Private Bag X05, Onderstepoort, 0110, South Africa*
[3]*Diagnostic Service Programme, Agricultural Research Council-Onderstepoort Veterinary Research, Private Bag X05, Onderstepoort, 0110, South Africa*
[4]*School of Veterinary Medicine, Faculty of Medical Sciences, The University of the West Indies, St. Augustine, Trinidad and Tobago*

Introduction: Zoonotic tuberculosis (TB), mainly caused by *Mycobacterium bovis*, a member of the *Mycobacterium tuberculosis* complex bacteria, remains a global public health hazard. Information based on knowledge, practices, and risk factors is crucial among high-risk occupations such as veterinarians and abattoir workers.

Methodology: A close-ended questionnaire was used to interview 103 abattoir workers during sampling visitations, and data relating to their knowledge, attitude, practices and potential risks of exposure to *Mycobacteria* were collected. The study was conducted at six red meat abattoirs in Gauteng province, South Africa.

Results: More males (87/103: 84.47%) participated in the study, with the majority (83/103: 80.58%) working in the slaughter and meat processing sections of the abattoirs. A high proportion (88.35%) of the participants were found to be knowledgeable about zoonotic TB, with the respondents' overall knowledge score of 42% (95% Confidence Interval: 37.48- 46.42, $p<0.001$). The study showed that 45% (95% CI: 35.28 – 56.02) of the participants were aware they could contract TB from animals and 44.6% (95% CI: 34.22 – 54.91) knew that diseased humans could transmit the disease to animals. As a result, personnel protective equipment (PPE), particularly clothing, was worn when handling carcasses at abattoirs (95.15%; CI: 90.92–99.37). Only a few of the respondents consumed undercooked meat (10.68%; CI: 4.61-16.75), while a concerning proportion consumed raw milk (25.24%; CI: 16.71 –33.77).

Conclusion: The study revealed a high proportion of good practices by workers regarding donning PPE when handling carcasses, hence minimizing the potential for transmission of zoonotic diseases such as TB. Raw milk consumption remains a major risk factor for zoonotic TB transmission, hence awareness programmes regarding control and prevention are crucial.

Molecular characterization of resistant *Brucella* spp isolated from livestock in the Eastern Cape, South Africa

Fonkui Y. Thierry[1]; Botopela S. Euphodia[1]; Ezekiel Green[1]

[1]*Department of Biotechnology and Food Technology, Faculty of Science, University of Johannesburg, Doornfontein Campus, Johannesburg, 2028, South Africa - youmbifonkui@yahoo.com*

Brucellosis is one of the most widespread zoonoses transmitted by animals associated with serious public health consequences and significant economic implications. The incidence rate of human brucellosis in South Africa continue to rise amid a lack of controlled measures and the scarcity of vaccines. The aim of this study was to establish the antibiotic resistance pattern of *Brucella* isolates and their virulence associated genes based on their phenotype and genotype using molecular tools. Disk diffusion assay and polymerase chain reaction (PCR) were used to identify the resistance and virulence profiles of *Brucella* species from Eastern Cape, South Africa. One hundred and six (106) *Brucella* isolates were tested against tetracycline (30 µg), penicillin G (10 µg), cephalothin (30 µg), erythromycin (15 µg), doxycycline (30 µg), trimethoprim/ sulfamethoxazole (25 µg) and streptomycin (10 µg) using disk diffusion. The amplicon of *Tet(A)*, *tet(B)*, *sul1*, *sul2*, *BlaTem*, *dfrA1*, *strA-strB*, and *aadA1* were screened for using PCR. Data obtained revealed that 43% (46/106) of *Brucella* isolates under investigation were resistant to antibiotics normally used against brucellosis with cow's isolates highly resistant compared to sheep and goat's counterparts. Most MAR isolates and those with a MAR index greater

than 0.2 were found in cows (58.1%), sheep (25.8%), and goats (16.1%), respectively. Resistance was observed against streptomycin (87%), penicillin G (52%), cephalothin (50%), trimethoprim/ sulfamethoxazole (26%) and tetracycline (23%). No *tet(A)*, *tet(B)*, or *strA-strB* genes were recorded form the isolates studied. However, 8 out of 10 (80%), 7 out of 10 (70%), 19 out of 29 (67%), 18 out of 28 (62%) and 3 out of 7 (43%) isolates contained *dfrA1*, *sul1*, *BlaTem*, *aadA1* and *sul2* gene respectively. In isolates were *tetA* and *tetB* gene were absent, *Brucella* showed no characteristics resistance towards tetracycline antibiotic. The presence of virulence genes in *Brucella* isolates rarely investigated, further complicates therapeutic interventions. These findings highlight the emergence of antibiotic resistance as a significant public health concern. However, it is reassuring to note that all strains, including *B. melitensis,* remained susceptible to aminoglycosides, tetracyclines, and rifampicin. These findings could provide insight and guidance into improved therapeutic protocols.

Prevalence and risk assessment of *Coxiella burnetii* in sheep and goats of North-West and Free State province

Katleho Nthabiseng Mosikidi[1], Nomakorinte Gcebe[1] & Nthabiseng MB Mphuthi[2]

[1]Agricultural Research Council - Bacteriology and Zoonotic Diseases Diagnostic Laboratory, Onderstepoort Veterinary Research Institute, Private Bag X 05, Onderstepoort 0110, South Africa - knmosikidi14@gmail.com
[2]Department of Animal Health, Faculty of Natural and Agricultural Science, North-West University, Mafikeng Campus, Private Bag X 2046, 2735

Query fever (Q fever) is a zoonotic widespread disease caused by the bacterium *Coxiella burnetii* (*C. burnetii*) which infects a broad range of animals and arthropods. Whilst Q fever can cause abortions and still birth in cattle, sheep, and goats, it is a neglected zoonoses in South Africa, despite reports of its occurrence, prevalence, economic and public health impact in the South Africa and other parts of the worlds. The aim of this study was to investigate the prevalence and conduct risk assessment of *C. burnetii* in communal and commercial domestic ruminants (sheep and goat) in the North-West Province (NW) and the presented abortion cases from the Free State farms (FS).

A cross-sectional study was conducted to determine the seroprevalence of Q fever where 421 serum samples were collected from sheep (155) and goats (266) in the NW province and tested using the enzyme-linked-immunosorbent assay (ELISA). A total of 126 samples of milk, vaginal swabs, and sheath scrapping were collected from the same animals and 11 tissues samples of unresolved abortion cases from the FS province. The samples were subjected to a polymerase chain reaction (PCR) for the detection of *C. burnetii* targeting a 142bp fragment of IS1111. To determine the risk factors associated with this disease a questionnaire was administered to farmers/shepherds. Seropositivity of *C. burnetii* in the North-West province for goats was 30.83% (82/266) (95%CI: 25.58-36.62) and 39.35% (61/155) (95%CI: 32.01-47.21) for sheep. The positive pathogen detection rate was 61.11% (77/126) in sheep 53.45% (31/58) (95%CI: 40.80-69.79) and goats 67.64% (46/68) (95%CI: 55.85-77.56) in the NW province. The molecular occurrence of *C. burnetii* in the FS province was 54.54% (6/11). There was no significant association of any of the risk factors investigated with serological and molecular positivity.

The study determined the high prevalence of *C. burnetii* in NW and identified the bacterium as the cause of some of the previously unresolved abortion cases in small ruminants from FS province. More follow up studies are required to identify genotypes of *C.burnetii* circulating in both provinces.

Molecular epidemiology of *Brucella* spp. among cattle presented for slaughter at selected abattoirs in Gauteng

Simangaliso Petros Mkhatshwa[1], Nenene D Qekwana[2] & James Wabwire Oguttu[1]

[1]*Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, University of South Africa - crystalvetmiracle@gmail.com*
[2]*Department of Paraclinical Sciences, Faculty of Veterinary Sciences, University of Pretoria, South Africa*

Background: Although brucellosis is endemic in South Africa, there is a dearth of studies that investigate the molecular epidemiology of the disease among cattle presented for slaughter at abattoirs in Gauteng province. This is a presentation of the protocol for study of the molecular epidemiology of *Brucella* spp. among cattle presented for slaughter at the selected abattoirs in Gauteng.

Objectives: The study aims to investigate the molecular epidemiology of *Brucella* spp. in cattle during routine slaughterhouse operations at selected abattoirs in Gauteng.

Methods: A cross-sectional study design will be adopted to investigate *Brucella* spp. in cattle (n=218) destined for slaughter. A checklist will be used to gather demographic information of animals. Pooled tissue samples comprising of lymph nodes (retropharyngeal, parotid, submandibular, and mesenteric), spleen and liver will be systematically collected from the identified animals over 4 days from each abattoir. These tissues will be subjected to DNA extraction and analysed to identify the *Brucella* species circulating among cattle presented for slaughter, using 16S-23S ribosomal interspacer region (ITS) and Bruce-ladder PCR. STATA version 17 will be used to analyze the data. The study will be conducted from May 2023 to December 2023.

Expected outcomes: The current study is expected to identify all known and rare *Brucella* spp. including vaccine strains that could be circulating in cattle presented for slaughter at selected abattoirs in Gauteng.

Conclusion: Results generated in the study will contribute to better understanding of the epidemiology of bovine brucellosis and could be used to design strategies to control brucellosis in the study area.

Genetic and genomic characterization of *Coxiella burnetii* isolates from South African livestock

Vhahangwele Sadiki[1,2], Nomakorinte Gcebe[2] & Rian Pierneef[3]

[1]*Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Private Bag X04, Onderstepoort, Pretoria 0110, South Africa - Vhahangwele_sadiki@yahoo.com*
[2]*Agricultural Research Council–Bacteriology and Zoonotic Diseases Diagnostic Laboratory, Onderstepoort Veterinary Research, Private Bag X 05, Onderstepoort, Pretoria 0110, South Africa*
[3]*Department of Biochemistry, Genetics and Microbiology, Faculty of Natural and Agricultural Sciences, University of Pretoria, South Africa*

Coxiella burnetii, the causative agent of Q fever, is a neglected pathogen in South Africa. Previous studies are based mainly in serological detection of the bacterium. A seroprevalence of 33.96% have been reported in the North-West province in sheep and goats and 7.25% in another study in cattle, sheep and pigs. In Gauteng province, seroprevalence of 6.90% was reported in cattle, sheep and pigs while in Limpopo it was 24.28% in cattle. Positive results have been obtained when conducting diagnostic testing from abortion cases samples at the Agricultural research council. However, information about circulating strains as well as the genomic characteristics of South African strains is limited. To date, only one study by Mangena et al. (2021) has focused on characterizing *Coxiella* genotypes in South Africa, revealing two new genotypes. Currently, there is no information available regarding the genomic features of South African strains of *C. burnetii* including the antimicrobial genetic profiles, virulence gene profiles and mobile genetic elements. This retrospective study

aims to investigate the genetic and genomic diversity of *C. burnetii* isolates from livestock (cattle, sheep and goats from previous studies) in South Africa (North-West, Limpopo and Gauteng Provinces). A total of 250 *Coxiella*-positive samples (tissue, vaginal swabs, and sheath scrapings) will be used in this study. In addition, we will also conduct opportunistic sampling by including samples submitted for diagnostic testing of *C. burnetii* by the Agricultural Research Council. So far, we have identified *C. burnetii* DNA in a total of 88 samples from cattle, 31 samples from sheep, and 46 samples from goats, all of which came from healthy animals. Through diagnostic testing, we have found *C. burnetii* DNA in 8 samples from goats, 6 samples from sheep, and 4 samples from cattle that were associated with cases of abortion. Additionally, we have identified *C. burnetii* DNA in 6 samples from goats and sheep that were involved in cases of abortion in the Free State.

Differential antibody staining of Nigerian dog rabies viruses using a southern African monoclonal antibody panel

Mmantshuruge Miyen[1], Debrah Mohale[1], Chika I Nwosuh[2], Ishaya SiniTekki[2] & Claude T Sabeta[1,3]

[1]*Agricultural Research Council-Onderstepoort Veterinary Institute, WOAH Rabies Reference Laboratory, Onderstepoort 0110, South Africa -miyenmj@arc.agric.za*
[2]*National Veterinary Research Institute (NVRI), VOM, Plateau State, 930103, Nigeria*
[3]*University of Pretoria, Faculty of Veterinary Science, Department of Veterinary Tropical Diseases, Onderstepoort 0110, South Africa*

Rabies is a neglected and fatal zoonotic disease with a significant veterinary and public health threat for 95% of the global population and is endemic in Africa and Asia. An estimated 59 000 humans succumb to the disease annually. However, the lack of implementation of reliable rabies diagnostic techniques negatively impacts disease surveillance resulting in a gross underestimation of disease burden.

In this study, dog specimens (*n*=30) received for routine rabies diagnosis at NVRI (Nigeria) were subjected to the gold standard direct fluorescent antibody test. Thereafter, mouse-passaged rabies viruses were grown on neuroblastoma cells and antigenically typed against an anti-Nucleoprotein monoclonal antibody (Mab) panel. Subsequently, viral RNAs were extracted from the brain-infected tissues, reverse-transcribed and the complete nucleoprotein gene amplified and sequenced with the Sanger method and translated in ClustalW. All the dog samples were lyssavirus positive. Staining of the lyssavirus isolates passaged in cell culture with the Mab panel demonstrated 2 main staining patterns and 4 sub-patterns. The Mab panel could distinguish Nigerian dog rabies viruses from the South African canid and mongoose rabies biotypes, and the three rabies-related viruses. In particular, Nigerian dog rabies viruses were exclusively stained with Mabs M1335, M1386 and M1400 (but variably with M1407 and M1412). The differential monoclonal antibody staining could be explained by the variation in six amino acid residues of the South African and Nigerian dog rabies viruses.

In conclusion, the rabies viruses antigenically typed following passage in neuroblastoma cells all had the same staining pattern, consistent with nucleotide sequencing results. There however appears to be limited genetic diversity in the Nigerian isolates. Nonetheless, the rabies viruses circulating in Nigeria differ significantly from the South African rabies viruses, including the unusual Mokola, Lagos bat and Duvenhage lyssaviruses. Due to the high background staining observed with mouse brain-passaged materials, use of original brain tissue is highly recommended for variant typing, thus eliminating the need to passage viruses in cell culture. Overall, Mab panels are useful for rapid typing of lyssaviruses, have high throughput and are appropriate for identification of emerging lyssavirus variants in Africa, and should form part of routine rabies surveillance.

Molecular characterization of lyssavirus rabies from domestic and African wild cats confirmed between 2010 2020 and newly identified *Lyssavirus mokola* (MOKV)

Ernest Ngoepe[1], Kefentse Tsie[1], Baby Phahladira[1], Nelisiwe Khumalo[2] & Claude Sabeta[1,3]

[1]WOAH Rabies Reference Laboratory, Agricultural Research Council (Onderstepoort Veterinary Research), Onderstepoort, 0110, Pretoria, South Africa - ngoepee@arc.agric.za
[2]Central Veterinary Laboratory, Corner Althea Road and Central, Manzini, Eswatini
[3]University of Pretoria, Department of Veterinary Tropical Diseases, Private Bag 04, Onderstepoort, 0110, Pretoria, South Africa

Rabies is one of the most significant public and veterinary health problem, causing approximately 59 000 human deaths annually in the developing countries of Asia and Africa (1). The aetiologic agent, viral species of the *Lyssavirus* genus, is highly neurotropic and has a wide host range including terrestrial mammals and several Chiropteran species (3). The *Lyssavirus mokola* (MOKV) was first isolated in the late 1960s from organ pools of shrews (*Crocidura flavescens manni*) in the Mokola forest in Nigeria. To date, there is at least 30 confirmed MOKV isolates, and all have been identified in Africa (2). There is a limited knowledge about the epidemiology of MOKV and the host species still unknown. We report on a retrospective molecular characterization of rabies cases originating from domestic cat and African wildcat species and the identification of a new MOKV isolate from the Kingdom of Eswatini. A partial region of the nucleoprotein gene of the lyssavirus genome was analyzed using PCR generated nucleotide sequences. Apart from a MOKV isolate obtained from a domestic cat from the Kingdom of Eswatini, the majority of brain-infected materials included in the study were identified as *Lyssavirus rabies* (RABV) (98%). Further, the nucleotide sequences divergence between the recently identified MOKV isolate, and the historical isolates ranged from 6.8% and 8.3%. This study further highlights the association between the potential MOKV host species and the domestic cats. Therefore, continuous vaccination of domestic cats against rabies is crucial even after the elimination of dog-mediated rabies as the spill-over related to a sylvatic rabies cycle in South Africa is likely to occur.

REFERENCES

1. Hampson, K., Coudeville, L., Lembo, T., Sambo, M., Kieffer, A., Attlan, M., Barrat, J., Blanton, J. D., Briggs, D. J., Cleaveland, S., et al. (2015). Estimating the global burden of endemic canine rabies. PLOS Neglected Tropical Disease, 9: e0003709.
2. Kemp, G.E., Causey, O.R., Moore, D.L., Odelola, A., Fabiyi, A. (1972). Mokola virus: Further studies on IbAn 27377, a new rabies-related etiological agent of zoonosis in Nigeria. American Journal of Tropical Medicine and Hygiene, 21:356-9.
3. Walker, P.J., Siddell, S.G., Lefkowitz, E.J., Mushegian, A.R., Adriaenssens, E.M., Alfenas-Zerbini, P., Dempsey, D.M., Dutilh, B.E., García, M.L., Curtis Hendrickson, R., Junglen, S. (2022). Recent changes to virus taxonomy ratified by the International Committee on Taxonomy of Viruses (2022). Archives of virology, 167(11): 2429-2440.

Contamination of beef and beef products by *Listeria* spp. and molecular characterization of *L. monocytogenes* in Mpumalanga, South Africa

Khomotso Moabelo[1], Nomakorinte Gcebe[2], James Gana[1,3], Yusuf B. Ngoshe[4] & Abiodun A. Adesiyun[1,5]

[1]Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Private Bag X04, Onderstepoort, Pretoria 0110, South Africa - khomotsocmoabelo@gmail.com
[2]Bacteriology Department, Serology section, Onderstepoort Veterinary Research, Agricultural Research Council, Pretoria 0110, South Africa
[3]Department of Agricultural Education, Federal College of Education, Kontagora, Niger State, Nigeria
[4]Department of Production Animal Studies, Epidemiology Section, University of Pretoria, Private Bag X04, Onderstepoort, Pretoria 0110, South Africa

[5]*Department of Paraclinical Sciences, School of Veterinary Medicine, The University of the West Indies, St. Augustine, Trinidad and Tobago*

This study determined the prevalence, risk factors, and molecular characteristics of *Listeria* species detected in beef and beef products sampled in Mpumalanga province, South Africa. Four hundred beef and beef products were collected from 30 retail outlets in three districts (Bronkhorstspruit, Emalahleni, and Middelburg) within the province. Standard bacteriological and polymerase chain reaction (PCR) assays were used in the study. The overall prevalence of *L. monocytogenes* and other *Listeria* spp. in the samples was 8.3% (33/400) and 30% (120/400) ($p < 0.05$), respectively. For the five variables investigated, statistically significant effects were evident only for the region ($p < 0.001$) and type of product ($p < 0.0001$) for *L. monocytogenes*, the type of outlet ($p = 0.011$) and the type of product ($p < 0.0001$) for *Listeria* spp. Of the 20 types of beef and beef products tested, 15 (75%) and 17 (85%) were contaminated by *L. monocytogenes* and *Listeria* spp., respectively ($p = 0.429$). Among the four categories of products tested, the prevalence of *L. monocytogenes* was 7.3% (8/109), 10.6% (11/104), 7.5% (8/106), and 7.4% (6/81) for raw beef, ready-to-eat (RTE) products, milled beef, and offal & organs, respectively ($p > 0.799$). Among the 33 *L. monocytogenes* isolates, PCR genoserogroup IIa (42.4%, 1/2a-3a) was most frequently detected. All (100%) of the isolates carried one or more of the eight virulence-associated genes assessed, with genes inlC and inlJ detected in all the isolates. The overall prevalence of *L. monocytogenes* (8.3%) and the high frequency of virulent serogroups of *L. monocytogenes* commonly associated with human listeriosis pose a food safety risk to consumers of beef and beef-based products contaminated by *L. monocytogenes*.

Carp Edema Disease: An emerging global concern

Ekemini Okon[1], Reuben Okocha[2], Mashood Arinola[3] &Nelson Matekwe[4]

[1]*Faculty of Bioscience Engineering, Ghent University, Ghent, Belgium - okon.ekeminimoses@gmail.com*
[2]*Department of Agriculture, College of Agricultural Sciences, Landmark University, Omu-Aran, Kwara State, Nigeria*
[3]*Department of Zoology, Poznan University of Life Sciences, Poland*
[4]*Department of Agriculture Environmental Affairs, Rural Development and Land Reform, Veterinary Services, Northern Cape Province, South Africa*

The significance of global aquaculture output increases with the rising demand to feed the human population. Two of the most significant freshwater fish in global aquaculture are carp and koi. Regrettably, various diseases, such as viral infections, impact their production. In recent years, carp edema disease (CED), caused by the carp edema virus (CEV), has emerged as one of the fatal viral infections. Addressing this health challenge is vital and requires understanding the disease dynamics through a research database. Therefore, this study employed a mixed approach, integrating findings from field surveys, laboratory analyses, and data syntheses to assess the current understanding of CED, focusing on epidemiological and impact assessment. The United States of America, Germany, Japan, China, Poland, and the Czech Republic played major roles in CED research, contributing about 50% of the studies. However, limited information is available on the disease prevalence in Africa, which makes it difficult to assess the risk of the disease to the African fish population. Major CED risk factors were water temperature, seasonal variations, immune suppression, fish age, and fish pathogen levels. Most disease cases resulted in high mortalities at different fish life stages, indicating high virulence and severity of CEV infection. The virus pathogenesis involved a complex interplay between viral replication, immune response, and environmental factors, with water temperature being a crucial determinant for disease development. Fish without clinical signs of the disease could harbour a relatively high virus load, indicating that trade relations between countries can help spread the virus, with extreme difficulty in eradicating the pathogen. There were consistencies in disease prevention and control effectiveness, such as environmental modifications and vaccinations. Specifically, vaccination strategies have shown promise in relieving the severity and prevalence of CED, although further research is needed to optimise vaccine formulation and delivery methods. Furthermore, there is limited information on the relationship between the genetic composition of

the fish species and CED. This information is essential in understanding the basis of their susceptibility and developing effective disease prevention, control, and management.

Morphological identification of ticks and molecular detection of tick-borne pathogens from small ruminants in Matlwang, Potchefstroom

Mpho Tawana

North-West University (Potchefstroom campus) - mphotawana@yahoo.com

Ticks are the second largest arthropods following mosquitoes and the most important external parasites of small ruminants in South Africa. Ticks pose a serious thread towards animal production and socio-economic through direct impact of sucking blood and transmission of pathogens. The objective of the study was to determine the occurrence of ticks in Matlwang Village, Potchefstroom, South Africa. Using morphological and molecular techniques. A calculated total of 288 animals were examined for ticks infestation and 250/288 animals were found to be infested with ticks belonging to the family *Ixodidae*. The 1893 ticks collected from goats 83.33% (125/150) and sheep 90.52% (125/138). Of the 1893 ticks 99.26% (1879/1893) showed morphologically identification of *Rhipicephalus evertsi evertsi* and the remaining 0.74% (14/1893) nymphs were unknown. None of the blood samples amplified for any desired tick-borne pathogens. The level of infestation was highest in Kgapamadi (36.77%) and lowest in Radimo (28.10%) *Rhipicephalus evertsi evertsi* is a widely distributed tick in South Africa and currently at Matlwang village is the only tick spp. that can be found in sheep and goats. This tick is capable of causing severe animal production and public health concern. Therefore, it is critical to adjust the current tick prevention and tick management strategies to mitigate this high occurrence of *Rhipicephalus evertsi evertsi* in order to improve the health and production of small ruminants in Matlwang Village, Potchefstroom, South Africa.

Comparison of the immunogenicity of two locally formulated inactivated LEP flurry adjuvanted rabies vaccines and a standard modified live LEP flurry rabies vaccine

Dauda Bwala[2], Ugokwe I. N.[1], Asala O.F.[2], Fagbohun O.A[3], Tekki, I.[2], Ogunmolawa, O.[2], Darang, A.[2], James, D[2]

[1]*Pan African University of Life and Earth sciences Institute (PAULESI), University of Ibadan. Nigeria*
[2]*Viral Vaccine Production Department, National Veterinary Research Institute, Vom. Plateau state, Nigeria - dgbwala@yahoo.com*
[3]*Department of Veterinary Microbiology, Faculty of Veterinary Medicine, University of Ibadan, Ibadan, Oyo State, Nigeria.*

Modified Live Rabies vaccines (MLV) of Low Egg Passage (LEP) Flury origin is employed in dog vaccination in Nigeria for the control of rabies [1]. Although immunogenic, the limitation associated with the use of MLV [1, 2, 3] necessitated this study where the immunogenicity of two locally formulated inactivated-adjuvanted LEP flury rabies vaccines was compared with that of a standard MLV LEP flury.

The LEP flury rabies vaccine were propagated in embryonated chicken eggs, inactivated with 0.1M binary ethylenimine (BEI) [4] and adjuvanted using Montanide ISA 201 and Ictyolane 17. During the experiment, 60 mice and eight puppies were randomly allocated into three test groups (Inactivated LEP flurry + Montanide adjuvanted, inactivated LEP flurry + Ictyolane adjuvanted and Standard MLV LEP rabies), and a negative non-vaccinated control group. Test groups were vaccinated with their respective vaccines and a semi quantitative mouse specific anti-rabies virus glycoprotein ELISA assay was used to determine the presence of rabies glycoprotein antibody in the sera of experimental animals' sampled post-vaccination (**AEC/02/117/22**).

Egg propagation of the LEP flury rabies yielded harvest with titer of $10^{5.25}$ while the inactivation kinetics of the harvest using 0.1M BEI at 37°C gave an inactivating half-life (t 1/2) of 24.72 hours, and complete inactivation of the virus to 0.0 FFU/ml was achieved at 48 hour. Vaccination of the experimental mice (0.1 ml/ mouse) and puppies (1 ml/ dog) using the test vaccines with an antigenic load of $10^{4.75}$ proved safe 14 DPV for puppies and 28-days post double vaccination (14 days apart) for mice. Sera antibody analysis revealed that mice vaccinated with Montanide and Ictyolane adjuvanted LEP flury vaccines has OD of 0.380±0.087 and 0.361±0.010 respectively; comparable with MLV rabies (0.389±0.009). All were above the cut-off detection point (0.242). However, the OD values for vaccinated puppies fell below the cut off values but paired t-test of the pre- and post- vaccinate sera OD values revealed a significant difference ($p<0.05$).

This study concludes that vaccination with the locally formulated inactivated rabies vaccines produces antibody response comparable to that of MLV. This presents a supplemental rabies vaccine formulation for use in dog rabies control programs in Nigeria.

1. I.S. Tekki, C. Nwosu, and P.A. Okewole. “Challenges and prospects of anti-rabies vaccines production in Nigeria”. *Journal of Vaccines,* 4(8), 2013.
2. N. Ito, T. Okamoto, M. Sasaki, S. Miyamoto, T. Takahashi, F. Izumi, M. Inukai, S. Jarusombuti, K. Okada, K. Nakagawa, and Y. Fujii. “Safety enhancement of a genetically modified live rabies vaccine strain by introducing an attenuating Leu residue at position 333 in the glycoprotein”. Vaccine, 39(28), 2021: 3777-84.
3. N.A. Maurice, P.D. Luka, M.N. Maurice, N.E. Ochefije, Z.P. Nden, P. Mshelbwala, and L. Lombin. “Rabies in a set of eight-weeks-old puppies in Nigeria: The need for review of current dog Anti-rabies vaccination schedule. *African Journal of Infectious Diseases,* 12(2), 2018: 72–77.
4. S.K. Mondal, M. Neelima, K. Reddy, A. Rao, and V.A. Srinivasan. “Validation of the inactivant Binary Ethylenimine for inactivating Rabies Virus for Veterinary Rabies Vaccine Production. *Biologicals*, 33, 2005: 85-9.

Seroprevalence of brucellosis among communal cattle in Sekhukhune District Municipality, Limpopo Province. A retrospective study

M. B. Kgwete[1,2], S. Mbizeni[1], J. W. Oguttu[1] & D. N. Qekwana[3]

[1]*Department of Agriculture and Animal Health, College of Agriculture and Environmental Science, Florida Campus, UNISA, South Africa - makgethoa@gmail.com*
[2]*Limpopo Department of Agriculture and Rural Development, South Africa*
[3]*Department of Paraclinical Sciences, Faculty of Veterinary Science, University of Pretoria, South Africa*

Bovine brucellosis occurs in most developing countries with significant economic impact due to the loss of agricultural products and the cost associated with controlling the disease. However, little is known about the burden of the disease among communal cattle in the Sekhukhune District municipality of Limpopo Province.

Methods: A cross-sectional retrospective study was conducted using results from Veterinary Laboratory, collected between 2010 and 2020. The proportion of brucellosis cases was calculated based on location, year, season, and month. Chi-square and Fisher’s exact tests were used to assess simple associations between the predictor variables and positive reactors.

Result: A total of 37080 animals were tested over the study period, of which 1.45% (538/3780) tested positive on Rose Bengal Test (RBT), 23.87% (53/222) on the Complement Fixation Test (CFT), and 44.59% (33/41) on the Serum Agglutination Test (SAT). Therefore, 60.78% (327/538) of reactors on RBT were not tested using CFT. There was a significant difference ($p^{<}.0.0001$) in the percentage of RBT-positive cattle, with Groblersdal State Veterinary Office (SVO) reporting most cases (2.71%, 493/14894. There was a significant difference ($p^{<}.0.0001$) between the seasons, with the highest number of RBT-positive cattle reported in the spring season (2.54%, 153/6035) as compared to summer (0.96%, 184/19154).

Conclusion: Bovine Brucellosis has remained constant in the Sekhukhune district Municipality over the study period. However, results suggest that the occurrence of brucellosis among cattle in the study area differs based on the season, month, and location.

Recommendation: More effort is needed to stamp out brucellosis in the study area livestock owners should be encouraged not to mix their animals with others of unknown brucellosis status and vaccination programs for heifers and adult cattle need to be stepped up.

POSTER SESSION 2 – THURSDAY 24 AUGUST 2023, 12h20

THEME: REGIONAL EDUCATION IN ANIMAL DISEASE CONTROL

Effects of supplementary diet protein on growth performance and reproductive health of Tswana goats

Mpho Tsheole[1] & Mulunda Mwanza[1]

[1]North-West University, Mafikeng Campus, Department of Animal Health, Faculty of Natural and Agricultural Science, Mafikeng Campus, Private Bag X 2046, Mmabatho, 2735, South Africa - mpho.tsheole@nwu.ac.za

The experiment was to determine the impact of protein supplementation on goat reproductive performance, health, and on blood and hormonal parameters. To achieve this objective, an experiment was conducted using 24 weaned female Tswana goats (three months of age). The experiment was completely randomized. Blocking was done according to body weight and animals were allocated into three treatment groups of eight goats per treatment and their feeding regime consisted of protein (23.51%) and energy (8.55%) per kg of the body weight. The first group was given the Maintenance protein requirement (Diet 1); the second group was given twice the Maintenance requirement (Diet 2) and the third group was fed three times the Maintenance X3 (Diet 3). Blood samples were collected, and serum metabolites and reproductive hormones were measured at the beginning of the experiment and weekly. One-way analysis of variance (ANOVA) was carried out on blood nutritional metabolites, hormonal, growth, and reproductive performance data using the General Linear Model (GLM) procedure of the Statistical Analysis System. Results obtained showed that different levels of protein supplementation had significant ($P<0.05$) effects on glucose, albumin, albuglobulin and urea levels. The level of progesterone in Diet 2 was significantly higher with a value of 13.45 ppb, while for the other weeks, no significant effects were observed from week 0 up to week 20. The use of high levels of dietary protein supplements boosted the levels of progesterone in the study. In conclusion, supplementation with three times maintenance level improved growth and reproductive performance and health and concentrations of serum metabolites and hormones, which subsequently, improved reproductive hormones (progesterone) and some blood metabolites (blood glucose, albumin total protein, and albumin) during oestrus cycle.

Despite the cost of the source of protein in the diet of animals, there is a need to educate farmers on feed formulations, and balanced feeding to animals to increase productivity. It could, therefore, be concluded that improved feeding with better management could ensure improvement in the reproductive performance of Tswana goats.

Awareness and practices of biosecurity measures in smallholder pig production in South Africa: Case of Buffalo City Metro in the Eastern Cape Province

N. Nongauza[1], S. Mthi[2], M. Yawa[3], S. Tokozwayo[3], Z. Mpisana[4] & Z Dubeni[5]

[1]Department of Rural Development and Agrarian Reform, East London - nwabisan@yahoo.com

[2]*Department of Rural Development and Agrarian Reform, P.O. Box 112, Queenstown, 5320*
[3]*Döhne Agricultural Development Institute, P. Bag X 15, Stutterheim 4930, South Africa*
[4]*Department of livestock and Pasture Science, University of Fort Hare, Private Bag x11314, Alice 5700, South Africa*
[5]*Department of Botany and Zoology, Faculty of Science, University of Fort Hare, Alice, South Africa*

Biosecurity has been highlighted as the most important preventative measure to reduce and protect the introduction of diseases to a farm and minimise spread of diseases within a herd. There is little published information about biosecurity practices on smallholder pig farmers in South Africa. The study aimed to assess awareness and practices biosecurity measures in smallholder pig production in the Buffalo City Metro, Eastern Cape Province. The data was collected by administering questionnaires to 30 randomly selected pig farmers in the study areas as from April to May 2023. Results revealed that pig farming in the study areas was predominated by men (78%), and the majority (43%) were between 41-60 years of age. More than 40% had advanced secondary education with more than 10 years farming experience, holding a land between 2-5ha with a household size ranging 4-6 members. In terms of herd structure, sows accounted a higher proportion (62.2%). Cash income was the major (42.3%) reason for farming with pigs in the study areas. More than 50% of pig farmers were not aware of biosecurity protocol to control diseases. Regular cleaning of pig houses followed by cleaning of feeding and drinking and use of foot bath were the most practiced biosecurity measures. Keeping of sick pig separately, quarantine of new pig stock, use of protective clothes and disinfecting delivery vehicles were the least observed biosecurity practices. Farmers in the study areas have low level of awareness on biosecurity measures. We conclude that adoption of specific biosecurity practices by smallholder pig farmers is feasible but requires institutional support. There is a clear requirement for government in partnership with various stakeholders to sensitise farmers using bottom-up approach in designing, planning and implementation of biosecurity practices to enable enhanced adoption.

THEME: SCIENTIFIC DEVELOPMENTS & PREVENTATIVE MEDICINE

Seroprevalence of Brucellosis in communal and smallholder cattle farming in North-West Province, South Africa

Marumo Bontsi[1], Hlokwe Tiny Motlatso[1], Kayoka-Kabongo Prudence Ngalula[2]

[1]*Agricultural Research Council - Onderstepoort Veterinary Research, Pretoria, South Africa -* bontsim@gmail.com
[2]*Department of Agriculture and Animal Health, College of Agriculture and Environmental Science, University of South Africa, Florida, South Africa*

Brucellosis is an important bacterial zoonosis responsible for considerable economic losses in livestock and health-related burden worldwide. The objective of this study was to determine the seroprevalence of Brucellosis in communal and smallholder cattle farming in North-West province of South Africa. A total number of blood samples (n = 770) from farmed animals (n=378) and abattoir-slaughtered animals (n = 392) were collected. In addition, milk samples (n = 22) were collected from lactating farmed cows. Rose Bengal test (RBT), complement fixation test (CFT) and milk ring test (MRT) were used to detect antibodies against *Brucella abortus*. The RBT showed a seroprevalence of 2% at 95% Confidence Interval (CI: 1.35 – 3.35), CFT confirmed an overall sero-prevalence of 1.95% (95% CI: 1.14 – 3.12) for all four districts (i.e., Dr Ruth Segomotsi Mompati, Ngaka Modiri Molema, Bojanala platinum and Dr Kenneth Kaunda districts) sampled. Although the seroprevalence of brucellosis was found to be low, the possibility of undetected cases of the disease could not be ruled out. Overall, the findings of this study confirmed that Brucellosis is endemic in the surveyed areas of North-West Province of South Africa.

Movement patterns of equines into the African Horse Sickness controlled area of South Africa

John Duncan Grewar[1], Michael J. Koning[2], Debra Carter[1], Lesley S. van Helden[3], Kerry Loxley[4] & Camilla T. Weyer[1]

[1]South African Equine Health and Protocols NPC, Baker Square, Paardevlei, Cape Town, 7110, South Africa - john@saehp.com
[2]JDATA (Pty) Ltd, 28 Tambali Village, Sandbaai, 7200, South Africa
[3]Western Cape Department of Agriculture, Veterinary Services: Epidemiology, Elsenburg, 7607, South Africa
[4]Department of Agriculture, Land Reform and Rural Development, Animal Health: Disease control, Delpen Building, Pretoria, 0084, South Africa

Background and Objective: In South Africa, the control of African horse sickness (AHS) involves issuing movement permits for equines entering the AHS controlled area (AHSCA) from the AHS infected zone. This study aims to analyse equine movement data to determine routing patterns and assess the proportion of AHS risk during travel. Additionally, the study identifies potential locations and optimal days for veterinary control points along the routes.

Method and Materials: The route taken (a spatial polylines object) for each equine movement during 2022 was established using the Open Source Routing Machine (OSRM). Veterinary movement permits for AHS movement control are not issued without the receipt of an AHS area status declaration (AHS high, partial, low or unknown risk) for the state veterinary (SV) region of origin. This status was established per day per SV area. All routes, with their AHS profiles and equine counts, were aggregated through rasterization and extraction functions in R.

Results: Movements originate primarily from the Western Cape Province (38%), Gauteng (19.4%), Kwa-Zulu Natal and the Eastern Cape Province (both 15.3%) with movement origins varying through the year. For the four risk classes: the median proportion of the routes made up of each class was 0.95 (95%CI: 0.43- 1) for AHS low-risk, 0 (95%CI: 0- 0.03) for AHS high-risk, 0 (95%CI: 0- 0.27) for AHS partial-risk and 0.03 (95%CI: 0- 0.18) for AHS unknown risk. In the AHS protection zone, the points most likely to intersect equines moving into the controlled area included Touwsriver and Swellendam on the eastern boundary of the zone and Caledon and east of Paarl on the western edge of the zone.

Discussion and Recommendations: The study reveals well-defined and predictable patterns in equine movements towards the AHSCA, primarily through AHS low-risk areas. The travel time ranges from approximately 6 hours in May to 13 hours in December, excluding breaks. Understanding these patterns can help efficiently establish control points to regulate movement and establish the baseline risk profile for AHS risk regions equines move through enroute to the AHSCA.

Reverse genetics as a platform for manufacturing of Bluetongue Vaccine

Tendai A.M. Mlingo[1], Jacobus M. Pretorius[1], Jacques Theron[2], Nobalanda B. Mokoena[1]
[1]Onderstepoort Biological Products SOC Ltd,100 Old Soutpan Road, Onderstepoort, 0110, South Africa - tendai@obp.vaccines.co.za
[2]Department of Biochemistry, Genetics and Microbiology, University of Pretoria, Pretoria 0002, South Africa

Control of bluetongue (BT) disease in domestic ruminants is predominantly through vaccination with licenced inactivated or live-attenuated vaccines (LAVs). Manufacturing and formulation of LAV in endemic countries requires a high number of Bluetongue virus (BTV) serotypes for effective protection against circulating types. The production process must consider different growth profiles of the serotypes contained in the vaccine. Herein, we evaluated a plasmid DNA-based reverse genetics platform for manufacturing of a polyvalent BT vaccine. The synthetic virus was characterised by a common backbone with exchange of the outer capsid

proteins (VP2 and VP5). For this purpose, the BTV1 reference strain selected as the background serotype was successfully rescued. Recombinant South African vaccine serotypes 1, 5 and 14 were successfully rescued by exchanging the VP2 capsid protein on the BTV1 backbone. BTV6 rescue was achieved after exchanging both VP2 and VP5 capsid proteins. Virus particles ranging between 52 and 78nm were obtained and comprised a mixture of partially and fully assembled BT particles. All serotypes were characterised by homogenous plaque size morphology except serotyped BTV5 that displayed a diversity of plaques. Serotypes 1, 5 and 6 growth profiles were distinct from their respective conventional vaccine viruses. Induction of cytopathic effect was more rapid in serotyped BTV1 when compared to the BTV1 vaccine strain, while serotyped BTV5 and BTV6 exhibited slower growth profiles. Growth kinetics of the BTV14 vaccine and synthetic viruses were indistinguishable. Virus disintegration was evident within one month of storage at 4°C,-40°C and-80°C when synthetic viruses were evaluated for stability. Virus particles formulated with a stabiliser-maintained titres for the longer period when compared to unformulated antigens. The plasmid DNA-based reverse genetics approach was found to be suitable for application in non-endemic areas as an alternative manufacturing platform.

Ethnoveterinary use of plants to treat livestock diseases in the Eastern Cape province, South Africa

Siza Mthi[1], Jean Rust[2], Sive Tokozwayo[2] & Zimasa Dubeni[3]

[1]Döhne Agricultural Development Institute, P. Bag X 15, Stutterheim 4930, South Africa - sizamthie@gmail.com
[3]Department of Rural Development and Agrarian Reform, P.O. Box 112, Queenstown, 5320
[3]Department of Botany and Zoology, Faculty of Science, University of Fort Hare, Alice, South Africa

Medicinal plants are used to cure and prevent a wide range of illnesses all over the world. It is vital that such data be recorded for the sake of conservation of indigenous knowledge as well as verification to determine efficacy of treatment. This is the first ethnoveterinary study to determine incidence of use as well as target conditions through the use of statistical tools such as informant consensus factors (icf) and fidelity levels (fl). The study was conducted with the aim to document traditional knowledge of local plants being used to treat various livestock diseases. Data obtained from the survey questionnaire were analysed using statistical indices like informant consensus factor and fidelity level to calculate the relevance of use and status of the local flora. Samples of plants claimed to have medicinal value were collected and botanically identified. The study revealed that 12 plants species belonging to 9 families were used. The family fabaceae was most frequently reported species (27%). Trees (75%) were the main source of ethnoveterinary medicine preparation followed by shrubs (25%). The leaves (58.3%) and bark (25.0%) were commonly utilised parts of plants. Based on the icf, the highest value was recorded for improving fertility (0.88) followed by diarrhea (0.84). As far as fl was concerned, the highest value was recorded in the case of *acacia karroo* (90%) for diarrhea/wound healing and *grewia occidentalis* (83.9%) to enhance fertility/wound healing. In conclusion, people in the study areas possess extensive ethnoveterinary knowledge to cure livestock diseases. Due to rapid deforestation, some of these medicinal plants are threatened, and the availability of modern drugs is rendering this traditional ethnoveterinary knowledge obsolete. Results from the study indicated that there are various plants in the specific study area that have great ethnobotanical potential to treat various diseases.

THEME: PUBLIC HEALTH & ENVIRONMENTAL HEALTH

Cost implications for coping with inadequate water supply in locals of Lephalale Municipality, Limpopo, South Africa

N. A. Modimola[1], L.S. Mudau[1] & M.M. Mokoena[1]

[1]*Department of Environmental Health, Tshwane University of Technology, P/Bag X680, Pretoria, 0001, South Africa* - *nthabiseng.modimola@yahoo.com*

Water is an essential need for survival daily with no substitute. However, the impact of poor water supply has been felt to a point where residents adopt coping strategies to ensure that there is adequate water in the household. Therefore, the strategies adopted co have implications that affect the financial and health implications, productivity due to fetching water from distant water sources and hygiene due to unavailability of water. A survey was carried out in the Local Municipality of Lephalale using an online questionnaire. The results showed that water reuse (n = 44; 22%) which affect the health and hygiene of participants. Participants could waterborne diseases through unhygienic practices. On the other hand, (n=40: 20%) purchase water from retail stores and neighbours which cost them over R1,50 per litre for over 20 days summing to R180.00 per month for drinking water only. Meanwhile, (n = 37; 18%) fetch water from far distance impacting physically, time cost and productivity. In addition, (n = 29; 15%) store water in a bigger container which are cleaned once in a while compromising their health. It has been reported that while water carrying containers grow algae and biofilm. Furthermore, (n = 22; 11%) privately drill of the boreholes costing the communities more money. It has reported that communities spend approximately R16 000 for full functional of boreholes excluding monthly purchasing of electricity. Therefore, it was concluded that communities suffer cost implications through health, financials and hygiene due to inadequate water supply.

Comparative Genomics of *Listeria* Species recovered from meat and food processing facilities

Itumeleng Matle[1], Thendo Mafuna[2], Kudakwashe Magwedere[3], Rian Pierneef[4] & Olega Reva[4]

[1]*Bacteriology Division, Agricultural Research Council: Onderstepoort Veterinary Research, Onderstepoort, Pretoria, South Africa* - *Matlel@arc.agric.za*
[2]*Department of Biochemistry, University of Johannesburg, Auckland Park, South Africa*
[3]*Directorate of Veterinary Public Health, Department of Agriculture, Land Reform and Rural Development, Pretoria, South Africa*
[4]*Centre for Bioinformatics and Computational Biology, University of Pretoria, Pretoria, 0001, South Africa*

Listeria species (spp.) are contaminants that can survive in food, on equipment, and on food processing premises if appropriate hygiene measures are not used. Homologous stress tolerance genes, virulence gene clusters such as the *prfA* cluster, and clusters of internalin genes that contribute to the pathogenic potential of the strains can be carried by both pathogenic and nonpathogenic *Listeria* spp. To enhance understanding of the genome evolution of virulence and virulence-associated properties, a comparative genome approach was used to analyze 41 genome sequences belonging to *L. innocua* and *L. welshimeri* isolated from food and food processing facilities. Genetic determinants responsible for disinfectant and stress tolerance were identified, including the efflux cassette *bcrABC* and *Tn6188_qac_1* disinfectant resistance determinant, and stress survival islets. These disinfectant-resistant genes were more frequently found in *L. innocua* (12%) than in *L. welshimeri* (2%). Several isolates representing the presumed nonpathogenic *L. innocua* still carried virulence-associated genes, including *LGI*2, *LGI*3, *LIPI*-3, and *LIPI*-4 which were absent in all *L. welshimeri* isolates. The mobile genetic elements identified were plasmids (*pLGUG1* and *J1776*) and prophages (PHAGE_Lister_vB_LmoS_188, PHAGE_Lister_LP_030_3, PHAGE_Lister_A118, PHAGE_Lister_B054, and PHAGE_Lister_vB_LmoS_293). The results suggest that the presumed nonpathogenic isolates especially *L.*

innocua can carry genes relevant to the strain's virulence and stress tolerance in the food and food processing facilities. This study provides genomic insights into the recently expanded genus in order to gain valuable information about the evolution of the virulence and stress tolerance properties of the genus *Listeria* and the distribution of these genetic elements pertinent to the pathogenic potential across *Listeria* spp. and clonal lineages in South Africa (SA).

Comprehensive analysis of *Staphylococcus aureus* isolates from subclinical mastitis dairy cows in Free state Province, South Africa using whole genome sequencing

N. G. Khasapane[1], Z. T. H. Khumalo[2,3], S.J. Nkhebenyane[1], S. Kwenda[5] & M. M. O. Thekisoe[4]

[1]*Department of Life Sciences, Centre for Applied Food Sustainability and Biotechnology, Central University of Technology, Bloemfontein, 9300 - nkhasapane@cut.ac.za*
[2]*Department of Veterinary Tropical Diseases, Faculty of Veterinary Sciences, University of Pretoria, Private Bag X04, Onderstepoort, 0110, South Africa.*
[3]*Clinvet International, Study Operations, Uitsig Road, Universitas, Bloemfontein*
9338
[4]*Unit for Environmental Sciences and Management, North-West University, Potchefstroom, 2531*
[5]*Sequencing Core Facility, National Institute for Communicable Diseases, National Health Laboratory Service, Johannesburg, South Africa*

Significant financial losses to the dairy sector are caused by bovine mastitis on a global scale. *Staphylococcus aureus* is one of the major bacteria which a frequent cause of bovine mastitis. Understanding the frequency of virulence traits and antimicrobial resistance would shed light on the molecular epidemiology of *S. aureus* strains linked to mastitis. In the current investigation, 38 mastitis-associated *S. aureus* strains obtained from the Free state Province, South Africa, were subjected to whole genome sequencing and comparative genomic analysis. The 38 strains were grouped by the *in silico* MLST into seven sequence types (STs) (ST 97, 352, 152, 243) and three new STs (novels 1-3). The average GC content of the 2.7 Mbp genome was 32.7%. Thirty-eight strains were divided into 13 primary clusters by the genome-wide SNP-based phylogenetic analysis. *Spa-types* t2883 accounted for the majority of isolates at 12 (31.57%), followed by t416 with 11 (28.94%) and t2844 with 5 (13.15%), among the 9 distinct *spatypes* that were found. The data also revealed the identification of four (4) plasmids, with Rep_N (rep20) accounting for the majority of isolates with 17 (44.73%), followed by Inc18 (repUS5) with 2 (5.26%). These isolates included 11 distinct antimicrobial resistance (AMR) genes, and all of the isolates used in this investigation were methicillin susceptible. Additionally, we discovered 23 genes linked to virulence. Due to the virulence traits of *S. aureus* that play a role in the mastitis disease process, characterisation is essential for risk assessment. The results of our study on genes associated with virulence and antibiotic resistance are relevant due to the implications for public health.

Exploration of the Use of Moringa *oleifera* in Aquaculture: A Review

Zimasa Busisiwe Dubeni[1*], Lisa Vallencia Buwa-Komoreng[1] & Siza Mthi[2]

[1]*Department of Botany, Faculty of Science and Agriculture, University of Fort Hare, Alice, 5700, South Africa - zdubeni@ufh.ac.za*
[2]*Department of Rural Development and Agrarian Reform, P.O. Box 112, Queenstown, 5320, South Africa*

Over the years, global aquaculture development increased rapidly in recent years, and the sector has become one of the fastest-growing industries in the animal-derived food production system. Nevertheless, microbial contamination and lipid oxidation, through an advanced level of intensification remain the main causes of meat deterioration rendering it unacceptable to the consumer. Antibiotics and synthetic antibiotics have been used to prevent meat spoilage throughout the product's shelf-life. However, antibiotics applied have been restricted

globally against aquatic disease outbreaks due to their apparent accumulation in the tissues, which imposes on the development of resistant bacteria. The aquaculture industry now considers natural alternatives to control the growth of microbes in fish. Plant extracts, increasingly recognized as consumer friendly, represent a valuable source of active compounds, mostly polyphenols, with potent anti-microbial and antioxidant activities. This paper aims to provide information on the use of the *M. oleifera* plant in the treatment of bacterial and parasitic diseases in fish and other marine species and their preservation thereof. Also, details on the identified secondary metabolites, the mechanisms of action, and various uses of *M. oleifera* in the preservation of *M. oleifera* will be highlighted.

A descriptive epidemiological study of food-borne diseases in Mhlontlo Local municipality, O.R. Tambo District, Eastern Cape Province, South Africa: A one health approach

N. N. Ndlame[1,2], T. P. Mbombo-Dweba[2] & J. W. Oguttu[2]

[1]*Department of Rural Development and Agrarian Reform, Eastern Cape, South Africa - 34773002@mylife.unisa.ac.za*
[2]*Department of Agriculture and Animal Health, Florida Campus, UNISA, South Africa*

Background: People in rural South Africa believe that there is no justification for throwing away meat. This attitude promotes the occurrence of food-borne diseases (FBDs). Considering this there is a need to investigate of FBDs among people from rural areas of South Africa.

Method and Materials: A cross-sectional study design using retrospective data of cases of FBDs collected by a health facility in O.R. Tambo District between 2016 and 2020 were used in this study. Descriptive statistics were computed in terms of time and place.

Results: Consumption of meat from a dead cow, and a cow injected with medicine was observed in eight and five locations respectively. Consumption of meat from dead sheep was reported in four locations. FBDs associated with eating meat from a cow bitten by a snake, a dead goat, ready-to-eat meat, sick chicken, chicken served at school and spoilt chicken meat, were each observed in one location. 2016, 2018 and 2020, recorded a spike in the number of FBDs between January and June. In 2017 and 2019 another spike was observed between September and December. The highest number of cases of FBDs was recorded in 2018 (52.98 %). The least number of cases was reported in 2019 (4.30%) and 2020, (8.59%).

Discussion and Recommendations: Consuming meat from dead cattle is the most common cause of FBDs in study area. This was expected since cattle are the most reared, and meat from a cow can serve many people. The incidence of diseases among animals tends to increase during the warm months (December to May) of the year. Hence an increase in the number of animals that get sick during these months. Sick animals and those that get treated that fail to recover are consumed, causing spikes in cases of FBDs.

Conclusion: Consumption of beef that should be condemned is the main driver of FBDs in the study area. This should be considered when planning health education initiatives. A one-health approach is needed to address occurrence of FBDs, with the veterinary team emphasizing the need to adhere to withdrawal periods for medicines following treatment of animals.

POSTER SESSION 3 – FRIDAY 25 AUGUST 2023, 12h20

Virulence characterisation and antimicrobial resistance profiles of Shiga toxin-producing *Escherichia coli* and Enteropathogenic *Escherichia coli* isolates from dairy cattle in South Africa

Alaba Olawole[1], Mogaugedi Malahlela[1], Munyaradzi C Marufu[2], Alan Kalake[3] & Musafiri Karama[1]

[1]*Veterinary Public Health Section, Department of Paraclinical Sciences, Faculty of Veterinary Science, University of Pretoria, Onderstepoort 0110, South Africa - leye277@gmail.com*
[1]*Veterinary Public Health Section, Department of Paraclinical Sciences, Faculty of Veterinary Science, University of Pretoria, Onderstepoort 0110, South Africa*
[2]*Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, Onderstepoort 0110, South Africa*
[3]*Gauteng Department of Agriculture and Rural Development, Johannesburg 2001, South Africa*

Shiga toxin-producing *Escherichia coli* (STEC) and Enteropathogenic *E. coli* (EPEC) cause foodborne disease characterised by mild diarrhea (EPEC) and mild to severe bloody diarrhea (STEC). In this study, 157 STEC and 48 EPEC isolates from dairy cattle were characterised for virulence-associated genes and antimicrobial resistance profiles. Virulence-associated genes including *stx1a, stx1c, stx2c, stx2d, espP, saa, pagC,* and *terC* were detected in the majority of STEC isolates. Plasmid encoded virulence genes *katP, espP* and *etpD* were significantly found in STEC isolates commonly associated with severe human disease. However, a lower prevalence of plasmid encoded virulence genes was observed among EPEC: *espP* (35.8%), *etpD* (9.4%), *katP* (5.7%), *saa* and *subA* (0%). Among STEC strains previously incriminated in human infections (N=78), *stx1a* (74%), *stx1c* (64%) and *stx2c* (65%) were the common *stx*-subtypes while *espP* (56%), *saa* (68%) *and subA* (56%) were the common plasmid encoded virulence genes. Furthermore, the virulence marker genes encoded on the pathogenicity islands were highly prevalent (82-100%) among STEC O26:H2, O26:H11, and O157:H7 which are considered the “top 7” serotypes incriminated in human disease. Antimicrobial resistance against 10/14 of antimicrobial agents tested was detected in 13.4% (21/157) of STEC isolates. Furthermore, multi-drug resistance was observed in 4.6% (7/157) of isolates mainly among STEC O54:H2, O61:H16, O136:H16 and O157:H7 strains. Among the EPEC isolates, antimicrobial resistance was detected in 40% (19/48) and multi-drug resistance in 21% (10/48) of isolates. The highest antimicrobial resistance levels among STEC isolates were recorded for tetracycline (8.3%) and ampicillin (5.1%). Similarly, antimicrobial resistance against tetracycline (31%) and ampicillin (15%) was also observed among EPEC isolates. The findings in this study demonstrated the significance of dairy cattle as reservoir of virulent STEC and EPEC strains which have been previously incriminated in human disease. Furthermore, the high number of virulence-associated genes in STEC O26:H2 and O136:H16 is a public health concern which highlights the need for surveillance and monitoring of emerging virulent STEC strains in South Africa. In addition, further characterisation and surveillance studies on STEC in South Africa will be needed to acquire more knowledge that can be used to improve food safety.

Prevalence and antimicrobial resistance of *Staphylococcus* spp. isolated from human specimens submitted to diagnostic laboratories in South Africa, 2012–2017

Themba Titus Sigudu[1,2], James Wabwire Oguttu[1] &Daniel Nenene Qekwana[3]

[1]*Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, University of South Africa, Johannesburg, South Africa - 39515885@mylife.unisa.ac.za*
[2]*Department of Health and Society, School of Public Health , Faculty of Health Sciences, University of Witwatersrand, Johannesburg, South Africa*
[3]*Section Veterinary Public Health, Department of Paraclinical Sciences, Faculty of Veterinary Science, University of Pretoria, Pretoria, South Africa*

Background: Antimicrobial resistance is a growing concern in both human and veterinary medicine as it limits traditional treatment options and increases costs. Understanding the prevalence and the magnitude of the problem and identifying its determinants is important for guiding control efforts.

Objectives: This study characterise the proportion of antimicrobial resistant staphylococcal isolates among human specimens submitted to diagnostic laboratories in South Africa, 2012–2017 and to identify predictors of antimicrobial resistance (AMR) and multidrug resistance (MDR).

Method and materials: Retrospective records of 404 217 diagnostic laboratory submissions assessed for antimicrobial susceptibility against 35 antimicrobials from 2012 to 2017 were included in this study. The Cochran-Armitage trend test was used to assess temporal trends for each antibiotic. Logistic regression models were used to investigate predictors of AMR and MDR.

Results: Overall, 74.4% (300 779/404 217) of Staphylococcus species isolated were *S. aureus*. Of these, 80.2% (240924/300 779 were AMR, while 40.2% (120913/300 779) were MDR. The highest level of resistance was against ampicillin (72.1%), and the least resistance was observed against linezolid (0.3%). There was a significant (p = 0.022) decreasing trend in AMR. The proportion of AMR isolates were at their highest in 2014 (81.0%) and their lowest in 2017 (70.0%). In contrast, there was an increasing temporal trend in MDR (p = 0.001) over the study period. The proportion of MDR isolates began at its lowest point in 2012 (23.0%) before reaching the highest level in 2016 (34.0%). A Significant (p < 0.05) associations were observed between age, species of organism and province of origin, with AMR outcome. Similarly, significant (p < 0.05) associations were identified between specimen type and age, with MDR outcome.

Discussion and recommendations: The high proportions of AMR to a number of antimicrobial agents observed in this study are concerning as they suggest that the levels of AMR are high for both pathogenic and non-pathogenic *Staphylococcus* spp. Therefore, continued monitoring of AMR among *Staphylococcus* spp. and judicious use of antimicrobials in human medicine should be promoted.

Antibiotic resistance and virulence profiles of *P. mirabilis* isolated from broiler chickens in North-West Province, South Africa

Kealeboga Mileng[1], Tsepo Ramatla[2], Kgaugelo E. Lekota[2] & Oriel Thekisoe[2]

[1]*Unit for Environmental Sciences and Management, North-West University, Potchefstroom, 2531, South Africa* - K.mileng@gmail.com
[2]*Unit for Environmental Sciences and Management, North-West University, Potchefstroom, 2531, South Africa*

Proteus mirabilis has been identified as an important zoonotic pathogen causing several illnesses such as diarrhoea, keratitis and urinary tract infections. This study assessed the prevalence of *P. mirabilis* in broiler chickens, its antibiotic resistance (AR) patterns, ESBL-producing *P. mirabilis* as well as the presence of virulence genes. A total of 26 isolates were confirmed as *P. mirabilis* from 480 pooled broiler chicken faecal samples by polymerase chain reaction (PCR). Disk diffusion method was used to evaluate the antibacterial susceptibility test, while nine virulence genes and 26 AR genes were also screened by PCR. All 26 *P. mirabilis* isolates harboured the *ireA* (siderophore receptors), *ptA*, and *zapA*, (proteases), *ucaA*, *pmfA*, *atfA*, and *mrpA*, (fimbriae), *hlyA* and *hpmA* (hemolysins) virulence genes. The *P. mirabilis* isolates were resistant to ciprofloxacin (62%) and levofloxacin (54%), whilst 8 (30.7%) of the isolates were classified as multidrug resistant (MDR). PCR analysis identified *blaCTX-M* gene (62%), *blaTEM* (58%) and *blaCTX-M-2* (38%). Further screening for AMR genes identified *mcr-1*, *cat1*, *cat2*, *qnrA, qnrD*, and *mecA*, 12%, 19%, 12%, 54%, 27%, and 8% respectively *P. mirabilis* isolates. The prevalence of the integrons integrase *intI1* and *intI2* genes was 43% and 4% respectively. The rise of ciprofloxacin and levofloxacin resistance as well as MDR strains is a public health threat that points to a challenge in the treatment of infections caused by these zoonotic bacteria. Furthermore, the presence of *blaCTX-M*-producing *P. mirabilis* in broilers should be controlled due to the importance of cephalosporins and the zoonotic potential of ESBL-producing *P. mirabilis*. This is the first study undertaken to isolate *P. mirabilits* from chicken faecal samples and investigate its antibiotic resistance status as well as virulence profiles in South Africa.

Occurrence, serotypes and virulence characterization of Shiga toxin-producing *Escherichia coli* isolates from goats on communal rangeland in South Africa

Mogaugedi N. Malahlela[1], Beniamino T. Cenci-Goga[1,2], Munyaradzi C. Marufu[3], Thierry Y. Fonkui[1], Luca Grispoldi[2], Eric Etter[4,5,6], Alan Kalake[7], & Musafiri Karama[1]

[1]*Veterinary Public Health Section, Department of Paraclinical Sciences, Faculty of Veterinary Science, University of Pretoria, Onderstepoort 0110, South Africa - mogaugedi.malahlela@gmail.com*
[2]*Department of Veterinary Medicine, Laboratorio di Ispezione Degli Alimenti di Origine Animale, University of Perugia, 06126 Perugia, Italy*
[3]*Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, Onderstepoort 0110, South Africa*
[4]*Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Onderstepoort 0110, South Africa*
[5]*Centre de Coopération Internationale en Recherche Agronomique Pour le Développement (CIRAD), Unité Mixte de Recherche (UMR), Animal Santé, Territoires, Risques et Ecosystèmes (ASTRE), 97170 Petit Bourg, France*
[6]*ASTRE, University Montpellier, CIRAD, INRAE, France Baillarguet International Campus, University of Montpellier, 34070 Montpellier, France*
[7]*Gauteng Department of Agriculture and Rural Development, Johannesburg 2001, South Africa*

Shiga-toxin-producing *Escherichia coli* (STEC) are zoonotic foodborne pathogens associated with gastrointestinal human diseases ranging from mild or severe bloody diarrhea, hemorrhagic colitis and hemolytic uremic syndrome. "Top 7" STEC including O157:H7 serotype and non-O157 serogroups (O26, O111, O45, O145, O121, and O103) are the most incriminated in human illness worldwide. In this study, a total of 289 goat fecal samples were examined for the occurrence of STEC in Gauteng, South Africa. STEC were detected and characterised by microbiological culture and PCR (Polymerase Chain Reaction). Furthermore, 628 goat STEC isolates were serotyped (O:H) and virulotyped for virulence markers by PCR. Overall, STEC was found in 80.2% goat fecal samples. Herd STEC occurrence was as follows: 75.3% (116/154) for herd A; 90.6% (39/43); herd B; 78.8% (41/52), herd C and 90% (36/40) in herd D. Serotyping of 628 STEC isolates revealed 63 distinct serotypes including four which belong to the top seven STEC serogroups were detected in 12.1% (35/289) of goats: O157:H7, 2.7% (8/289); O157:H8, 0.3%, (1/289); O157:H29, 0.3% (1/289); O103:H8, 7.6% (22/289); O103:H56, 0.3% (1/289); O26:H2, 0.3% (1/289); O111:H8, 0.3% (1/289) and 59 non-O157 STEC serotypes. Of the 63 STEC serotypes found, twenty-four were previously isolated from patients with human disease worldwide including South Africa. Genes encoding major virulence genes were distributed as follows: *stx1*, 60.6% (381/628); *stx2*, 72.7% (457/628); *eaeA*, 22.1% (139/628) and *hlyA*, 78.0% (490/628). Both *stx1* and *stx2* together were found in 33.4% (210/628) of isolates, respectively. It is concluded that goats are reservoir of STEC and carrier of diverse STEC serotypes which have been incriminated in life-threatening human STEC disease in South Africa. Further surveillance of STEC in goats will be necessary to fully understand the importance of goats as a reservoir of STEC in South Africa. In addition, comparative molecular characterisation studies are needed to evaluate to what extent goats may be a source of human STEC disease in South Africa.

Seroprevalence of *Toxoplasma gondii* in free-range pigs within Ngaka Molema District Municipality District, North-West Province

Naomi Masango[1], Rendani Victress Ndou[1] & Kopano Kgomari[1]

[1]*School of Agricultural Studies, Centre of Animal Health Studies, North-West University, Mafikeng Campus, Private Bag X2046, Mmabatho, 2735 - bathabilenaomi@gmail.com*

Free-range pigs are considered a good indicator of environmental contamination with *Toxoplasma gondii* (*T.gondii*), this is because they feed directly on the ground that may contain *T.gondii*oocysts. Though the disease in pigs is asymptomatic, the consumption of infected pigs by humans may lead to human toxoplasmosis with dire consequences. This study aimed to determine the seroprevalence of *T.gondii* in free-range pigs at two local municipalities within Ngaka ModiriMolema District Municipality. The study used the convenience sampling method to collect a total of 298 blood samples from 37 farming operations within 12 villages. Sera were tested for antibodies specific to *T. gondii* using the ID screen toxoplasmosis indirect multi-species ELISA test kit. A relatively high prevalence of 20.1% (60/298) was obtained, ranging from 0% to 57,9%. The high seropositivity obtained in this study indicates not only high environmental contamination but also a high potential risk for food safety. Therefore, this study concludes that there is a great need for the education of farmers and the public about zoonotic diseases.

Trend-analysis of generic *E. coli, Salmonella spp*. and total bacterial count detected in imported poultry meat into South Africa (2016 – 2018)

M. E. Machedi[1] M E1 & A. Singh[2]

[1]*Department of Agriculture, Land Reform & Rural Development, South Africa - memachedi@gmail.com*
[2]*Department of Environmental Health, Faculty of Health Sciences, University of Johannesburg, South Africa 2104 John Orr Building, Doornfontein Campus*

Background: South Africa is the net importer of poultry meat and has been since the early 2000s. The country produces 85% of local consumption and the self-sufficiency ratio has been steadily declining. On average South Africa imports 560 000 tonnes of poultry meat annually. With increasing consumption, the risk of contamination of poultry meat with food-borne pathogens becomes an important public health issue that can lead to catastrophic diseases in humans.

Objectives: The aim of the study was to analyse the microbiological reports of imported poultry meat that came through the port of Durban, South Africa from January 2016 to December 2018. The objective was to first study the correlation between Total Bacterial Count (TBC), generic *E. coli* and *Salmonella* species by looking at the country of origin, product, period and species as the variables. Secondly, the comparative risk profiles of exporting countries were also examined.

Methods: The study design selected was a retrospective cross-sectional study. The secondary data analysed was obtainable and available from the State Veterinarian Office in Durban with permission and the approved SANAS (South African National Accreditation System) accredited laboratories that conducted the poultry meat compliance tests. Only microbiological data (total bacterial count, *Escherichia coli* and *Salmonella* sp.) from poultry products that have been subjected to microbiological testing on frozen full carcasses, chicken feet, legs, breasts, offal and chicken skins were recorded. The data was collected from the period 2016-2018 and captured onto the Microsoft Excel spreadsheet every month. The total number of samples recorded for frozen imported poultry consignments that were bacteriologically tested for the presence and counts of a total bacterial count, *E. coli*, and *Salmonella* species, was n= 34161. The analysis of the statistical data was accomplished using SPSS Software v 27.0. The data was abstracted for the following variables i.e., period, species, product, country of origin and microbiological results. The data was cleaned, checked for completeness, categorised and

transformed to fit data analysis based on the objectives of the study. Statistical significance was determined at $p < 0.05$. Descriptive analysis was performed for estimating the relationships and or trends between variables.

Results: This study showed that in 2018, the Total Bacterial Count (TBC) in poultry meat was significant when it was analysed against the period of importation. The majority of poultry meat imports 40.8% (13 929) occurred in 2018. Fewer imports 23.4% (7 995) were recorded in 2016. The distribution of poultry cuts is almost evenly spread, with unrecognisable cuts accounting for 51.7% (17 646) and recognisable cuts with 48.3% (16 515) of all imported consignments over the three-year investigated period. South America has the highest distribution of all the countries that imported to Republic of South Africa, with 20 782 (60.8%) poultry consignments, followed by Europe 7 790 (22.8%) and North America 5 200 (15.2%). Africa has the lowest distribution of 1 (0.01%). Most of the poultry species over this period were chicken with 93.4% (31 909). Of all the consignments tested for *E. coli*, 94% (32 107) were less than the threshold of 1 x 10^3cfu/g. The overall prevalence of *Salmonella* in imported poultry meat was 2.9% for the study period. In 2016, the *Salmonella* prevalence was 4.96%, 2.11% in 2017 and 1.3% in 2018. The countries from South America had the highest number of consignments that were tested for *Salmonella spp* in 2016 (6.5%) while Europe has the highest *Salmonella spp* prevalence of 2.8% in 2017 and 2018 (1.88%). The unrecognizable cuts of the product amounted to 51.5% (16 536) of all the products tested for *Salmonella spp.* and of those 3.6% (597) were positive ($p<0.05$).

Conclusion: The prevalence of food-borne pathogens is relatively low in frozen imported poultry meat compared to other studies. Food safety controls and protocols in international trade play an important role in reducing the incidence of food-borne pathogens in poultry meat.

THEME: SOCIOECONOMIC/CULTURAL DYNAMICS

Use of remedies by illiterate small-scale farmers for treatment of livestock diseases in Lubala Village of the Eastern Cape Province in South Africa

Tandile N. Ndobeni [1] & Patrick J. Masika[2]

[1]*Directorate of Veterinary Services, Primary Animal Health, Gauteng Department of Agriculture Rural Development and Environment - ndobenitn@gmail.com*
[2]*Department of Livestock and Pasture Science, Faculty of Science and Agriculture, University of Fort Hare*

Background: Remedies used by small-scale farmers for their livestock production are divided into two; conventional and non-conventional. Both remedies are important and are used to improve livestock production globally.

Objective: Assess the factors that influence the use of remedies by small-scale livestock farmers.

Materials and Methods: The study was conducted at the Lubala village in Lusikisiki in the Eastern Cape in 2011. Purposive sampling was used to identify farmers to participate in this study. The questionnaires to be used for interviews comprised of gender, age, household size, level of education, employment status, and lastly the type of medication used for livestock. All primary data was obtained using questionnaires from respondents were entered in an Excel spreadsheet and analyzed using SPSS 16.0.

Results: A total of 60 farmers were interviewed, with 60% males and 40% females. The household size was arbitrarily grouped according to the number of household members; small (2 – 6), medium (7 – 13) and large which was (14 – 25). Majority of livestock treatment was done by household head (57%), however both genders together with children less than 15 years all participated. Of the respondents (37%) received government pensions, (23%) were unemployed, (18%) self-employed, (16%) were employed and (6%) were students. Respondents had different levels of education, with majority (51%) having primary school level, (33%)

had not gone to school at all, and the rest had attained secondary (12%) and (4%) tertiary education. Most respondents (65.5%) used conventional remedies to treat livestock, while (34.5%) used non-conventional remedies.

Discussion and Recommendations: The results showed that illiteracy had an effect in the use of conventional remedies, while employment status does not have an effect on types of remedies used. In addition, knowledge of non-conventional remedies is passed orally from generation to generation by the elders to females that they work closely with. Therefore, there is an urgent need to document and validate information on the use of non-conventional remedies.

Socio-economic dynamics influencing livestock farmers to apply primary animal health care practices in Gauteng Province

Xolisiwe Yolanda Potelwa[1] & Zimbini Mdlulwa[2]

[1]*Gauteng Department of Agriculture, Rural Development, and Environment* - xolisiwei@gmail.com
[2]*North-West Department of Agriculture and Rural Development*

The Gauteng Department of Agriculture, Rural Development and Environment (GDARDE) had earmarked a total of ten smallholder livestock farmers (SHLF) to be commercialized by 2024/25. The commercialization programme (CP) was initiated to increase the Gauteng Province (GP)'s agricultural gross value share (AGVS) from 0,4% to 2% and to ensure that the sector continues to increase its contributions to export earnings. Furthermore, the CP is also aimed to improve the SHLF support programme in the province. A situation analysis was conducted in 2021 to determine the livestock landscape and social economic dynamics that could influence CP. Farms visits and face-to-face interviews were conducted on SHLF using a structured questionnaire. The analysis revealed that SHLF are faced with several challenges that include limited agricultural land, animal handling facilities, and limited production and marketing infrastructure. The limited land size inhibits SHLF from increasing their livestock, practising rotational grazing, and separating different livestock species. These limitations create a platform for the spread of infectious diseases as farmers are constrained to practice isolation of new herds and sick animals. Lack of handling facilities such as neck clamps, sliding gates, and crush pens were highlighted as major limiting factors for SHLF to practice disease management (vaccination, deworming, hoof trimming etc). Lack of production and marketing infrastructure such as auction facilities were identified as contributors to the spread of infectious diseases as livestock is moved long distances including beyond the borders of the province. Farmers indicated that local auction facilities could assist in the reduction of stock theft, and animal movement while enabling traceability, and collaborative efforts towards infectious disease prevention and control. Healthy animals with good body conditions will benefit SHLF with better market prices while local auctions will assist with the reduction of transaction costs and market access. It is recommended that for an efficient and effective livestock CP, GDARDE implements a holistic approach to livestock production and marketing. This approach will assist the province to ensure a sustainable disease-free sector, thereby contributing towards the growth of AGVS of the Province and improved socio-economic impact as well as diversifying the export market for better earnings.

The socio-economic profile of communal cattle farmers and tick infestation levels among communal cattle in Sinthumule - Kutama area

Makhado P. Sedina[1], M. M. Mayanja[2], J. W. Oguttu,

[1]*Department of Agriculture and Animal Health, Florida Campus, UNISA, South Africa* - sidinamp@gmail.com

Background: Ticks are external blood sucking parasites responsible of many tick-borne diseases in the livestock industry. In addition, ticks cause damage to hides and irritate animals. While livestock in rural areas play an important role in social, cultural, and financial aspects of communities, this is constrained by high tick infestation. This study investigated the socio-economic status of small-scale cattle farmers and tick infestation amongst communal cattle in Sinthumule – Kutama area.

Methodology: A quantitative cross-sectional study design was adopted for this study. Systematic random sampling was used to recruit households. Data was collected using semi-structured face to face interviews and a checklist. Data was analysed using STATA (Version 17) to compute descriptive statistics.

Results: A total of 28 cattle owners participated in this study and 133 cattle were sampled around Sinthumule – Kutama areas of Makhado local municipality. Most cattle farmers were males (85.71%) and married (64.29 %). The dominant age group was over >60 years, accounting for 39.29% followed by the 47- 60-year-old (35.71%). Most of farmers were of Vhavenda ethnicity (92.86 %). Majority had attained secondary (42.86 %) and primary (36.9 %) schooling. Majority of farmers were either self-employed or unemployed (32.14 %). Cattle farmers who depended on salary and pension pay outs, each constituted 25 % of the study population. The estimated monthly household income for majority of farmers (78.57 %) was <R5000. Majority of farmers kept crossbreeds (59.40%), while Simmentaler (1.50 %) were the least reared breed. Majority of cattle (49.62 %) were old (>8 years) followed by adult cattle (>2 to 8 years) (18.05 %). Female cattle (81.95 %) were the majority. Cattle with a body condition score of 4 constituted 60.90% while very thin cattle made up only 2.26 % of all cattle sampled. The average tick count was highest on the ears (M = 52; IQR = 63), lower perineum (M =25; IQR =30) followed the dewlap (M = 24; IQR =36).

Discussion and recommendations: Cattle farming is mostly practiced by old males with very low education and income levels. Old female cattle form majority of the communal herd. The preferred cattle breed is the crossbreed. The average tick count on cattle was high. Tick control awareness programs should be conducted to capacitate cattle farmers.

Are socio-economic dynamics a threat to infectious diseases prevention and control? The narratives of animal health practitioners and smallholder farmers in South Africa

Zimbini Mdlulwa[1], M. Lungwana[2] & N. Ngcobo[2]

[1]*North-West Department of Agriculture and Rural Development, Stadium Road, Mahikeng, South Africa - ZMdlulwa@nwpg.gov.za.*
[2]*Agricultural Research Council, 1134 Park Street, Hatfield, Pretoria, South Africa*

Globally, there is a realization that socio-economic dynamics must be considered when evaluating the effectiveness of farm management including the incidence and prevalence of diseases on livestock farms. This is more compelling in rural areas as literature has highlighted a relationship between animal disease and socio-economic dynamics of smallholder farmers (SHFs). As livestock is managed by humans, it is not surprising that culture can influence the epidemiology of animal diseases. This paper sought to investigate socio-economic dynamics that pose a threat on prevention and control of infectious diseases. In 2022, a study commissioned by the European Commission for the Control of Foot-and-Mouth Disease and the Food and Agriculture Organisation (FAO) was conducted by the Agricultural Research Council to determine the socio-economic dynamics affecting animal disease management. Focus group discussions (FGDs) were held with 112 Animal Health Practitioner (AHPs) and 269 SHFs in North-West and Eastern Cape provinces of South Africa. Qualitative and quantitative methods were used to analyse the data. The analysis has revealed that socio-economic dynamics such as gender, cultural beliefs and age have an impact on animal disease management. SHFs revealed limited knowledge on biosecurity measures such as handling of aborted fetuses and sick animals. Mishandling of abortions renders SHFs vulnerable to zoonosis such as contagious abortion (CA) and Rift Valley fever (RVF). Cultural beliefs in other areas limit female AHPs from entering the livestock kraals, making it difficult for them to deliver the required animal health services. Furthermore, livestock owned by women is more vulnerable to infectious diseases due to them being restricted to enter the kraal when in mourning. Whilst One Health is a holistic approach to infectious disease management, it was found that elderly AHPs were not knowledgeable about the One Health approach while the younger ones had proper understanding of the approach and its application. Findings of this study suggest that socio-economic dynamics such as culture, gender, education and age should be taken into account when strategising on approaches for holistic management on infectious diseases. Training for SHFs and AHPs on One Health approach is recommended to achieve optimal health outcomes.

Reflections on ancient veterinary practices in Africa and contextual relevance to primary animal health care

Alfred Tlotlo Kgasi

University of Pretoria - alfred.kgasi@up.ac.za

Even though we have modern and advanced practices in veterinary medicine and science, it is believed that veterinary medicine was practised long before written records could be made (Mark, 2020). It is reported that humans domesticated various animals such as dogs, cats, cattle, goats, horses, and sheep from their wild counterparts as far back as between 13,000 and 2,500 BC. The domestication of animals led to the development of what can be characterised as a human animal bond. The human animal bond is a mutually beneficial and dynamic relationship between people and animals that is essential to the health and well-being of both (Melvin, 2021).

It has further been cited the rough evolution of veterinary practice dates back to ancient civilizations in Mesopotamia, Africa, China and India. This is believed to be long before it arrived in Greece and Rome where it was later developed throughout Europe (Mark, 2020). Physicians of other regions were practicing veterinary medicine long before the written records could attest to it. Some scholars, in fact, have argued that veterinary practice in Egypt is among the earliest in the world dating back at least to the time of the Old Kingdom (c. 2613-2181 BC) if not earlier (Conni Lord, 2015). Livestock keepers relied on these traditional practices before introduction of Western medicines. Centuries of local people's empirical observation and experience contributed to creation of indigenous knowledge systems (McCorkle and Mathias-Mundy, 1992).

According to WHO, at least 80% of people in developing countries depend largely on indigenous practices for the treatment and control of various diseases in both humans and animals. Recognition of the rich history of ancient veterinary practices in Africa can benefit the principle of Primary Animal Healthcare in creating acceptance and recognition people’s identity and their socio-culturally roots. The recognition also dispels the myth that western medicines practices are the only solution to disease control problems, and thus creates space for co-existence of options of treatment. Indigenous knowledge systems may play a role in dealing with modern scientific challenges such microbial drug resistance.

THEME: ONE WELFARE

Socio-economic and welfare aspects of working equines in the peri-urban areas around Mogalakwena Municipality in Limpopo Province, South Africa

D. B. Molapo[1,2], J. W. Oguttu[1] & C. M. E. McCrindle[1]

[1]*Department of Agriculture and Animal Health, Florida Campus, UNISA, South Africa - bettymolapo@gmail.com*
[2]*Department of Agriculture, land Reform and Rural Development, South Africa*

Background: Equines play an important role as working animals in peri- urban areas, employed for carting. Their work can support food security and reduce poverty in low-income communities. However, few studies have investigated socioeconomics, health, breeding, and management of these animals including their role in communities in such areas. This study investigated the socioeconomic and animal welfare aspects of working equines in the study area.

Methodology: A quantitative cross-sectional questionnaire-based study design was adopted for this study. Semi structured face-to-face interviews using a pre-tested questionnaire and a checklist were used to collect data from selected participants.

Results: Fourteen (n=14) Peri-Urban areas around Mogalakwena Local Municipality were surveyed. A total of 111 equine owners participated in this study. Majority of the equine owners were males (n=90; 80.8%). The dominant age group was 31–50-year-olds, and it constituted (n=49;44.14%), with the least being 18-30 years (n=26;23.43%). Sources of income for working equine owners ranged from donkey carting (n=85;76.58%), government social grants (n=21;18.92%) and salaries (n=8;7.21%).However, Equines in the study primarily carried external wounds on the areas of hindquarters (n=27;6.44%), mouth (n=19;4.53%), neck(n=19;4.53%) and belly(n=18;4.30). About 30% (27.21%; n=114) of the equines had their ears mutilated, nineteen (n=19; 4.58%) were branded using hot iron method.

Discussion and recommendations: Working equines plays an important role in the livelihoods of people in Mogalakwena, through income generation, poverty reduction and food security. The majority of working equines are owned by middle-aged males who use them as their sole means of generating income and supporting household economy. Despite the very important role they play, working equines were raised under primitive conditions and their welfare was poor. Interventions to enhance their health and working life are needed.

A review on the methods for detection and identification of *Klebsiella pneumoniae* from various sources

Katlego L. Ndlovu[1], Mulunda Mwanza[1], Itumeleng Matle[2] & Lubanza Ngoma[1]

[1]*Department of Animal Health, School of Agriculture, North-West University, Private Bag X2046, Mmabatho, 2735, South Africa - katlindlovu1@gmail.com*
[2]*Bacteriology Division, Agricultural Research Council – Onderstepoort Veterinary Research, Onderstepoort, Pretoria, South Africa*

The *Klebsiella pneumoniae* complex is highly diverse both genetically and ecologically, being commonly recovered from humans, livestock, plants, food, soil, water, and wild animals. It is also a leading cause of multidrug-resistant human infections. Thus, it represents a highly pertinent taxon for assessing the risk to public health posed by animal, food, and environmental reservoirs. Although extensive reviews of methods for bacterial detection exist, most are skewed towards common bacteria such as *Escherichia coli*, despite the increasing relevance of *K. pneumoniae*. Therefore, the aim of this review was to highlight different methods for detection and identification of *K. pneumoniae* from veterinary and human clinical samples, as well as food and environmental sources. This review has shown that culture-based methods allied with new approaches are beneficial for the detection of *K. pneumoniae* in food, veterinary, and clinical settings. However, an optimal culture method and bacterial medium for recovering *K. pneumoniae* from food matrices is still debateable. The application of immunoassay methods, especially indirect ELISA for detection of antibodies to *K. pneumoniae* in animals, is reviewed. The use and benefits of nucleic acid-based PCR methods and next-generation sequencing-based methods for detection of *K. pneumoniae* and its antimicrobial determantants as well as virulence genes are also reviewed. This review has, therefore, shown that different modern methods exist for the detection of current and emerging *K. pneumoniae* strains. It provides further evidence that the full utilization of these tools can lead to the early detection and control of *K. pnuemoniae* infection, enhancing public health and reducing the frequency of disease outbreaks.

THEME: ETHNOVETERINARY MEDICINE (INDIGENOUS KNOWLEDGE)

Documentation and promotion of ethnoveterinary medicine used by amaNdebele in Nkangala District Municipality

Fikile Mbali Maseko[1], M. Mwanza[1] & R. V. Ndou[1]

[1]NWU Mafikeng campus, Private Bag X2046, Mmabatho 2745 - fikilembalimaseko@gmail.com

Ethnoveterinary medicine (EVM) is the scientific term that defines indigenous knowledge systems that are used for animal health care. The knowledge covers a wide range of practices including ethno-diagnostics, medicinal plant use, non-plant remedies and metaphysical, surgical and non-surgical procedures. This knowledge was neglected when modern veterinary medicine was introduced. However, modern veterinary medicine has its limitations including side effects, costs and inaccessibility to some farmers in poor and remote areas. Thus, in recent years, the value of EVM as a sustainable alternative is being recognised. This study concurrently documented the knowledge of EVM as practised by amaNdebele from selected (six) areas of Mpumalanga, South Africa. In addition, promoted knowledge to the youth. A mixed-method research design was adopted for the study. In first objective, qualitative research methods including the snowball sampling method and semi-structured interviews were used to document the knowledge of EVM. Thirty-one (31) medicinal plants were documented belonging to twenty-one (21) plant families, treating 24 different diseases and conditions. The family Asphodelaceae being the most common. *Aloe asborescens* Mill, *Elephantorrhiza elephantine* (Burch.) Skeels, *Euphorbia clavariodes* Boiss and *Dichapetalum cymosum* cited as the most common medicinal plants and *Dichapetalum cymosum* being poisonous and problematic. Furthermore, diarrhoea, fractures, chicken pox and dystocia are the most common diseases and conditions treated with more than one plant. Furthermore, this study also revealed elders concerns about knowledge preservation. In second objective, quantitative research methods were used to obtain and analyse the awareness, perceptions, and intervention feedback data from the youth on EVM. The study revealed an awareness of 61.9% and 97.6% interest in acquiring the knowledge and a high percentage (91.6%) of the youth would want this knowledge as part of their school curriculum. The challenges on EVM application arise because of how the know is acquired, since it is not verified and documented. In conclusion preservation and promotion of knowledge of EVM is a matter of great priority, one of the channels is the substantial addition of knowledge to the school curriculum. Further documentation of the knowledge in unexplored areas is also suggested.

- - END POSTER PRESENTATIONS - -

Thank you for joining us for the 20TH Annual SASVEPM Congress

SOUTHERN
AFRICAN
SOCIETY FOR
VETERINARY
EPIDEMIOLOGY &
PREVENTIVE
MEDICINE

20TH ANNUAL CONGRESS

SAVETCON
EVENT MANAGEMENT