

PROGRAMME & ABSTRACTS



Epi Africa

**21st Annual
SASVEPM CONGRESS**



21 - 23
AUGUST 2024



LAGOON BEACH
HOTEL, CAPE TOWN





SASVEPM EXCO 23 - 25



President:
Dr Mohamed Sirdar



Vice President:
Prof Chris Marufu



Secretary:
Dr Oonagh Pretorius



Treasurer:
Dr Itumeleng Matle



Training and capacity building:
Dr Wonderful Shumba



Communications officer:
Dr Tandile Ndobeni



Table of Contents

History of SASVEPM.....	4
Participant Information.....	10
On-site Conference Support.....	11
Foreign Delegate Information.....	12
Sponsors & Partners.....	14
Programme.....	15
Keynote Presentations.....	21
Lifetime Achievement Award.....	24
Willie Ungerer Award.....	25
Oral Presentations.....	26
Poster Presentations.....	53

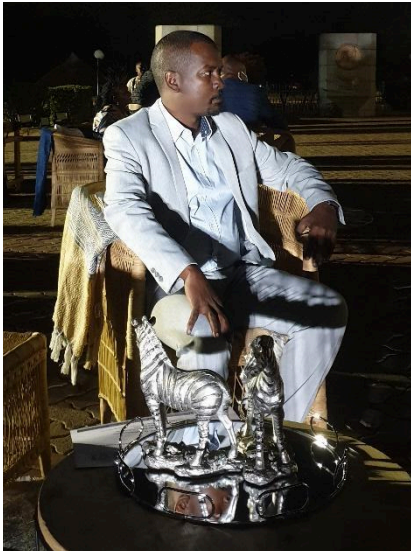
Welcome

Dear SASVEPM Members, Esteemed guests and Congress participants,

We extend our warmest welcome to you as we kick off the 21st Congress of the Southern African Society for Veterinary Epidemiology and Preventive Medicine (SASVEPM) in beautiful Cape Town, South Africa!

Africa is arguably the continent at highest risk from infectious diseases, but often struggles to implement internationally recommended veterinary surveillance and control measures successfully. This is not only due to severe resource limitations and lack of capacity, but also inexorably linked to the highly heterogeneous nature of our terrain, peoples, animals, and climate. To truly understand the complex eco-epidemiological landscapes of Africa requires creative approaches to data collection and disease surveillance, holistic control measures, participatory approaches, interdisciplinary efforts, and community involvement.

This year's SASVEPM congress features the unique problems and circumstances faced in animal health and welfare on the African continent and explores practical and sustainable local and regional solutions. We believe that only by developing Afro-centric approaches to address global problems will we have a chance at finding the sustainable solutions we need to flourish as a continent.



The 21st SASVEPM Congress serves as a strong multinational networking platform to build and foster collaborative research and enhance communication across disciplines, professions, and sectors.

Joining us in our 21st Congress anniversary is highly appreciated, and we anticipate delivering an inspiring and informative event under the theme **“Epi for Africa: Global Problems | Local Solutions”**.

We are delighted to introduce you to our distinguished keynote speakers: Dr. Locksley Messam, Prof. Daniel Nenene Qekwana and Dr. Anne Conan. These remarkable professionals are experts in their respective fields and will be sharing their insights and knowledge during the Congress.

The keynote speakers, oral and poster presentations, sponsors exhibitions, gala dinner and other activities are all designed to facilitate attendee networking, explore creative approaches to veterinary epidemiology and preventive medicine, and bolster involvement within the SASVEPM community.

We look forward to making this year's Congress a memorable and rewarding experience that warrants your return next year and continued contribution to this amazing Society!

Warm regards,

Dr. Mohamed M. Sirdar

President, SASVEPM



History of SASVEPM

How it began

SASVEPM's 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 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 society's 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 ran 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 conferences. *"We obtained sponsorship for our society from two major organisations, Bayer Animal Health and Geographical Information Systems and had the support of the 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 the SASVEPM President's 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

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

Congress #	Year	Congress theme	Place	Workshops
1 st	2001	CE: Investigating an unknown disease in a population	Onderstepoort, GP, South Africa (SA)	Disease Outbreak Investigation
2 nd	2002	CE: Theory, practice and application of surveys/ surveillance	Onderstepoort, GP SA	Risk Analysis course
3 rd	2003	CE: Economics of animal disease control	Pretoria, GP SA	
4 th	2004	CE: Evaluation of diagnostic tests	Pretoria, GP, SA	
5 th	2005	CE: One Medicine	Irene, GP,SA	
6 th	2006	CE: Epidemiology in Practice	Durban, KZN, SA	
7 th	2007	CE: Wildlife epidemiology	Somerset West, WC, SA	
8 th	2008	CE: Rinderpest & PPR. One disease of the past and one of the future	Kopanong, GP, SA	
-	2009	ISVEE 12 & SASVEPM	Durban, KZN, SA	

Congress #	Year	Congress theme	Place	Workshops
9 th	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
10 th	2012	Outbreak Investigation: Science and Intuition	Pretoria, GP, SA	Databases for vets
11 th	2013	Preventing Disease for Better Health	Salt Rock, KZN, SA	Brucellosis
12 th	2014	Innovative Epidemiology	Port Elizabeth, EC, SA	Tracing the Source Workshop
13 th	2015	Wildlife-Livestock-Community Interface	Bloemfontein, FS, SA	
14 th	2016	Epidemiology on the Edge: Economics, Trade, and Movement	Cape Town, WC, SA	
15 th	2017	SASVEPM & SAVA Joint Conference	Boksburg, GP, SA	
16 th	2018	SASVEPM & RuVASA Joint Conference	Boksburg, GP, SA	
17 th	2019	Field Epidemiology in Action	Umhlanga, KZN, SA	Epidemiology & interdisciplinary approach
-	2020	<i>No congress due to COVID-19</i>	<i>African Swine Fever - online workshop Foot and Mouth Disease - online workshop Animal Health and Economics - online workshop</i>	
18 th	2021	Creative Animal Health Solutions for Sustainable Economic Growth	Bela-Bela, LP, SA	Data Management Lab Biosecurity
19 th	2022	One Africa, One Health, One Welfare	Buffalo City, EC, SA	Rabies workshop
20 th	2023	One Health Without Borders	Gaborone, Botswana	Disease Outbreak Investigation
21 st	2024	Epi for Africa: Global Problems Local Solutions	Cape Town, WC, SA	Essential Practices in Laboratory Biosafety and Method Validation



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, 2001-2024

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 (<i>in 2013 it became the Willie Ungerer Memorial Epidemiology Prize</i>)
2014	John Grewar
2015	Grietjie de Klerk
2016	Johann Kotze
2017	Peter Geertsma
2018	Geoffrey Fosgate
2019	Cheryl McCrindle
2020	<i>No prize given</i>
2021	Michael Modisane
2022	Mpho Maja
2023	Misheck Mulumba
2024	Moetapele Letshwenyo



SASVEPM Epidemiology Prize Winners over the years





Databases for Veterinarians Workshop, Pretoria, 2012



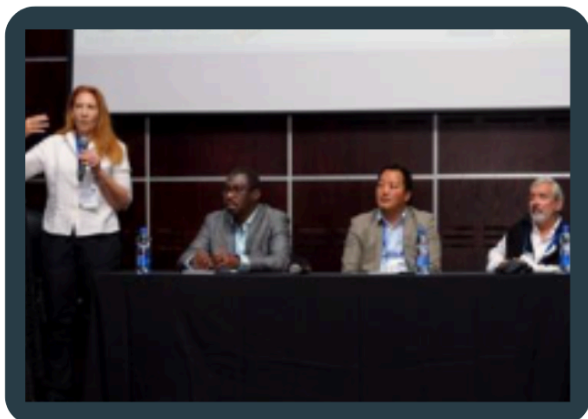
Tracing the Source Workshop, Pretoria, 2014



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



Lifetime Achievement Award:
Prof. Bruce Gummow



Willie Ungerer Epidemiology Prize:
Dr Misheck Mulumba



Gavin Thomson Award for Best Oral
Presentation: Munyaradzi C Marufu



Animal Health Technician Award: Katleho N Mosiki



Post-Graduate Award for Best Oral
Presentation: Oluyemisi A. Akerele



Best Poster Presentation Award: Tendai A. M
Mlingo



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 20 August: 17:00

Wednesday 21 August: 07:00 – 08:00

Thursday 22 August: 07:00 – 08:00

Friday 23 August: 07:00 – 08:00

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

Mrs Madaleen Schultheiss | +27 (0) 82 575 6479

Mrs Katlego Legodi | +27 (0) 76 461 1365

Mr Prosper Lukhele | +27 (0) 78 261 2561

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) 82 575 6479 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. EZShuttle is recommended. Make a booking here:

<https://www.ezshuttle.co.za/index.shtml>

myCity buses can also be used - see schedules here: <https://www.myciti.org.za/en/home/>

Flights

Should you require any assistance with flights, please approach the Registration staff.

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.

Travel, Health and Accident insurance: Every participant should buy their own travel, health and accident insurance

Electrical Supply

South Africa operates on a 230V supply voltage and 50Hz. Type M (most common) as well as Type C

Gratuity Guide

10% Gratuity (tips) is customary for services rendered at restaurants, bars, hotels, etc.

Emergency Numbers

Emergencies from Mobile	112
Emergencies from Landline	107
South African Police Service	10111
Medical & Fire	021 535 1100

Currency: ZAR

Banks

Major credit card brands, namely MasterCard and Visa, are widely accepted here, and debit cards and cheque cards, which give you access to your bank account in your home country, can generally be used over the counter and at ATMs wherever there's a MasterCard or Visa sign.

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.

Language: South Africa has 11 official languages of which three are spoken in the Western Cape. English is predominantly used in business and education

Local time: SAST

Passports: Every person wishing to enter South Africa must be in possession of a valid passport for travel to South Africa and, where necessary, a visa. (Exempt countries:

<https://www.dha.gov.za/index.php/immigration-services/exempt-countries>)

- Passengers travelling to South Africa must be in possession of a passport with two unused pages required for endorsements. The two unused pages when presented for purposes of endorsing a port of entry visa, visa, permanent residence permit, or entry of departure stamp.
- The passport must be machine readable however, the foreigner may be admitted into or depart from South Africa with a non-machine-readable passport provided that:
 - He or she is from a foreign country that is issuing machine-readable passports and has not completely phased out the non-machine-readable passports; and On entry to South Africa, a visa is considered to be a visitor's permit. The permit's period of validity is calculated from the date of entry into the country and will be set out under the heading "conditions" on the visa label.

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.

Value Added Tax

- Tax: 15% Value Added Tax

To claim 15% VAT refund for total value of goods purchased, 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.

Weather: The city has a Mediterranean climate, with rainy winters and dry summers. Cape Town is a summer paradise, with balmy temperatures and sunny days. Cape Town gets almost all its rainfall in winter, so expect warm and cloudless days but make provision for sudden cold weather.

Dress code: Dress code for the congress is Business Casual.

Sponsors & Partners

With appreciation to our 2024 Congress Sponsors & Partners



Programme

Tuesday, 20 August 2024	
17:00	Registration opens
18:00	Welcome Reception - Lagoon Beach Hotel
-19:30	
0	

Wednesday, 21 August 2024			
Time	Theme	Title	Speaker
07:00	Registration - Arrival Coffee & Tea in Exhibition Area		
	SESSION CHAIR: Dr. Mohamed Sirdar		
08:00	Opening Session	Welcome & Opening Remarks	Mohamed Sirdar (SASVEPM President)
08:30		Keynote 1: The (un)Common Sense of Epidemiologic Inference: Why Training is A Must	Locksley Messam
09:30	Epidemiological Methods	Descriptive epidemiology and spatio-temporal analysis of African swine fever outbreaks in South Africa: 2012-2023	Oonagh Pretorius
09:50		Veterinarians' perceptions of beef cattle farmer's knowledge and practices of biosecurity in Western Australia	Lebogang Mnisi
10:10		Introduction of Sponsors	Chris Marufu (SASVEPM VP)
10:20	Mid-morning refreshments		
	SESSION CHAIR: Dr. Tandile Ndobeni		
10:50	Epidemiological Methods	Evaluation of expert opinion elicitation in the context of foot-and-mouth disease control	Mohamed Sirdar
11:10		Gut microbiome of wildtype <i>Tabanus par</i> (Walker, 1854) using metagenomics approach.	Emily Emsley
11:30	Animal Welfare	Welfare status of dairy cows reared from large scale dairy farms in Midlands Province –Zimbabwe	Zivanayi Matore
11:50		Are you an ethical professional? The updated South African National Standard for the Care and Use of Animals for Scientific Purposes (SANS 10386:2021)	Bert Mohr
12:10	Special Theme	Income generation and curbing fuel costs by use of Donkeys, Mules and Horses	Benedict Mhletywa
12:30	Poster Session 1		
13:00	Lunch		
	SESSION CHAIR: Prof. Nkululeko Nyangiwe		
14:00		Context-specific solutions for African Horse Sickness in South Africa: enhancing ASD through integrated reporting	Camilla Weyer
14:20	Unique African Epidemiological Challenges & Solutions	State veterinary laboratory's role in the control of diseases: challenges and perspectives.	Mulunda Mwanza
14:40		Molecular and serological prevalence of corridor disease (buffalo associated <i>Theileria parva</i> infection) in cattle populations at the livestock/game interface of Kwazulu-Natal Province, South Africa	Sikhumbuzo Mbizeni

15:00		Dog-mediated human rabies elimination in Nigeria by 2030 - will dog markets stifle progress towards elimination?	Ukamaka Eze
15:20	Special Theme	Sharing elephant dung with traditional healers: from dung heap to beacon of hope	Lin-Mari de Klerk-Lorist
15:40		Wellness Tea	
15:50	Wellness session	How to cultivate mental-emotional wellbeing, reduce stress and anxiety, and be well from the inside out – practical tips and exercises to change your life forever	Bert Mohr
16:30		End of Day One	

Thursday, 22 August 2024			
Time	Theme	Title	Speaker
07:00		Registration - Arrival Coffee & Tea in Exhibition Area SESSION CHAIR: Dr. Oonagh Pretorius	
08:00		Keynote 2: One Health: Is Conceptualisation a Barrier to its Operationalisation?	Anne Conan
09:00	One Health Approaches: Integrating Human, Animal, and Environmental Health	A “One Health” perspective of Africa-wide distribution and prevalence of Giardia species in humans, animals and environment: A systematic review and meta-analysis	Mpho Tawana
09:20		Unravelling bacterial communities in Diptera flies from livestock kraals and residential dumping sites using metataxonomic approach	Lara de Wet
09:40		In-vitro antimicrobial activity of crude extracts of Combretum molle leaf- A One Health Approach	Joshua Ngwisha
10:00		Occurrence and characterization of Shiga toxin-producing Escherichia coli and Enteropathogenic Escherichia coli isolates from cattle and calves on communal rangeland in Gauteng, South Africa.	Mogaugedi Malahlela
10:20		Mid-morning refreshments SESSION CHAIR: Dr. Wonderful Shumba	
10:50	Disease Prevention & Control in Low Resource Settings	Enhancing Veterinary Service Provision for Smallholder Farmers in Zimbabwe: An Integrated Approach	Leonard Maposa
11:10		Knowledge of ticks and tick-borne diseases and tick control strategies among communal farmers in Mafikeng Local Municipality	Pfano Theweli
11:30		Gold sponsor presentation - OBP	
11:50	Disease Prevention & Control in Low Resource Settings	“Guilty until proven innocent”, the only way to optimize control of transboundary animal disease in South Africa, an African swine fever case report.	Agatha Raseasala
12:10		Bridging policy and science: Public-Private Partnerships revitalizing South Africa’s equine trade prospects	John Grewar
12:30		Poster Session 2	
13:00		Lunch SESSION CHAIR: Mrs. Thembakazi Xoxo	
14:00	Disease Prevention & Control in Low Resource Settings	Evaluation of the proper use of medication available over the counter by subsistence in Mpumalanga Province.	Japhta Mokoete
14:20		FAO Expert Consultation on acaricide resistance of cattle ticks: A case study of the Eastern Cape Province in South Africa	Nkululeko Nyangiwe



14:40	Special Theme	Meat safety risk of unapproved stamped carcasses sold at butcheries of Mpumalanga	Mpendulo Xashimba
14:55		Mid-afternoon refreshments	
15:15	SASVEPM AGM		
17:00		End of Day Two	

SASVEPM 21st ANNUAL CONGRESS CELEBRATION & AWARDS	
	Moyo – Kirstenbosch Botanical Gardens Dress code: Unique African Dress
17:30	First shuttle departs Lagoon Beach Hotel
18:00	Last shuttle departs Lagoon Beach Hotel
18:30	Arrival Drinks & Entertainment
19:00	Congress Dinner & Awards
21:30	First shuttle leaves back to LBH
23:00	Last shuttle leaves back to LBH

Friday, 23 August 2024			
Time	Theme	Title	Speaker
07:00		Registration - Arrival Coffee & Tea in Exhibition Area SESSION CHAIR: Prof. Chris Marufu	
08:00		Keynote 3: Antimicrobial Stewardship: understanding the African context.	Nenene Qekwana
09:00	Antimicrobial Resistance	Antibiotic quality and use practices amongst dairy farmers and drug retailers in central Kenyan highlands	Dishon Muloi
09:20		Molecular comparative study of antibiotic resistance of Salmonella enterica from animals, food and environment isolated over 62 years.	Nozipho Maphori
09:40		Genomic characterization of generic Escherichia coli from food-producing animals and products of animal origin, in South Africa	Refiloe Malesa
10:00		Antimicrobial patterns of ESKAPE pathogens isolated from the hands of students in a Veterinary Academic Hospital, South Africa.	Dikeledi Sebola
10:20		Veterinary antibiotic traces in formal and informal red meat slaughtered food animals in the West Coast District of the Western Cape	Victor Twala
10:40		Mid-morning refreshments SESSION CHAIR: Dr. Itumeleng Matle	
11:10	State of the Continent: Disease rich, data poor	Analysis of mannose-binding lectin protein and mRNA levels on selected chicken breeds in South Africa	Peter Ayodeji Idowu
11:30		The bacterial community harboured by Amblyomma hebraeum ticks from livestock in North West Province, South Africa	Kealeboga Mileng
11:50		Bacillus anthracis in South Africa, 1975-2013: are some lineages vanishing?	Kgaugelo Lekota
12:10		Temporal and Serotypic Dynamics of Actinobacillus pleuropneumoniae in South African Porcine Populations: A Retrospective Study from 1985 to 2023	Emmanuel Seakamela
12:30		Poster Session 3	
13:00		Lunch SESSION CHAIR: Dr. Nyeleti Manganyi	

14:00	State of the Continent: Disease rich, data poor	Rift Valley fever: questioning dogma and debunking myths	Peter Thompson
14:20		Retrospective Analysis of Serotype Distribution in <i>Mannheimia haemolytica</i> , <i>Pasteurella multocida</i> , and <i>Bibersteinia trehalosi</i> Isolates: Insights from 50 Years of Specimen Data at Onderstepoort Veterinary Research Laboratory.	Itumeleng Matle
14:40	Wildlife Epidemiology	Tuberculosis in a Skukuza vervet monkey troop – a monkey on the back of the One Health concept?	Lin-Mari de Klerk-Lorist
15:00		Species composition of ticks (Acari: Ixodidae) infesting selected wild ungulates from two protected wildlife management areas in Northern Botswana	Obuile Owen Raboloko
15:20		Black-backed jackal-associated rabies case in white rhino from North-West Province, South Africa	Chuene Ernest Ngoepe
15:40		Translocation risk assessment model for white rhinoceroses (<i>Ceratotherium simum</i>) from wildlife populations infected with tuberculosis, South Africa	Oonagh Pretorius
16:00	Closing Ceremony	Closing, vote of thanks, awards	Mohamed Sirdar & Oonagh Pretorius
16:30		End of Congress	

OFFICIAL CONGRESS CELEBRATION & AWARDS

Venue: **Moyo - Kirstenbosch Botanical Gardens**
 Time: **18:30**
 Dress code: **Unique African Dress or Semi-formal**



POSTERS

12:30 Wednesday, 21 August 2024

Poster Session 1 :

<u>Abstract</u>	<u>Title</u>	<u>Speaker</u>
4	Prognostic indicators of survival in dogs with clinically suspected canine distemper infection in Harare, Zimbabwe	Takudzwanashe Matiza
7	Husbandry practices among peri-urban free-roaming pigs in Gert Sibande District Municipality, Mpumalanga Province, South Africa	Priscilla Munzhelele
25	Student Voice in the Development of a Pedagogic Model for Integrating Ethnoveterinary Medicine into the Curriculum of Animal Health Education	Rendani Victress Ndou
28	Systematic review on traditional medicinal plants used for the treatment of livestock diseases in the Eastern Cape Province	Siza Mthi
30	Prevalence and associated risk factors of Cryptosporidium in domesticated ruminants in the Rust de Winter area, Gauteng Province, South Africa	Tebogo Atlivia Seanego
34	Evaluation of the qualitative economic impact of African swine fever virus outbreaks using the Outcost tool in the Mpumalanga Province, South Africa	Taelo Sibi
44	Detection of Theileria haneyi in South African equids using a newly developed quantitative real-time PCR assay.	Tshenolo Mbaba
46	Knowledge, attitude and practices: an investigation and assessment of the medicinal plants' potential to heal wounds in communal cattle at Ephraim Mogale Municipality, Limpopo Province	Malebo Lekgethisho
60	Comparison of the Bionote NSP Ab ELISA and Priocheck FMDV NS ELISA	Khomotso Moabelo
61	Construction of three foot-and-mouth disease virus peptide phage display libraries as a tool for the identification of important epitopes	Naledi Sekgobela
68	Conservation and economic benefits of medicinal plants used to treat livestock ailments in the Eastern Cape Province, South Africa	Nwabisa Nongauza
70	The effect of the COVID-19 pandemic on vaccination of domestic dogs and incidence of canine parvoviral disease in Pretoria, South Africa	Josef Hanekom
78	Comparing udder health status in cattle belonging to small-scale farmers in Eastern Cape and Gauteng provinces, South Africa	Nyeleti Manganyi

12:40 Thursday, 22 August 2024

Poster Session 2:

<u>Abstract</u>	<u>Title</u>	<u>Speaker</u>
1	Knowledge, attitudes and practices of communal goat farmers towards the control of gastrointestinal nematodes	Khanyisani Ndwandwe
10	Dog - mediated Human Rabies Elimination in Kenya: Status, and assessment of knowledge, attitude, and practices of Rabies Elimination Strategy implementation in Selected Counties.	Ruphline Anyango
12	Histology of the gizzard and proventriculus of indigenous chickens fed wheat offal-based diet supplemented with maxigrain and polyzyme	Babatunde Falana
29	In the light of one health approach, a general overview of zoonotic impacts of West Nile virus in Africa	Ahmed Ibrahim
32	Tick control measures and tick infestation levels on communal cattle: a case study of Sinthumule – Kutama Area, Limpopo Province	Makhado Sedina
33	Temporal changes in the prevalence of Staphylococcus aureus colonisation among humans in South Africa: Retrospective study from 2013 to 2017	Onalenna Mabalane
37	Coagulase Positive Staphylococcus aureus Isolated between 2010 and 2014 from specimens submitted to diagnostic laboratories in Mpumalanga Province, South Africa.	Mojaki Nyabela
38	Tuberculosis at the wildlife/livestock/human interface in southern Bushbuckridge, Mpumalanga, South Africa	Oupa Rikhotso
41	Seroprevalence of bovine brucellosis and risk factors associated with occurrence of the disease in cattle in Dr. Kenneth Kaunda District of North West Province	Eunice Matome
43	The impact of comorbidities and physiological conditions on the burden of food-borne disease: A case study of rural Eastern Cape, South Africa.	Nandisa Ndlame
63	Evaluation of a commercial probiotic on the biological performance of Nile tilapia (Oreochromis Niloticus) during sex-reversal and extended nursing in Kenya	Gugulethu Moyo
73	Genome Sequences of the Fifteen Bluetongue Virus Vaccine Strains Incorporated in the South African Live-Attenuated Vaccine	Tendai Mlingo
83	Evaluation of overdose safety of Lumpy Skin disease vaccine	Sbahle Zuma

12:30 Friday, 23 August 2024

Poster Session 3:

<u>Abstract</u>	<u>Title</u>	<u>Speaker</u>
2	Safety and Immunogenicity of the serotype-reduced Bluetongue vaccine in sheep	Ntombikayise Nkomo
11	Antimicrobial use and practice in aquaculture production systems in Nairobi, Kenya	Elvis Waga
18	Bacterial pathogens associated with bovine mastitis and their antimicrobial resistance profiles in the JB Marks Municipality of North West Province, South Africa	Cecilia Sizana-Kgaje
24	Antibiotic resistance patterns, virulence gene profiles, and genetic diversity of Salmonella enterica subsp enterica serovar Typhimurium isolated from the environment, animal and food products in South Africa (1999-2021)	Nkagiseng Moatshe
36	Prevalence of Staphylococcus pseudintermedius species isolated from canine specimens submitted to a veterinary diagnostic laboratory in South Africa, 2012 – 2017	Themba Sigudu
53	Ticks population dynamics (Acari: Ixodidae) on and of bovine hosts	Mandla Yawa
54	Whole genome-based analysis revealed novel sequence types of Klebsiella pneumoniae, K. variicola and K. michiganensis from sheep and goat faeces as well as water sources in Matlwang, Potchefstroom	Tshepang Motlhaping
55	Molecular detection of Coxiella species from sheep ticks in Matlwang, Potchefstroom	Jody Howard
56	Antimicrobial sensitivity testing of preserved S. enterica and E. coli isolates from 2000 to 2021 in the agricultural sector	Masabata Motaung
69	Molecular identification and characterization of selected food-borne pathogens in imported dried fish sold in informal markets around Gauteng province in South Africa.	Rendy Nkosi
76	The occurrence of gastrointestinal parasitic infections in sheep and goats in the Eastern Cape, South Africa.	Mlungisi Jansen
77	Distribution of slaughtered of bush and warthog pigs in Gert Sibande District and disease spread risks	Mpendulo Xashimba
80	Systematic Reviews of Epidemiology of Porcine Cysticercosis in South Africa from 2003 to 2023	Naomi Masango

Keynote Presentations

The (un)Common Sense of Epidemiologic Inference: Why Training is A Must

Dr. Locksley Messam

School of Veterinary Medicine, University College Dublin, Ireland



Biography: Dr. Messam is a tenured lecturer at University College Dublin's School of Veterinary Medicine. He is a veterinary epidemiologist with both methods-related and applied research interests, including epidemiologic study design, the validation and application of diagnostic tests and the effects of human-animal interactions on human health and wellbeing. A staunch advocate of the application of epidemiologic approaches to study design, data analysis and inferences, he maintains that studies claiming to be epidemiologic in nature, should be designed, conducted, and make inferences in ways that are recognisably consistent with the central concepts and methods of the discipline.

Having conducted research in Europe, North America and the Caribbean, Dr. Messam has substantial experience in the efficient conduct of epidemiologic studies requiring empirical data collection in a variety of cultural contexts. A native Jamaican, he is a graduate of the University of the West Indies, Jamaica, University of Veterinary Sciences, Hungary, and the University of California Davis, USA, where he did his undergraduate, veterinary and doctoral studies, respectively. A firm believer that formal training in epidemiology is invaluable to grasping the discipline's approach to inference, he has taught epidemiology to veterinary and graduate students in the Caribbean, North America and Europe and has conducted a number of workshops on epidemiologic methods at the Society for Veterinary Epidemiology and Preventive Medicine's (SVEPM) conferences. Since 2022, Dr. Messam has also been a member of SVEPM's executive committee.

Abstract:

It is a common view that basic intelligence and/or scientific training is enough to make sound epidemiologic inferences. This was evident worldwide during the recent Covid-19 pandemic, with social media, the news and scientific articles replete with the opinions of armchair epidemiologists on, among other things, the pandemic's cause, the vaccines' safety, and the most current R_0 for SARS-CoV-2. Indeed, the word "epidemiology" and its derivatives are widely used by the untrained public in everyday discussions about disease.

What is not widely appreciated is that epidemiology is a well-defined discipline with its own approach and body of methods, and that sound epidemiologic inference depends on both being applied correctly. It is not understood, that applying common sense in making epidemiologic inferences is only helpful if it is supported by a knowledge of epidemiologic methods and that this knowledge only comes from being trained in the discipline (Rothman, 2002).

The aim of this talk is to show, that the application of just common sense is not only inadequate for making correct epidemiologic inferences but also leads to incorrect conclusions. Using examples from bovine Brucellosis, I first contrast common sense conclusions with those resulting from an understanding and application of epidemiologic principles and methods. I follow this with a brief discussion of why this

misunderstanding about epidemiology persists, and then close with suggestions of helpful approaches to epidemiologic training, primarily for non-epidemiologists working in the discipline.

Bibliography

Kenneth J. Rothman (2002) *Epidemiology: An Introduction*. Oxford University Press

WEDNESDAY 21 AUGUST: 08:30

One Health: Is Conceptualisation a Barrier to its Operationalisation?

Dr. Anne Conan

CIRAD: Southern Africa, Harare, Zimbabwe



Biography: Dr. Anne Conan is a researcher in epidemiology at the French Agricultural Research and International Cooperation Organization (CIRAD, France) and is attached to the Research Platform - Production and Conservation in Partnership ([RP-PCP](#)) based at the University of Zimbabwe. She specializes in infectious diseases and zoonoses in low-income areas.

Her main research topics include the surveillance of infectious diseases at the wildlife interface, the consequences of intensification of chicken farming in Asia ([One Health Poultry Hub](#)), the epidemiology of African swine fever in pigs, the epidemiology of *Coxiella burnetii* in humans and livestock, and the control of rabies in humans and dogs. She is a research fellow at the [One Health](#)

[Research Foundation](#).

Dr. Conan completed her DVM and MSc in epidemiological surveillance in 2008. She worked at the Public Health and Epidemiology Department in Pasteur Institute in Cambodia for five years. After completing her PhD in Epidemiology in 2013, Dr Conan started a post-doctorate fellowship at the Department of Veterinary Tropical Diseases at the University of Pretoria (South Africa). She then joined Ross University School of Veterinary Medicine (St. Kitts and Nevi, West Indies) in 2015 as a post-doctorate fellow before becoming an Assistant Professor in Epidemiology. After spending three years at City University of Hong Kong as research assistant professor and then research associate professor, she joined CIRAD in November 2022.

Abstract: Emerging from the concept of & One Medicine & developed by Dr. Calvin Schwabe, the term & One Health & began its conceptualization more than 20 years ago with the SARS and H5N1 epidemics and the formulation of the 12 Manhattan Principles. Since then, numerous researchers and organizations have developed opinions and created diagrams to define One Health. The Tripartite, later expanding to the Quadripartite, followed this trend and established the OHHLEP (One Health High Level Expert Panel), which officially defined One Health in 2023. They also developed the Theory of Change for One Health, which is used in the Quadripartite OH Joint Plan of Action. Unfortunately, despite these definitions and guidelines, the operationalization of One Health still faces various challenges. The focus on zoonotic diseases shows the misunderstandings and misinterpretation of the concept among funders, governments, and researchers. Thus, One Health actors still report two main barriers to operationalisation: the work in silos, often excluding ecosystem health, and the lack of institutionalisation. In Africa, however, some countries, such as Kenya, Senegal, Rwanda, and Cameroon, have already institutionalized One Health, while others have begun the process with the assistance of projects like COHESA (Capacitating One Health in Eastern and Southern

Africa) and/or the Quadripartite. As the institutional barriers have been gradually overcome, the conceptualization and operationalization of ecosystem health within the One Health approach remain the next challenge.

THURSDAY 22 AUGUST: 08:00

Antimicrobial Stewardship: understanding the African context

Dr. Nenene Qekwana

Department of Paraclinical Sciences, Faculty of Veterinary Science, University of Pretoria, South Africa



Biography: Dr. Daniel Nenene Qekwana is a recognized specialist in veterinary public health and an associated professor in the Department of Paraclinical Sciences at the Faculty of Veterinary Science, University of Pretoria where he is involved in teaching and training of undergraduate and postgraduate students in epidemiology, food safety, zoonotic diseases, and public health. After completing his PhD in epidemiology, he has conducted research on various topics including spatio-temporal changes in disease outbreaks, drivers of antimicrobial resistance in humans and animals, and the impact of policy decision/formulation from a justice perspective.

Dr. Qekwana is currently the Head of the Department of Paraclinical Sciences and a member of the Faculty of Veterinary Sciences research ethics committee. He has served as part of the Ministerial Advisory Committee on Antimicrobial Resistance (MAC-AMR) until the end of 2023 and continues to

serve as a member of the Gauteng Provincial Antimicrobial Stewardship Committee.

FRIDAY 23 AUGUST: 08:00

Lifetime Achievement Award

The Southern African Society for Veterinary Epidemiology and Preventive Medicine would like to honour **Dr. Sewellyn Davey** for her dedication to the South African Veterinary Services and the invaluable contribution she made to veterinary disease control and public health throughout her career.

Dr. Sewellyn Davey



After majoring in Microbiology and Zoology for a Bachelor of Science degree in 1975, Dr. Davey graduated with a Bachelor of Veterinary Science in 1980 from the Onderstepoort Veterinary Faculty of the University of Pretoria. Early in her career, she was stationed at first at Ermelo, Mpumalanga, and later in Kroonstad, Free State. As a laboratory vet in these regional laboratories, she concentrated on disease investigation and diagnosis and in 1982 headed up the serology section in the Kroonstad Laboratory. In 1987 Sewellyn was appointed State Veterinarian for Animal Health in Malmesbury in the Western Cape. Disease control was her mandate. Sewellyn has consulted in South Africa and abroad. She served on the OIE ad hoc committee tasked with the rewriting of the Terrestrial

Code chapters on Brucellosis and Tuberculosis. From 2016 until 2020 she was chairperson of the Ministerial Technical (Min Tech) Working Group on bovine brucellosis, and member of the Min Tech working group on bovine tuberculosis. She was an inspirational leader while in her post and always provided support and advice in the veterinary field to her younger colleagues. She had wonderful rapport with her Animal Health Technicians and always encouraged them to further their knowledge in disease control. In 2020 she retired from government service. She then registered with the South African Veterinary Council and is a private consultant for bovine brucellosis, MAP and bovine TB; to assist her colleagues with the diagnosis, management and control of these diseases.

Willie Ungerer Award

The Southern African Society for Veterinary Epidemiology and Preventive Medicine are honoured to announce the recipient for the 2024 Willie Ungerer Award:

Dr Moetapele Letshwenyo

Dr Moetapele Letshwenyo is the current World Organisation for Animal Health (WOAH) Sub-Regional Representative for Southern Africa (or SADC) countries. He is a veterinarian by profession, with a Bachelor's Degree in Veterinary Medicine and Surgery from Edinburgh University, a Master of Preventive Veterinary Medicine from the University of California, Davis and a Masters of Business Administration from the University of Botswana. For most part of his veterinary career, he worked for the Department of Veterinary Services of Botswana primarily as a field veterinarian in several veterinary districts, such as Francistown, Selibe Phikwe, and Maun, before settling at Ministry Headquarters initially as the Department epidemiologist. In this role, he was responsible for all sanitary and phyto-sanitary matters and assisted in setting up the Veterinary Epidemiology and Economics Unit which was responsible for establishing the livestock identification and traceability system (LITS) of Botswana in 2001, among others.



He coordinated the control and eradication of several outbreaks of foot and mouth diseases in the country and made presentations and talks on animal disease control in Botswana at conferences and seminars worldwide, organized by various international organizations such as OIE, FAO, AU IBAR, SADC, etc. He was a member of various technical committees of these Organisations.

All this culminated with an award of a "Meritorious Honour" by the then OIE (now World Organisation for Animal Health). This medal is awarded "in recognition of outstanding technical, scientific and administrative contribution to the field of veterinary science and animal disease control". He progressed to become the Director of Veterinary Services and OIE (WOAH) Delegate for Botswana in 2008.

In 2009 he became a Deputy Permanent Secretary in the Ministry – a policy level assignment, which was broader than just veterinary work, as it encompassed animal production and agribusiness. He held this position until joining the World Organisation for Animal Health (commonly called OIE: Office International des Epizooties) as the Sub-Regional Representative for Southern Africa in 2014.

The World Organisation for Animal Health is a standard setting body on matters of animal health, welfare and veterinary public health (zoonosis). It works closely with member countries, through the Veterinary Services to ensure compliance to international standards, in order to facilitate safe trade in animals and their products. As the sub-regional representative Dr Letshwenyo is responsible for driving the mandate and



representing the OIE in the sixteen member countries of the SADC sub-region, as well as in meetings with Collaborating Partners.

He has been an active member of SASVEPM and participated in the last two congresses as Keynote speaker and supports the organization in releasing technical staff to support SASVEPM workshops.

Scientific Publications

1. M. Letshwenyo, N. Mapitse and J. M.K. Hyera; A case of foot-and-mouth disease in a kudu in Botswana. *Veterinary Record* (In Print)
2. M. Letshwenyo, M. Fanikiso & M. Chimbombi – “The Control of Foot-and Mouth Disease in Botswana: Special Reference to Vaccination” published in *Development in Biologicals* (2005); Vol. 119. Pages 403-411.
3. E.K. Baipoledi, J.M.K. Hyera, G. Matlho, M. Letshwenyo, M. Chimbombi, E.K. Adom and D.J. Paton. Re-emergence of Foot-and-Mouth Disease (FMD) in Botswana: Disease outbreak, virus isolation, typing and characterization
4. M. Letshwenyo & K. Kedikilwe – “A goat-sheep hybrid born under natural conditions in Botswana” published in the *Veterinary Record* (June 2000)
5. Main author in the dossiers submitted to the OIE for the re-instatement of the “FMD Free Zone Without Vaccination”, following the 2002 & 2003 FMD outbreaks in Botswana.
6. J. M.K. Hyera; M. Letshwenyo, K.B. Monyame, G. Thobokwe, A.R. Pilane, N. Mapitse and E. K. Baipoledi. A serological survey for antibodies to foot-and-mouth disease virus in indigenous Tswana goats and sheep in Kasane, Maun and Shakawe districts in north-western Botswana. *Onderstepoort Journal of Veterinary Research*, 73: 143 – 147 (2006).
7. Co-published several papers on rabies control in Namibia.



Oral Presentations

in order of appearance as on the programme

THEME: **Epidemiological Methods**

Descriptive epidemiology and spatio-temporal analysis of African swine fever outbreaks in South Africa: 2012-2023

Oonagh Pretorius¹, Jose Pablo Gomez Vazquez¹ & Carlos Gonzalez-Crespo¹

¹*Center for Animal Disease Modeling and Surveillance, University of California, Davis.*

A need for improved understanding of ASF epidemiology and updated spatiotemporal studies has been identified to evaluate the recent occurrence of multiple outbreaks in South Africa (SA) and identify key areas for intervention.

Study objectives were to describe the epidemiology of historical ASF outbreaks in SA from 2012 to 2023 and investigate the presence of spatiotemporal clustering to identify effective strategies for controlling and eradicating the disease.

Data were extracted from national biannual disease reports submitted to WOAHA over the past 11 years. Point data were compiled and explored in Microsoft Excel and all maps were generated in ArcGIS Pro 3.2.1 using a Gauss conform projection with the Hartbeesthoek 1994 geodetic datum.

To evaluate the presence of clusters of high rates of disease we used the space-time permutation scan statistic in SaTScan. The temporal window was set to 36% of the study window. Maximum spatial cluster size was 50% of population at risk and maximum reported spatial cluster size was set to a circular area with a radius of 250km. P-values less than 0.05 were considered statistically significant.

Eleven ASF outbreaks were reported consisting of 271 events at 175 unique locations, affecting areas outside the ASF Control zone of 8 Provinces. Outbreak duration varied from ten to upwards of 1484 days. Median event duration was 202 days. 19179 cases were reported in domestic pigs and one bushpig. 27 highly significant (p-value < 0.000001) spatiotemporal clusters were identified.

Temporal visualisation of outbreak events indicates increasing extent and severity of ASF outbreaks each year. Spatiotemporal cluster radii were of such size and number that identifying key areas for intervention was not possible. Rather, the analysis clearly illustrates that outbreaks of this disease are of national concern. Current policy and control strategies should be evaluated for appropriateness to the current disease outlook.

WEDNESDAY, 09:30

Veterinarians' perceptions of beef cattle farmer's knowledge and practices of biosecurity in Western Australia

Lebogang Mnisi^{1,2}, Kirsty Bayliss², John Edwards²⁻³

¹. *Potchefstroom Food Security, Agriculture District Centre, Chris Hani Street, Potchefstroom, 2531*

². *Murdoch University, Food Security Department, 90 South St, Murdoch WA 6150*

³. *Ausvet Pty Ltd, 5 Shuffrey St, Fremantle WA 6160*



Effective biosecurity measures are crucial for livestock producers to protect the Australian animal industry from diseases. The study conducted, aimed to assess how Western Australian veterinarians perceived local cattle farmers' knowledge, understanding, and practices on biosecurity.

This research project used mixed methods including literature reviews, meta-analysis, and policy examination. Questionnaires were distributed to eleven biosecurity expert veterinarians from different sectors in Western Australia (WA). The calculated sample size for the study was 301, and the questionnaire was sent to the respondents. However, the response rate was only 16% as such the study had to apply a contingency plan to account for this limitation targeting veterinarians that provides services for the 301 prospective respondents who never fully responded to the survey.

Considering the fact that getting response through the administration of questionnaires was very poor. It is well noted that future study should consider the participatory approach to address this limitation. Data was analysed using Microsoft Excel 2013, NVivo queries, and explores. The small number of participants (n=11) limited the study to descriptive analysis.

The study revealed that many beef farmers lack a proper understanding of biosecurity and fail to take necessary measures to ensure it on their farms. Although WA has biosecurity measures and policies in place, producers have low adaptation to quality assurance programs like the Livestock Assurance Program and J-BAS. However, producers conform to National Livestock Identification and Vendor Declaration systems without fail. Findings from this study suggest a need to improve farmers' understanding of on-farm biosecurity through improved interaction with veterinarians.

WEDNESDAY, 09:50

Evaluation of expert opinion elicitation in the context of foot-and-mouth disease control

Mohamed Sirdar and G. T. Fosgate ²

¹World Organisation for Animal Health, WOAHS Sub-Regional Representation for Southern Africa, Gaborone, Botswana

²Epidemiology Section, Department of Production Animal Studies, Faculty of Veterinary Sciences, University of Pretoria, Onderstepoort, 0110, South Africa

In South Africa, foot-and-mouth disease (FMD) is a controlled disease in accordance with the South African Animal Diseases Act (Act 35 of 1984). The FMD Veterinary Procedural Notice (VPN) stipulates disease control measures including restriction of susceptible animal movement and products, prophylactic vaccination of cattle, clinical surveillance of susceptible species, and disease control fencing to separate livestock from wildlife reservoirs. The FMD protection zone with vaccination (PZV) of Mpumalanga and Limpopo Provinces had a total of 223 dip-tanks and during the period between 2007-2016, reported a total of 998 cattle FMD cases. These cases occurred within six outbreaks affecting a total of 29 dip-tanks with all outbreaks attributed to infection with Southern African Territories (SAT) serotypes.

The objective of this study was to evaluate differences in expert opinion predictions to actual reported outbreaks as a validation criterion.

All reported SAT FMD cases in domestic cattle from 2006 to 2016 in the PZV for both Limpopo and Mpumalanga Provinces of South Africa were identified. The unit of analysis (case) was defined as the affected/non-affected dip-tank.

Eleven risk factors important for FMD occurrence and spread were used to build a weighted linear combination (WLC) score based on expert opinion elicitation. Pairwise comparisons were conducted by ten experts based on their own assessment of the evidence available in the literature and personal experience. Analyses were performed for FMD occurrence and spread independently. Smoothed Bayesian kriged maps

were generated for individual risk factors, as well as the overall WLC scores for FMD occurrence and spread. Data generated from experts' prediction were extracted for each dip tank using the zonal statistics tool of the ArcGIS (version 10.4 ESRI, Redlands, CA, USA). Individual risk factor and WLC scores were compared between outbreak and non-outbreak dip-tanks using a Mann–Whitney U tests. Statistical analysis was performed using SPSS 24.0 for Windows (SPSS Inc. Chicago, IL, USA) and results were interpreted at $p < 0.05$.

Expert opinion suggested that FMD occurrence was influenced predominantly by proximity to game reserves and cattle density. Cattle populations and vaccination practices were considered most important for FMD spread. Vaccine matching was also believed to have a great influence on FMD occurrence and spread. This study supports expert-opinion elicitation exercises as a reliable measure for obtaining information to support disease control.

WEDNESDAY, 10:50

Gut microbiome of wildtype *Tabanus par* (Walker, 1854) using metagenomics approach.

Emily Emsley¹, Moeti Taioe^{1,2}, Tsepo Ramatla^{1,3}, Kgagelo Lekota¹, Oriel Thekiso¹

¹*Unit for Environmental Sciences and Management, North-West University, Potchefstroom, 2531, South Africa*

²*Epidemiology, Parasites and Vectors, Agricultural Research Council – Onderstepoort Veterinary Research, Onderstepoort, 0110, South Africa*

³*Centre for Applied Food Safety and Biotechnology, Department of Life Sciences, Central University of Technology, 1 Park Road, Bloemfontein, 9300, South Africa*

The horse fly, *Tabanus par*, is amongst economically important hematophagous pests of livestock and wildlife. Horse flies are required blood feeders, and although they also carry diseases, they need the help of microflora to metabolize the blood diet. This study was aimed at identifying the gut microbiome of *T. par* using shotgun metagenomics sequencing from 60 adult pooled DNA flies collected at Charters Creek in KwaZulu-Natal Province. Metagenomics analysis of *T. par* showed that the most abundant bacteria phyla was Pseudomonadota (59%) of which genus *Aeromonas* (25%) was identified as the most prevalent assigned genus, consisting of pathogenic species *A. hydrophila* (12%). *Acinetobacter* spp. (12%) was the second most prevalent bacterium, with *A. johnsonii* and *A. schindleri* making up 8% of the species that were determined. *Trichoplusia ni* TED virus (17%) and *Vespertiliovirus* (15%) were the most abundant phages identified belonging to the family of Metaviridae and Plectroviridae, respectively. Plasmids in abundance included *Burkholderia vietnamiensis* (10%) *Escherichia coli* O85:H1 (5%) and *Acinetobacter pittii* (5%). The prevailing fungal was a saprobic species of *Synchytrium microbalum* (3%). This study has pioneered the detection of bacterial, viral, and fungal genera of "One Health" and symbiotic relevance in *T. par*. This finding expands on our knowledge of the microbial species that *T. par* carries and opens up new avenues to investigate the role of phages, and pathogens play in vertebrate hosts during blood meals.

WEDNESDAY, 11:10



Welfare status of dairy cows reared from large scale dairy farms in Midlands Province –Zimbabwe

Zivanayi Matore, Pamela SA Woods, Tonderai Mutibvu

University of Zimbabwe, Department of Livestock Sciences, Faculty of Agriculture, Environment and Food Systems Harare, Zimbabwe

In Zimbabwe a lot of studies have been done on nutrition, breeding, physiology and health of farm animals but with little or no consideration of the impacts of these studies on animal welfare. The aim of this study was to evaluate the welfare status of dairy cows from large scale dairy farms through an assessment of risk factors/drivers and indicators of animal welfare. For this study 728 dairy cows from all the 31 large scale dairy farms in Midlands Province, Zimbabwe were selected for the study noting down risk factors and indicators of dairy cow welfare during both the dry and rainy season. Human 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 ($\chi^2=115$, DF=9, $P<0.0005$). From the study 95% of the cows examined were not lame (score 1) and for those that were lame only 0.6 % (n=4) had severely impaired mobility (score 5). Whereas 30 % of the cows observed during the rainy season were heavily soiled with manure (score 4), only 1% of the cows observed during the dry season were heavily soiled (score 4). Cow cleanliness was significantly associated with manure accumulation in housing and handling facilities in both study 1 ($\chi^2=18$, DF=6, $P=0.006$) and study 2 ($\chi^2=47$, 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 study 1 and study 2 was fair (BC=3) and body condition was significantly associated with the breed of animal in both study 1 ($\chi^2=22$, DF=12, $P=0.039$), and study 2 ($\chi^2=38$, DF=12, $P<0.005$). Exotic breeds like the Holstein generally fared low when compared to locally adapted breeds like the Ayrshire.

WEDNESDAY, 11:30

Are you an ethical professional? The updated South African National Standard for the Care and Use of Animals for Scientific Purposes (SANS 10386:2021)

Bert Mohr, BVSc(Hons), MMedVet(Med), DPhil (Oxford), Diplomate ECVIM-CA
Scientific Veterinary Consulting Inc. <https://scientificveterinaryconsulting.com>

Would you like peace of mind in your care and use of animals in research, testing and teaching?

Come learn about the core principles of the updated South African National Standard for the Care and Use of Animals for Scientific Purposes (SANS 10386:2021) - the minimum standards for animal care and use in research, testing, teaching, training, validation, diagnostics, field trials, observation, and the production (breeding) of animals for related purposes in South Africa.

Essential knowledge and skills required to oversee and conduct ethical, responsible, and impactful scientific activities with animals - for Animal Ethics Committee members, research managers, principal investigators, scientists, students, veterinarians, para-veterinary professionals, facility & laboratory managers, and animal caretakers

Do you know about the new foundational principles, preserving the dignity of animals?



Are you aware of the specific requirements for the education and training of scientists, students, animal caretakers and Animal Ethics Committee members?

Do you need to update your Animal Ethics Policy, Terms of Reference, SOPs and Forms of your Animal Ethics Committee (AEC), but don't know where to start?

Are you compliant with the requirements for an independent external review of institutional operation (i.e., governance, AEC & facilities) at least every 4 years?

Come learn more about this fascinating field - and see why it's actually really cool to be compliant.

WEDNESDAY, 11:50

SPECIAL THEME: Success Stories

Income generation and curbing fuel costs by use of Donkeys, Mules and Horses

Benedict Mhletywa

Introduction: The use of donkeys, mules and Horses in rural areas is predominantly seen practiced in some rural areas to ensure that household does not remain without something to do and generate income for the health of the home. The practice of using animals is taking place through partnership that is between the farmers that own animals and those who are in need of them to perform household activities in rural areas of Qumbu. Since the household head have responsibilities on ensuring that the household chores are kept functional in all times. Among the activities performed by the animals both agricultural and non-agricultural includes the following: Ploughing, planting, cultivation, fire wood, rhex, sand, water, maize and manure.

Purpose: The main purpose is to share the use of Donkeys, Mules and Horses to perform agricultural and non-agricultural activities in some rural areas of Qumbu. To know what activities performed by Donkeys, Mules and Horses in the household livelihood. To find out how Donkeys, Mules and Horses used to generate income. To determine the difference in using fuel using transport against donkeys or mules. To see if there is assistance from government if not what can be done for them.

Method or Data sources: The method of collecting data done through identification of farmers who own animals and those who hire from them. The total number of farmers interviewed from the structured questionnaire that was developed were 30, 15 of those who own animal and 15 of those who hire the owners. The questionnaire was designed to suit both groups with parameters designed to gather relevant information. Factors that were covered in the questionnaire include the demographics, social, economic, risk and other factors to broaden the information that the author would like to depict in the entire exercise. Since the topic could not be the first time to be presented, available literature will be reviewed to enrich the topic with the relevant citation.

Results: The findings on the income generated has been shown as something possible in household through the use of donkeys, horses and mules used in agricultural and non-agricultural activities. It has been evident the fact horses are contributing higher income followed by donkeys and mules contributed lower income. In terms of the parameter set to find the practice of animal against fuel using transport. The animal use found to be the cheapest against the fuel using transport.

Conclusion: The use of Donkeys, Mules and Horses in rural areas is one of the practiced activities to enable living and sustaining livelihood in a less cost. Looking at issues like high cost of living, high cost of fuel and other related socioeconomic constraints found that this practice may contribute relief to the aforementioned issues through savings spend lesser than the situation warrant outside. In elaboration to the factors and issues raised in the entire document linked to the theme of the congress Epi for Africa: Global Problems Local Solutions linked to local success stories sub theme.



WEDNESDAY, 12:10

SPECIAL THEME: Unique African Epidemiological Challenges & Solutions

Context-specific solutions for African Horse Sickness in South Africa: enhancing ASD through integrated reporting

Camilla Weyer, John D. Grewar¹

¹*South African Equine Health and Protocols NPC, Baker Square, Paardevlei, Cape Town, 7110, South Africa; camilla@sae hp.com; john@sae hp.com*

South Africa maintains an African horse sickness (AHS) free zone in the southwestern part of the country to support horse exports. This zone is safeguarded by stringent movement controls, requiring permits only from areas designated as low-risk by the resident State veterinarian through an AHS Area Status Declaration (ASD). This classification depends heavily on epidemiological data, notably the reporting of confirmed and suspected AHS cases from the origin area and its surroundings.

Currently, all laboratory-confirmed cases are reported to the permit-issuing body by laboratories, significantly influencing the ASD classification. A major limitation, however, is the delayed reporting of non-laboratory confirmed cases, documented monthly at the provincial level and not formally shared with the Western Cape permit authority. Although mitigation measures, like mandatory laboratory testing for at least one case per State Vet area, are in place, gaps still occur. For example, during the 2023 AHS outbreak in the Eastern Cape, 177 cases were reported through the government system, but only 9 through the ECOD system used for ASD. Horse movements from the informal sector in the Eastern Cape are rare, minimizing the risk of AHS spreading into the controlled area.

Improving the integration between formal laboratory reports and monthly disease reporting could substantially enhance the robustness of the ASD risk-based system, thereby strengthening disease control across South Africa. Employing risk-based movement control approaches is crucial for managing endemic diseases in African countries, where zonal strategies are essential for facilitating trade.

WEDNESDAY, 14:00

State veterinary laboratory's role in the control of diseases: challenges and perspectives.

Mulunda Mwanza

State veterinary services play an important role in diseases and particularly controlled diseases diagnostic. This paper aims to reflect on different challenges faced by most state veterinary laboratories and the implication on disease diagnostics. Studies have shown that these laboratories face several challenges, from financial availability and efficacy: to staffing. While few laboratories have expanded to most advanced diagnostic methods with accuracy and precision, some laboratories still run basic tests that are not always accurate. While most of state laboratories are being accredited, there is a need to increase the number of laboratories in the country to expedite diagnostics and the need of improving different tests. This will help to laboratories to respond effectively and with efficacy.

WEDNESDAY, 14:20

Molecular and serological prevalence of corridor disease (buffalo associated *Theileria parva* infection) in cattle populations at the livestock/game interface of Kwazulu-Natal Province, South Africa

Sikhumbuzo Mbizeni^{a,b,d,*}, Ben J Mans^{b,c,d}, Samson Mukaratirwa^{b,e}, Abdalla A Latif^b

^a*Department of Agriculture and Animal Health, University of South Africa, South Africa*

^b*School of Life Sciences, University of KwaZulu-Natal, Durban, South Africa*

^c*Department of Life and Consumer Sciences, University of South Africa, South Africa*

^d*Epidemiology, Parasites and Vectors, Agricultural Research Council - Onderstepoort Veterinary Research, Pretoria, South Africa*

^e*One Health Center for Zoonoses and Tropical Veterinary Medicine, Ross University School of Veterinary Medicine, Basseterre, Saint Kitts and Nevis, West Indies*

The increase in reports of Corridor disease (CD) outbreaks in recent years has raised questions about the probability of adaptation of buffalo-derived *Theileria parva* strains in cattle herds adjacent to game reserves. A cross-sectional study was conducted to investigate the extent of occurrence of *T. parva* infections in cattle population in the CD-controlled area of KwaZulu-Natal province. Blood samples were collected from 1137 cattle from 14 herds and analysed by quantitative real-time PCR (qPCR) and indirect fluorescent antibody test (IFAT) to determine the prevalence of *T. parva*. A total of 484 samples from 4 of the 14 herds were further tested on qPCR for the presence of *T. taurotragi* infections. Data was analysed using descriptive statistics and a chi-square test was used to assess association between variables. The overall prevalence of *T. parva* was 1.3% (95%CI:1-2%) and 19.9% (95% CI:17-22%) on qPCR and IFAT, respectively. The qPCR-positive samples were detected in March and May and IFAT positive samples were detected in all seasons sampled, with higher numbers during summer months. The chi-square test showed that *T. parva* prevalence rates based on both qPCR and IFAT were positively associated with herds with previous history of CD outbreaks ($\chi^2 = 8.594$, $P = 0.003$; 69.513 , $P < 0.001$, respectively). The overall prevalence of *T. taurotragi* was 39.4% (95% CI: 35-44%) with the herd-level prevalence ranging between 35.0% and 43.4%. Results from this study demonstrates the extent of occurrence of subclinical carriers of *T. parva* infections in cattle populations at a livestock/game interface area of KwaZulu-Natal province. The molecular and seroprevalence rates were low when compared with areas where cattle-adapted *T. parva* infections are endemic. The adaptation of buffalo-derived *T. parva* in cattle population resulting in cattle-cattle transmissions seem to be unlikely under the current epidemiological state

WEDNESDAY, 14:40

Dog-mediated human rabies elimination in Nigeria by 2030 - will dog markets stifle progress towards elimination?

Ukamaka Eze,²Kenneth Ikejiofor Ogbu,³ Romanus C Ezeokonkwo,¹Boniface M Anene,⁴Claude T Sabeta

¹*Department of Veterinary Medicine, Faculty of Veterinary Medicine, University of Nigeria, Nsukka, Nigeria.*

²*Department of Animal Health, Federal College of Animal Health and Production Technology, National Veterinary Research Institute Vom, Plateau State, Nigeria*

³*Department of Veterinary Parasitology and Entomology, Faculty of Veterinary Medicine, University of Nigeria, Nsukka 41001, Nigeria;*

⁴*Department of Veterinary Tropical Diseases, University of Pretoria, Pretoria 0110, South Africa*

Introduction: The contribution of dog meat consumption and markets to rabies epidemiology in south-eastern Nigeria is not fully understood. Interestingly, fewer local dog breeds compared to exotic breeds are vaccinated against rabies. In this context, a prevalence study to assess lyssavirus antigen and



anti-rabies circulating antibodies in dogs slaughtered for human consumption between 2023-2024 was undertaken and the findings compared to those from a 2015-2016 study.

Methodology: A cross-sectional survey was undertaken on dog marketers (n=120) to ascertain their perceptions and participation towards rabies vaccination of traded dogs. An equal number of brain and serum samples (n=231 each) were collected from dogs brought for slaughter for human consumption between 2023 and 2024. The samples were tested for lyssavirus antigen and anti-glycoprotein rabies antibodies using the direct fluorescent antibody test and a blocking ELISA, respectively. The findings were later compared to previously obtained results on a panel of brain and serum samples collected from the same geographical region for the 2015-2016 period.

Results: Of the 116 participants in the survey, 81% indicated that they would not present dogs (0-3 years old) for vaccination. The majority, 96% would not present dogs in the markets for vaccination. Laboratory analyses demonstrated that 9% (n=21) of brain tissues were lyssavirus-positive and 5.2% (n =12) of the tested sera (2023-2024) had circulating antibody levels of ≥ 0.5 IU/ mL. Slightly lower prevalence rates were obtained (8.3% for antigen, and 2.5% serum) in the 2015-2016 study.

Discussion: The reluctance of dog marketers to vaccinate dogs for human consumption predisposes dog handlers to a public health risk as there is a strong correlation between reduced number of dogs and protective rabies antibodies.

Conclusion: This study demonstrated significant public health risks associated with dog meat processing and handling in south-eastern Nigeria, and the likely draw-back towards elimination of dog-mediated human rabies by 2030.

WEDNESDAY, 15:00

SPECIAL THEME: Success Stories

Sharing elephant dung with traditional healers: from dung heap to beacon of hope

Lin-Mari de Klerk-Lorist

The Kruger National Park has a long history of engagement with traditional healers. Through various conservation programmes, relationships between the park and traditional healers living and working adjacent to the park have been growing. During this time, the issue was raised that elephant dung is an important ingredient for a variety of traditional medicines. However, it was apparent that local traditional healers found it difficult get hold of such valuable but “discarded” products.

Subsequent demand surveys supported this, and a pilot project started in 2022 to test the feasibility and impact of donating elephant dung for local traditional medicine. The longer term objective included informing whether or not it will be desirable and feasible to roll such a project out at a larger scale, and to inform the development of the required governance documentation to support the programme. The pilot project was supported by Environmental Education services, Ranger services, Conservation Management, Scientific Services and the State Veterinary Department.

The elephant dung parcels were well received in all cases, and recipients were positive about the project. The pilot study suggests this is a feasible benefit sharing option, that comes with low ecological, social and economic costs and risks, yet has significant benefits linked to the positive relationship building outcomes that have been observed.

WEDNESDAY, 15:20



SPECIAL SESSION: Wellness

How to cultivate mental-emotional wellbeing, reduce stress and anxiety, and be well from the inside out – practical tips and exercises to change your life forever

Bert Mohr

In a stressful world, it can be easy to lose track of our inner values, lose touch with our deeper emotions, and forget why we became veterinary or para-veterinary professionals in the first place – can you still remember now?

Animal welfare science tells us that animals are sentient beings, i.e., conscious of their existence and capable of experiencing pleasures, suffering, and complex emotions. However, most of us work in environments where animals are used for their benefits to humans, rather than being respected for their inherent value as individuals. This creates a moral tension for the animal carers, who need to operate outside their moral comfort zones and “toughen up” to be able to seemingly function in the workplace.

Thus we become distanced from our true emotions and may suppress difficult feelings - with the people who instinctively care the deepest, ending up caring less over time.

This cost of caring can weigh heavily, draining the reserves in our mental-emotional “tanks”. Our training taught us much about animals, but less about our own wellbeing! This is not so much a failing of a curriculum, but rather of a system where performance may be valued above our holistic wellbeing as humans.

The first step on our journey to reclaiming our own wellbeing is realising that we are struggling – and that it’s OK to struggle! This can be especially hard to admit when we have an over-active “busy” mind, or experience tough emotions! The solution is to become aware of our experience as an observer, in a non-judgemental, curious and gentle way, leading to understanding and acceptance of our own minds and emotions.

Come learn some really easy practical tools that you can apply on a daily basis to reduce stress, and find deep peace – while rekindling your passion for animals!"

WEDNESDAY, 15:50

THEME: One Health Approaches: Integrating Human, Animal, and Environmental Health

A “One Health” perspective of Africa-wide distribution and prevalence of *Giardia* species in humans, animals and environment: A systematic review and meta-analysis

Mpho Tawana^{1,3}, ThankGod Onyiche², Tsepo Ramatla¹, Oriel Thekiso¹

¹Unit for Environmental Sciences and Management, North-West University, Potchefstroom, 2531, South Africa

²Department of Veterinary Parasitology and Entomology, University of Maiduguru, Maiduguru, 600230, Nigeria

³Department of Zoology and Entomology, University of the Free State, Phuthaditjhaba, South Africa.

DOI: <https://doi.org/10.1017/S0031182023000513>

Giardiasis caused by *Giardia duodenalis*, is a leading cause of diarrhoea in resource-poor countries. To gain a better insight into the epidemiology of *Giardia* in Africa, we undertook a robust study to comprehend the distribution and prevalence of *Giardia* infection in humans, animals and their dispersal in the environment. Our protocol was registered with PROSPERO with registration number CRD42022317653. Deep literature search from five electronic databases, namely, AJOL, Google scholar, PubMed, ScienceDirect and Springer Link was performed using relevant keywords. Meta-analysis was performed using a random-effects model and heterogeneity among studies was evaluated using Cochran's Q and the I^2 -statistic. More than 500 eligible studies published from 1st January 1980 until 22nd March 2022 were retrieved. In humans, exactly 48,124 *Giardia* spp. infection cases were registered from the 494,014 stool samples examined resulting in a pooled prevalence estimate (PPE) of 8.8% using microscopy. Whilst serology and molecular diagnostic methods generated PPE of 14.3% and 19.5% respectively, with HIV+ subjects and those with diarrhetic stool having infection rates of 5.0% and 12.3% respectively. The PPE of *Giardia* spp. infection in animals using molecular methods was 15.6%, which was most prevalent in pigs (25.2%) with Nigeria registering the highest prevalence at 20.1%. The PPE of *Giardia* spp. contamination from waterbodies was 11.9% from a total of 7950 samples which were detected using microscopy, with Tunisia documenting the highest infection rate of 37.3%. This systematic review and meta-analysis highlights the necessity of "One Health" approach for consolidated epidemiological studies and control of *Giardiasis* in the African continent.

THURSDAY, 09:00

Unravelling bacterial communities in Diptera flies from livestock kraals and residential dumping sites using metataxonomic approach

Lara de Wet,¹ J.J. Bezuidenhout¹, T. Ramatla^{1,2}, O. Thekiso¹, K.E., Lekota¹

¹Unit for Environmental Sciences and Management, North-West University, Potchefstroom 2531, South Africa

²Centre for Applied Food Sustainability and Biotechnology, Department of Life Sciences, Central University of Technology, Bloemfontein, 9300.

Although Diptera flies can harbour a wide range of microorganisms, it's not yet well-known which bacteria are circulating in Matlwang livestock kraals and Ikageng residential dumping sites, Potchefstroom. A meta-taxonomic approach was utilized to investigate the gut bacterial diversity of Diptera. The study utilized the *Cytochrome Oxidase 1 (CO1)* gene amplification and sequencing in addition to morphological features to identify Diptera flies. The fly-gut bacterial communities were investigated by amplifying V3-V4 of the *16S rRNA* gene. The prevalent Diptera in livestock kraals were *Hemipyrellia* spp. (31%), *Tabanus* spp. (24%) and *Chrysomya* spp. (12%), lastly (33%) of Diptera were not categorized in the 3 main genera. Dumping site was dominated by *Hemipyrellia* spp. (88%), followed by *Sarcophagidae* spp. (7.2%), *Chrysomya* spp. (1.9%), and *Synthesiomyia* spp. (1.6%), lastly (1.3%) of Diptera were not categorized in the 4 main genera. Alpha-diversity concluded that the gut microbiome of Diptera found in the dumping site proved to be more diverse than in the livestock kraals. *Tabanus* spp. demonstrated more diversity than any other genera. Meta-taxonomic analysis showed that the Diptera from dumping site and livestock kraals consisted of 74.50% and 63.62% Proteobacteria phyla. Comparative analysis of Simpson diversity index shows significantly higher values in dumping site relative to livestock kraals. This is augmented by *Chrysomya* spp. showing higher diversity in dumping site in relation to livestock kraals based on Shannon index. The high

abundance of bacterial community found in the dumping site is due to the wide variety of feeding resources available as compared to the livestock kraals. *Pseudomonas* species were more prevalent in the dumping site (55.90%) than in livestock kraals (30.80%). *Rickettsia* spp. was prevalent in livestock kraals with a relative abundance of 32.20% and 11.00% for dumping site. The study demonstrated that Diptera are carriers of a wide variety of bacterial communities. Proteobacteria phyla was the highest detected phyla in both sites containing potential pathogens such as *Pseudomonas* species. This study highlights the first report of the *R. rickettsii* group from flies collected in Matlwang, Potchefstroom. The study has brought attention to the importance of bacterial pathogens that Diptera flies carry, which are important for both veterinary and public health.

THURSDAY, 09:20

In-vitro antimicrobial activity of crude extracts of *Combretum molle* leaf- A One Health Approach

Joshua Ngwisha

Background: This study, with the participation of traditional knowledge, chemists, veterinarians and microbiologists, aimed to explore the antimicrobial activity of *Combretum molle*, a plant native to Zambia, as a potential source for novel antimicrobial agents. With the global rise in antimicrobial resistance (AMR), there is an urgent need for alternative therapies. Traditional medicinal practices involving plants offer a promising avenue for combating the AMR crisis.

Methods: The study utilized four solvents for exhaustive extraction of dried leaf extracts of *Combretum molle*. These extracts were then screened against a panel of bacterial isolates including *Staphylococcus aureus*, *Streptococcus agalactiae*, *Pseudomonas aeruginosa*, *Escherichia coli*, *Klebsiella pneumoniae*, *Acinetobacter*, and *Aeromonas*. Antimicrobial activity was assessed using disk diffusion and broth microdilution techniques, with minimum inhibitory concentrations (MICs) determined via spectrophotometry. The positive control used was tetracycline.

Results: The results revealed significant antimicrobial activity of *Combretum molle* leaf crude extract, with inhibition zones ranging from 6 to 26 mm. Hexane extracts exhibited the highest antimicrobial activity, with MIC values ranging from 3.6 to 50.4 mg/ml. Notably, the ethanol extract showed comparable activity to tetracycline, with no statistically significant difference in their antimicrobial activity (P-value < 0.05). These findings highlight the therapeutic potential of *C. molle* extracts as an alternative to conventional antimicrobial agents in combating multi-drug resistance.

Conclusions: The study demonstrates the antimicrobial potential of *Combretum molle* extracts, validating their possible utilization in traditional medicine as an alternative to conventional antimicrobial agents. This multi-stakeholder collaborative research contributes to addressing the challenge of antimicrobial resistance and underscores the importance of exploring natural sources for novel antimicrobial compounds.

THURSDAY, 09:40

Occurrence and characterization of Shiga toxin-producing *Escherichia coli* and Enteropathogenic *Escherichia coli* isolates from cattle and calves on communal rangeland in Gauteng, South Africa.

Mogaugedi Malahlela¹, Munyaradzi C Marufu², Musafiri Karama¹

¹Veterinary 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*

Shiga toxin-producing *Escherichia coli* (STEC) and enteropathogenic *Escherichia coli* (EPEC) are food-borne pathogens responsible for mild to severe gastroenteritis in humans. Cattle are the primary reservoir of STEC and EPEC. This study investigated the occurrence of STEC and EPEC in 646 faecal samples from apparently healthy adult cattle (n=322) and calves (n=324) on communal rangeland in Gauteng, South Africa. In addition, 216 STEC isolates from adult cattle and 274 from calves were characterized by serotype and possession of major virulence genes. Microbiological culture and Polymerase chain reaction (PCR) were used for detection, virulence characterization and serotyping of STEC and EPEC. PCR revealed that STEC was present in 78.8% of adult cattle and 53.08% of calves. EPEC was present in 11.18% of adult cattle and 20.06% of calves. The distribution of major virulence genes among the 216 STEC isolates which were recovered from adult cattle was as follows: *stx1* only, 21.29%; *stx2* only, 37.96%; *stx1* and *stx2* concurrently, 40.74%; *eaeA*, 17.12% and *hlyA*, 72.68% of STEC isolates. Among the 274 STEC isolates which were recovered from calves, 25.54% carried *stx1* only, 42.33% possessed *stx2* only and 32.11% carried both *stx1* and *stx2*. The *eaeA* was found in 28.46% and *hlyA* was detected in 79.92% of STEC isolates. Partial serotyping revealed 51 STEC serotypes and 11 EPEC serogroups including strains which have been associated with disease in humans. This is the first study reporting on the presence of STEC and EPEC in adult cattle and calves raised on communal rangeland in Gauteng, South Africa. Further STEC and EPEC characterization studies comparing cattle and human isolates will be needed to evaluate to what extent cattle may be a source of STEC and EPEC disease for humans consuming food products or in contact with cattle raised on communal grazing rangelands of Gauteng, South Africa.

THURSDAY, 10:00

THEME: Disease Prevention & Control in Low Resource Settings Enhancing Veterinary Service Provision for Smallholder Farmers in Zimbabwe: An Integrated Approach

Leonard Maposa, (BVSc, MBA, MSc (VTD), PhD)

Livestock Department, Tongaat Hulett Zimbabwe, P Bag 801, Triangle, Zimbabwe. leomaposa@gmail.com

Smallholder farmers form the backbone of Zimbabwe's agricultural sector, with livestock playing a critical role in their livelihoods. However, livestock diseases pose significant challenges to sustainable livestock production, leading to economic losses and jeopardizing food security. The study aimed at developing a sustainable institutional arrangement for veterinary service (VS) provision to smallholder farmers in Zimbabwe. This study explored the current state of VS for smallholder farmers, highlighting the limitations of existing systems and recommended ways of improving service delivery.

Employing a mixed methods approach, the study investigated the drivers of veterinary service demand, identified key service providers, assessed their roles and institutional gaps, and evaluated the cost-effectiveness of various service arrangements in Mwenezi and Mberengwa Districts. Data collection involved a semi-structured questionnaire (N=382), focus group discussions (N=8), and interviews (N=17), complemented by continuous observations.

Data analysis incorporated descriptive statistics, multivariate probit analysis, and cost-effectiveness assessments. Notably, animal diseases emerged as a significant challenge, with 67.8% of respondents identifying them as the primary constraint to livestock production. The most dominant service provider was government veterinary services (86.7%). In comparison, 24.4% accessed the services of community animal health workers, and the private sector veterinary drug suppliers provided 67.8% of the drug supply. Key factors influencing farmer preferences for veterinary service providers included disease control effectiveness, response time, technical expertise, and availability of veterinary drugs.



The study concluded that the challenge of animal diseases in the smallholder sector was huge and not adequately addressed under the current arrangement for veterinary services. The study recommends an integrated approach, emphasizing collaboration among state veterinary services, the private sector, and community-based animal health workers in order to improve accessibility, affordability, and quality of veterinary services for smallholder farmers. The study contributes to enhanced veterinary service provision in resource constrained communities.

THURSDAY, 10:50

Knowledge of ticks and tick-borne diseases and tick control strategies among communal farmers in Mafikeng Local Municipality

Pfano Theweli, Dr Rendani Victress Ndou¹ & Amogelang Khule¹ & Nothemba Ndukuya¹

¹*Centre of Animal Health Studies, School of Agricultural Studies North West University, Mafikeng Campus, Private Bag X2046, Mmabatho, 2735*

Ticks and tick-borne diseases (TBDs) have a major impact on livestock productivity in South Africa. TBDs included economically significant diseases such as heartwater, babesiosis, and anaplasmosis. Therefore, this study was conducted to evaluate the knowledge and practices of communal livestock farmers regarding ticks and TBDs in Mafikeng Local Municipality. Data was collected from 305 farmers (110 cattle, 95 goats, and 100 sheep) using a structured questionnaire. The data was analyzed for descriptive and inferential statistics using SPSS version 29. The findings revealed that a majority of cattle farmers had some knowledge of ticks and TBDs diseases. However, when shown pictures, only 45.44% of them were able to identify *Hyalomma* tick and 29.99% identified *Amblyomma* tick. Among goat farmers, 50% had sufficient knowledge of tick-borne diseases, but the majority could only identify *Amblyomma* tick, while none of them were able to identify *Rhipicephalus* tick. Surprisingly, 12% of sheep farmers did not believe that sheep can contract diseases from ticks, and a staggering 84% of them were unable to identify the *Amblyomma* tick from a picture. The most common tick control method used across all three enterprises was acaricides, with manual removal and ethnoveterinary medicine also being used. The Chi-Square test for independence with values $\chi^2=55,516a$, $df = 30$, and $p=0.003$ revealed that the level of education of farmers had a significant association with their knowledge of ticks and TBDs. The study concluded that farmers need more extension services on ticks and TBDs. Additionally, effective, affordable, sustainable, and environmentally friendly tick management strategies including those presented by ethnoveterinary medicine should be investigated, developed, and promoted. The study recommends that stakeholders collaborate and coordinate their efforts to address the challenges associated with ticks and TBDs in livestock production.

THURSDAY, 11:10

“Guilty until proven innocent”, the only way to optimize control of transboundary animal disease in South Africa, an African swine fever case report.

Agatha Raseasala Dr Farhanaaz Abdool-Khader

Department of Paraclinical Sciences, Faculty of Veterinary Science, University of Pretoria, Onderstepoort, 0110 South Africa

Gauteng Department of Agriculture & Rural Development, Johannesburg, 2000, South Africa

African swine fever (ASF) is a controlled disease in terms of the Animal Diseases Act, 1984 (Act 35 of 1984) that causes acute haemorrhagic disease and mortalities of up to 100%. It is highly resistant in the environment, allowing for human behaviour to easily facilitate disease spread. Diagnostic laboratories

which have compartmentalization, waste management, and decontamination protocols in place for porcine cases, are better equipped to prevent unintentional spread of ASF. A “guilty until proven innocent” approach is the ideal, whereby cases presenting with suspicious signs and history, are considered positive without a negative PCR test result from Transboundary Animal Diseases – Agricultural Research Council (TAD-ARC).

A pig was presented for necropsy at the Onderstepoort Pathology Section with a suspicious history for ASF. The post mortem evaluation revealed amongst others, nasal bloody discharge, generalized lymph node haemorrhage and fibrinous peritonitis, further supporting the ASF suspicion. This was immediately reported to the State Veterinarian (SV) for further disease outbreak investigation, while awaiting PCR test result from TAD-ARC, which later confirmed the positive result. Threats of legal action and intervention by the South African Police Services (SAPS), was necessitated by the SV in order to place the farm under quarantine and do backward tracing as part of the disease investigation.

Of note though, is that not all animals presenting with these lesions are definitively infected with ASF virus. Other diseases may present similarly, including Salmonellosis and Pasteurellosis to name a few. This case report, should encourage the maintenance of a high level of transboundary animal disease awareness amongst all veterinarians, in turn optimising the biosecurity and control of ASF. The collaborative efforts of the different stake holders in this case, contributed positively to prompt disease outbreak detection and mitigation of disease spread.

THURSDAY, 11:50

Bridging policy and science: Public-Private Partnerships revitalizing South Africa’s equine trade prospects

John Grewar, Vivien Malan², Kerry Loxley³, Camilla T. Weyer¹ & Beverley J. Parker¹

¹South African Equine Health and Protocols NPC, Baker Square, Paardevelei, Cape Town, 7110, South Africa, john@saehp.com; camilla@saehp.com; bev@saehp.com

²Western Cape Department of Agriculture, Veterinary Services: State Veterinarian Boland, Elsenburg, 7607, South Africa, vivien.malan@westerncape.gov.za

³Department of Agriculture, Land Reform and Rural Development, Animal Health: Disease control, Pretoria, 0084, South Africa, KerryL@Dalrrd.gov.za

In 2013, a European Union (EU) audit identified significant deficiencies in South Africa’s equine health controls, particularly concerning African horse sickness (AHS). This resulted in a sustained embargo on the direct export of live horses to the EU and other international equine markets. The last direct export from South Africa to the EU prior to the embargo, occurred in early 2011. In March 2024, there was a notable policy shift when the EU approved the reopening of South Africa’s designated equine export zone, reflecting a major turnaround in the country’s equine health management.

This abstract outlines the pivotal developments contributing to this reversal. Firstly, the establishment of the Equine Health Fund in 2014 and subsequently the South African Equine Health & Protocols (SAEHP) in 2018 centralized and focused efforts to address the 2013 audit findings, ensuring regulatory processes were a primary rather than secondary concern. Secondly, a robust public-private partnership (PPP) under the World Organisation for Animal Health (WOAH) guidelines involved SAEHP, the Western Cape Department of Agriculture (WCDOA), and the Department of Agriculture, Land Reform, and Rural Development (DALRRD), enhancing accountability and cooperation in AHS management. Thirdly, an output-based approach was adopted, centering on real-world applications of scientific research, such as risk assessments for horse movements and stringent compliance with the Animal Diseases Act and EU requirements. Lastly, international engagement became a strategic priority, with South African representatives actively participating in global scientific and policy forums to promote the country’s standards and practices, thereby fostering trust and collaboration with international partners.



These concerted efforts have not only addressed the specific issues flagged by the EU but also positioned South Africa as a credible and reliable participant in the global equine industry, highlighting the fact that industry and Government can find common ground and work together to achieve success.

THURSDAY, 12:10

Evaluation of the proper use of medication available over the counter by subsistence in Mpumalanga Province.

Japhta Mokoale

South Africa has two types of animal farming systems, being the commercial industry and subsistence farming in more rural areas, with commercial farmers having more access to veterinary services. To cater for the absence of sufficient veterinary service, the country allows farmers to access certain over the counter medications (stock remedies), as a way to assist them to farm sustainably and profitably. However, with any drug use, their true benefits are only realized following correct use. The aim of this study was to describe and assess the adequacy of the current use of veterinary drugs by rural-based farmers. A scheduled structured questionnaire with close-ended questions and direct observation was employed. The most important finding was the absence of proper training in the area, with 82.9% not receiving any training related to livestock production or use/handling of stock remedies, highlighting the urgent need for proper training. Of interest, a large proportion of the farmers (57.5%) left the care of their animals to herders. Concerns were also noted in the application of withholding periods, transport of medication, disposal of medication, calculation of drug doses, correct route of administration and carcass disposal with no difference in response between farmers receiving training and those who didn't. These findings not only indicate the importance of farmer training, but show that for such training to be effective, information should not only cover farming activities but must include primary animal health care and an understanding of information contained in package leaflets. It would also be important to ensure that herdsmen are also included in such training initiatives as they are the primary caregivers of the animals.

THURSDAY, 14:00

FAO Expert Consultation on acaricide resistance of cattle ticks: A case study of the Eastern Cape Province in South Africa

Nkululeko Nyangiwe,

*Department of Agriculture and Animal Health, University of South Africa, Florida, South Africa
Döhne Agricultural Development Institute, Private Bag X15, Sutterheim 4930, South Africa;
nyangiwe1@gmail.com*

The Food and Agriculture Organization of the United Nations (FAO) organized a virtual expert consultation on 9–10 November 2021 on the sustainable management of parasites in livestock challenged by the global emergence of resistance. The objective of the study was to provide FAO with advice on the way forward regarding parasite resistance management. The study involved tick data collected from communally grazed cattle using engorged ticks, firstly at 59 dip-tanks in the eastern regions of the Eastern Cape Province and secondly at 33 communities within the municipalities of Elundini, Senqu, and Walter in Joe Gqabi District Municipality. Ticks were immediately transported to the Acaricide Resistance Testing Laboratory at the University of the Free State's Department of Zoology and Entomology for acaricide resistance testing. Three groups of 10 engorged female ticks were used as treatment groups, and the 4th served as an untreated control group. Each group was immersed for 10 min in the test acaricide at the concentration recommended for its use in the field, namely amitraz at 0.025 %, cypermethrin at 0.015 %, and chlorfenvinphos at 0.05 %.

The results of the Shaw Larval Immersion Test (from 59 dip-tanks) indicated that there was emerging resistance to amitraz in *R. (B.) microplus* at 2 dip-tanks and resistance at a 3rd dip-tank. This tick was also resistant to cypermethrin at 1 dip tank, while emerging resistance to chlorfenvinphos at 8 tanks and resistance at 2 were also recorded. The Egg Laying Test detected no resistance to any of the acaricides in *R. (B.) microplus* or *R. appendiculatus*, while the Reproductive Estimate Test indicated emerging resistance to amitraz in *R. (B.) microplus* at 1 dip-tank. While results from the 33 communal dip-tanks showed a total of 49% of the *R. (B.) decoloratus* tick's larvae were susceptible to amidine, with 30% developing resistance and 21% ineffective reservation at a concentration of 250 ppm. Unlike one-host ticks, two- and three-host ticks were found to be much less exposed to acaricidal treatments and have a lower probability of developing resistance but are important for disease transmission.

THURSDAY, 14:20

SPECIAL THEME: Success Stories

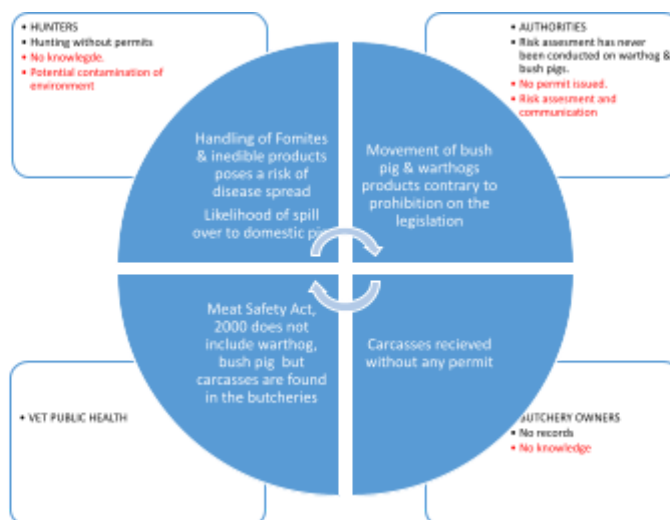
Meat safety risk of unapproved stamped carcasses sold at butcheries of Mpumalanga

Mpendulo Xashimba

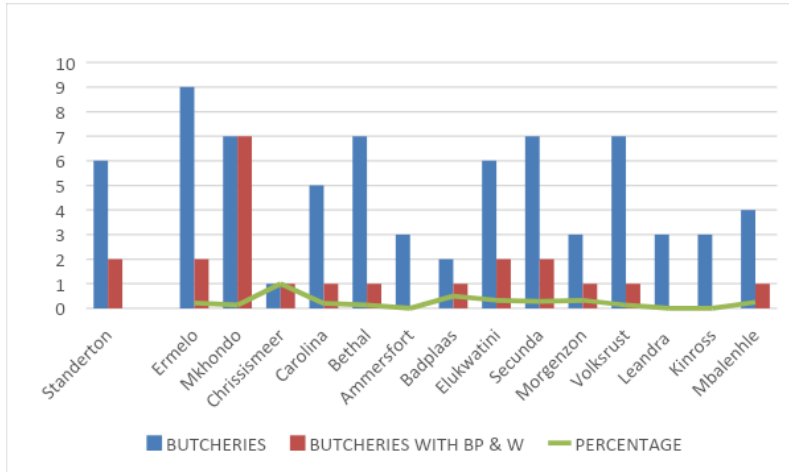
INTRODUCTION: The study was triggered by the bush and warthog pig carcasses found on butcheries, without any veterinary movement permits issued. Bush/Warthog pigs and ticks are carriers of ASF, and are capable of introducing the virus into their domestic counterparts if no control in place.

METHODS: Physically going during hunting and records gaps between ideal situation and what is actually happening. Evaluate the SOP's of issuing of permits if any, credibility of available data and risks thereof. To assess the knowledge levels of diseases that may spread by direct or indirect contact, by the hunters, veterinary authorities and butchery owners.

DISCUSSION



RESULTS



The figure 4.1. The distribution of bush and warthog pig carcasses.

CONCLUSION: Issuing of permits on all the slaughtered bush pigs for traceability reasons as it is the requirement from the Animal Disease Regulations. In order to have a written protocol for slaughtering of warthog or bush pig and destruction of inedible products i, e, offal, heads and feet, skin, and the handling of fomites as the transmission can also occur via contaminated fomites (non-living objects) such as shoes, clothes, vehicles, knives equipment. The lack of knowledge on all stake holders was noted, therefore information sessions will be facilitated to all the stakeholders.

THURSDAY, 14:40

THEME: Antimicrobial Resistance

Antibiotic quality and use practices amongst dairy farmers and drug retailers in central Kenyan highlands

Dishon Muloi,^{1,7*†}, Peter Kurui^{3*}, Garima Sharma¹, Linnet Ochieng¹, Fredrick Nganga¹, Fredrick Gudda¹, John Maingi Muthini³, Delia Grace^{1,4}, Michel Dione⁵, Arshnee Moodley^{1,6+‡}, Caroline Muneri²⁺

¹Animal and Human Health Department, International Livestock Research Institute, Nairobi, Kenya

²Department of Veterinary Surgery, Theriogenology and Medicine, Egerton University, Njoro, Kenya

³Department of Biochemistry, Microbiology and Biotechnology, Kenyatta University, Nairobi, Kenya

⁴Natural Resources Institute, University of Greenwich, Kent, United Kingdom

⁵Animal and Human Health Department, International Livestock Research Institute, Dakar, Senegal

⁶Department of Veterinary and Animal Sciences, University of Copenhagen, Frederiksberg C, Denmark

⁷Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, Neston, United Kingdom

Understanding antibiotic use in dairy systems is critical to guide antimicrobial stewardship programs. We investigated antibiotic use practices in small-holder dairy farms, antibiotic quality, and antimicrobial resistance (AMR) awareness among veterinary drug retailers in a mixed farming community in the central Kenyan highlands. Data were collected from 248 dairy farms and 72 veterinary drug stores between February 2020 and October 2021. A scale was developed to measure knowledge about AMR and antibiotic use using item response theory, and regression models were used to evaluate factors associated with antibiotic use and AMR knowledge. The active pharmaceutical ingredient (API) content of 27 antibiotic

samples was determined using high-performance liquid chromatography (HPLC). The presence and levels of 11 antibiotic residues in 108 milk samples collected from the study farms were also investigated using liquid chromatography tandem mass spectrometry (LC–MS/MS). Almost all farms (98.8%, n = 244) reported using antibiotics at least once in the last year, mostly for therapeutic reasons (35.5%). The most used antibiotics were tetracycline (30.6%), penicillin (16.7%), and sulfonamide (9.4%), either individually or in combination, and predominantly in the injectable form. Larger farm size (OR = 1.02, $p < 0.001$) and history of vaccination use (OR = 1.17, $p < 0.001$) were significantly associated with a higher frequency of antibiotic use. Drug retailers who advised on animal treatments had a significantly higher mean knowledge scores than those who only sold drugs. We found that 44.4% (12/27) of the tested antibiotics did not meet the United States Pharmacopeial test specifications (percentage of label claim). We detected nine antibiotics in milk, including oxytetracycline, sulfamethoxazole, and trimethoprim. However, only three samples exceeded the maximum residue limits set by the Codex Alimentarius Commission. Our findings indicate that antibiotics of poor quality are accessible and used in small-holder dairy systems, which can be found in milk. These results will aid future investigations on how to promote sustainable antibiotic use practices in dairy systems.

FRIDAY, 09:00

Molecular comparative study of antibiotic resistance of *Salmonella enterica* from animals, food and environment isolated over 62 years.

Nozipho Maphori², Lubanza Ngoma¹, Mulunda Mwanza¹, Itumeleng Matle²

¹ Natural and Agricultural Science: Northwest university.

² Agricultural Research Council: Onderstepoort Veterinary Research – Bacteriology Section, Pretoria, South Africa.

Introduction: *Salmonella enterica* is a zoonotic bacterial pathogen, poses significant risks to both veterinary and public health in South Africa. This study investigated the occurrence of antimicrobial resistance and molecular characteristics of *S. enterica* isolated from animal, food, and the environment between 1959 and 2023 in South Africa.

Methods: A total of 625 *Salmonella* strains were tested against 13 antibiotics using disc diffusion method. Conventional polymerase chain reaction was performed for screening of integrons (n=3), virulence (n=11), and antimicrobial resistance (n= 8) genes. Data was analyzed using the statistical package EpiCalc 2000 (version 2), and Frequency Procedure of SAS statistical software version 9.4.

Results: During the study period, a total of 109 *Salmonella* serotypes were identified. *Salmonella* Enteritidis was the most prevalent (20.3%; n=127), followed by *S. Typhimurium* (13.9%; n = 87) and *S. Heidelberg* (9%; n = 56). Many strains showed resistance to nitrofurantoin (94.1%), followed by ceftazidime (42.1%), and ampicillin-clavulanic acid (41.6%). Multidrug resistance (MDR) was observed against 72.6% (n=286) isolates with 8 *Salmonella* serotypes showing resistance to more than 5 antibiotics. Antibiotic resistance varied significantly over 65 years with high levels reported between the year 2010 and 2023. Most of the isolates harbored *qnrA* (36.3%), *sul1* (35.7%), *tetA* (33.6%) and *cat1* (24.2%) antibiotic resistance genes. Furthermore, the study uncovered substantial presence of virulence gene within the isolates including *invA* (92.5%), *SopB* (82.2%), *SspH1* (78.4%) and *SifA* (76.2%).

Discussion: Understanding the epidemiology of *S. enterica* in different animal reservoirs, food and environmental sources is essential to reduce its transmission to humans. The study reveals an elevated prevalence of AMR and virulence genes in *S. enterica* from South Africa. It also highlights the increase in distribution of antibiotic resistance genes which has negative impact on prophylaxis of the pathogen. The results offer valuable insights into the molecular mechanisms of AMR and pathogenicity of *S. enterica*.

Conclusion: These results suggest that *S. enterica* in animal, food and environment in South Africa should be monitored due to potential consequences in public and animal health.

Keywords: Virulence genes, Antibiotic resistance genes, *Salmonella* serotypes

FRIDAY, 09:20



Genomic characterization of generic *Escherichia coli* from food-producing animals and products of animal origin, in South Africa

Refiloe Malesa Rian Pierneef^{2,3}, Kudakwashe Magwedere⁴, Thendo Mafuna⁵ Itumeleng Matle^{1*}

¹Bacteriology Division, Agricultural Research Council-Onderstepoort Veterinary Research, Onderstepoort 0110, South Africa

²Department of Biochemistry, Genetics and Microbiology, University of Pretoria, Pretoria, 0001, South Africa

³Centre for Bioinformatics and Computational Biology, University of Pretoria, Pretoria, 0001, South Africa

⁴Directorate of Veterinary Public Health, Department of Agriculture, Land Reform and Rural Development, Pretoria, South Africa

⁵Department of Biochemistry, University of Johannesburg, Auckland Park, South Africa

Escherichia coli is found in diverse environmental niches, including meat and meat products, and is known for its significance in both food safety and public health. In South Africa, whole genomic sequencing (WGS) efforts for *E. coli* are overwhelmingly skewed toward human isolates with limited studies conducted on non-human isolates. Therefore, the aim of this study was to use WGS to characterize generic strains of *E. coli* isolated from animal specimens, meat, and meat-based products in South Africa. Based on WGS analysis, a total of 35 *E. coli* strains were grouped into five phylogroups (A, B1, B2, C, and E), with A (45.7%) being the most predominant. Virulence-associated genes identified the isolates as either extra-intestinal pathogenic *E. coli* (68.5%) or intestinal pathogenic *E. coli* (31.4%) pathotypes. Twenty-three different serotypes were identified, with O101:H37 (17.4%), O2:H4 (17.4%), O6:H5 (13.0%), and O64:H19 (8.7%) being the predominant ones. Among the 19 different sequence types (STs), ST1858, ST975, and ST10 were the most prevalent (11.42% each). Various virulence genes, antimicrobial resistance genes, and genetic mobile elements carrying Tn2, IS26, and Tn6196 elements were detected, with the disinfectant resistance *sitABCD* being the most predominant. The type 1 CRISPR system which functions by storing records of previous invasions to provide immunological memory for a rapid and robust response upon subsequent viral infections was detected in all isolates, consisting of subtypes I-E (85.7%), I-A (57.1%), and I-F (11.4%). The findings of this study provide an insight into the genetic diversity of generic *E. coli* isolates from animal species, meat, and meat-based products in South Africa.

FRIDAY, 09:40

Antimicrobial patterns of ESKAPE pathogens isolated from the hands of students in a Veterinary Academic Hospital, South Africa.

Dikeledi Sebola¹, James W. Oguttu², Mogaugedi N. Malahlela¹, Marleen M. Kock^{3,4}, Daniel N. Qekwana¹.

¹Section Veterinary Public Health, Department of Paraclinical Sciences, Faculty of Veterinary Science, University of Pretoria, Pretoria, South Africa

²Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, University of South Africa, Johannesburg, South Africa

³Department of Medical Microbiology, University of Pretoria, Pretoria, South Africa

⁴Tshwane Academic Division, National Health Laboratory Service, Pretoria, South Africa

Objective: *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* species termed 'ESKAPE' organisms are responsible for most hospital-acquired infections (HAIs). Although these bacteria are known to spread via the hands of healthcare workers (HCWs), there is a paucity of information on the occurrence of these organisms in veterinary settings. This study aimed to investigate the presence and antimicrobial patterns of this bacteria

isolated from the hands of students working in the intensive care unit (ICU) at a veterinary academic hospital.

Methods: A cross-sectional study was conducted among students working in an ICU at a veterinary academic hospital in South Africa. Students were sampled before the start of the ICU shift using a modified glove-juice method. Standard microbiological techniques and a series of polymerase chain reaction (PCR) assays were used to identify and characterize the bacteria. All the isolates were tested for resistance against a specific panel of antibiotics using the disk diffusion method. Proportions of bacterial species and their antimicrobial-susceptibility profiles were calculated.

Results: At screening, all the students (n=62) carried at least one of the ESKAPE organisms on their hands. *Escherichia coli* was the most isolated organism (76%, 47/62), followed by *E. faecium* (52%, 22/62), *P. aeruginosa* (48%, 30/62), *A. baumannii* (47%, 29/62), *K. pneumoniae* (27%, 17/62), and *S. aureus* (24%, 15/62). A reduced proportion of isolates were recovered from the samples, *E. coli* (26%, 12/47), *E. faecium* (27%, 6/22), *P. aeruginosa* (43%, 13/30), *A. baumannii* (21%, 7/29), *K. pneumoniae* (41%, 7/17), and *S. aureus* (20%, 3/15). Most of the organisms showed a high proportion of resistance to at least one antibiotic. Multidrug resistance (MDR) was reported among just over half (55%, 5/9) of *E. coli*, 33% (2/6) of *E. faecium*, 100% (13/13) of *P. aeruginosa*, and 33% (1/3) of *S. aureus* isolates.

Conclusion: Students working in the ICU carried several ESKAPE bacteria before contact with patients. Moreover, MDR was common among this group of organisms. The findings of the present study underscore the importance of infection prevention and control strategies to help reduce the likelihood of the spread of these organisms to personnel, owners, family members, and patients.

FRIDAY, 10:00

Veterinary antibiotic traces in formal and informal red meat slaughtered food animals in the West Coast District of the Western Cape

Victor Twala¹, DV Nkosi¹, TJ Morodi¹ & EJ Mkhwebane¹

¹Tshwane University of Technology, Pretoria, South Africa, nkosidv@tut.ac.za,

Tel.: (012) 382-5283; Mobile: 082-649-2685

²Western Cape Department of Agriculture, Elsenburg, South Africa, victor.twala@westerncape.gov.za,

Tel: 021 808 7631; Mobile 083 642 7387

Introduction: Veterinary antibiotics are vital for enhancing animal growth, preventing diseases, and ensuring product quality across various livestock sectors. However, their misuse had resulted in antibiotic resistance, posing risks to animal health public health concerns. The study aimed to assess the prevalence of veterinary antibiotic residues used in meat animal production, with a specific focus on abattoir-level practices, conducted in the West Coast District of the Western Cape Province, which heavily relied on both commercial and small-scale farming.

Materials and Methods: In a cross-sectional discipline-based investigation. A structured questionnaire was sent to fourteen (n=14), national and provincial veterinary public health offices across South Africa (n=9), and thirty (n=30) farms representing the farming sector, as well as all red meat abattoirs (n=5) in the West Coast District. Chi-square for association of variables compared differences in the districts and p-value <0.05 was regarded as significantly different. The research targeted ordinary processes from farm to fork, the regulatory bodies responsible for overseeing the Veterinary Medicines and Related Substances Control Act, which governed the appropriate use of antibiotics.

Results: Seventy percent ($X^2=4.8000$; $p=0.0285$) of farmers reported refraining from administering veterinary antibiotics to promote weight gain in healthy animals, while 37% ($X^2=12.3333$; $p=0.0150$) expressed concern over the potential emergence of resistant bacteria due to misuse. Additionally, only 34% ($X^2=17.3333$; $p=0.0017$) of respondents adhered to veterinary antibiotic usage solely under veterinarian



instruction, and the majority of abattoir managers were found to be non-compliant with regulatory laws, with many policymakers voicing concerns about limited resources.

Conclusions: The findings underscore the importance of enhancing farmer education on responsible antibiotic use and strengthening enforcement mechanisms to ensure compliance with regulatory laws. Addressing non-compliance among abattoir managers and policymakers' resource constraints was crucial for promoting safe and sustainable agricultural practices.

FRIDAY, 10:20

THEME: State Of The Continent: Disease Rich, Data Poor

Analysis of mannose-binding lectin protein and mRNA levels on selected chicken breeds in South Africa

Peter Ayodeji Idowu¹, Takalani J Mpofo¹, Oliver T Zishiri², Khathutshelo A. Nephawe¹ and Bohani Mtileni¹

¹*Tshwane University of Technology, Department of Animal Sciences, Faculty of Science, Private bag X680, Pretoria 0001, South Africa*

²*Discipline of Genetics, School of Life Sciences, University of KwaZulu-Natal, Private Bag X54001, Durban 4000, South Africa*

Introduction: Mannose-binding lectin (MBL) plays a crucial role in recognizing and eliminating pathogens by activating the complement system. This study aimed to detect and quantify the MBL protein concentration and expression in selected chicken breeds in South Africa.

Methods: Forty-five blood samples were randomly collected from three indigenous chicken breeds, Ovambo (OV = 9), Venda (VD = 9), and Potchefstroom Koekoek (PK = 9), and two exotic breeds: Rhode Island Red (RIR = 9) and Lohmann Brown (LB = 9). The concentration of MBL protein was determined using an ELISA sandwich assay. MBL mRNA expression was determined from the liver samples of two indigenous breeds (OV = 5 and PK = 5) and two exotic breeds (RIR = 5 and LB = 5) using qPCR techniques.

Results: MBL protein concentrations ranged from 5.26 µg/ml to 18.56 µg/ml. The LB breed had the lowest mean of 6.40 ± 0.80 µg/ml, while the PK breed had the highest mean concentration of 17.70 ± 0.24 µg/ml. At 12, 25, and 35 weeks, MBL proteins of OV, VD, PK, RIR, and LB varied significantly (p ≤ 0.05). mRNA MBL expression of OV and LB breeds showed a 1-fold decrease, RIR showed a 1-fold increase, and PK showed more than a 2-fold increase in MBL expression relative to the control.

Discussion: Differences in MBL protein among the breeds indicate that chickens with high MBL protein concentration activate the complement system faster, signifying a stronger immune response to bacterial diseases. Higher MBL protein and expression levels in chickens correlate with better disease resistance, which is crucial for breeding plans with minimal antibiotic use, thus reducing antimicrobial resistance.

Conclusion: The findings revealed differences in MBL protein concentration and expression levels among South African chicken breeds, highlighting the genetic diversity of the MBL protein gene, a tool for disease prevention.

FRIDAY, 11:10

The bacterial community harboured by *Amblyomma hebraeum* ticks from livestock in North West Province, South Africa

Kealeboga Mileng¹, J. Bezuidenhout¹, T. Ramatla^{1,2}, N.G Khasapane^{1,2}, O. Thekiso¹, K.E. Lekota¹

¹Unit for Environmental Sciences and Management, North-West University, Potchefstroom, 2531, South Africa.

²Centre for Applied Food Sustainability and Biotechnology, Department of Life Sciences, Central University of Technology, Bloemfontein, 9300.

Ticks of the genus *Amblyomma* are known vectors of various pathogens affecting both humans and animals. Understanding the bacterial communities associated with these ticks is important for clarifying their roles in disease transmission cycles and identifying potential intervention strategies. The study examined bacterial community of *Amblyomma hebraeum* collected from livestock in the Mahikeng, North West province, using high throughput sequencing. A total of 31 ticks from sheep (n = 12), goat (n = 7), and cattle (n = 12) DNA samples were amplified targeting the bacterial V3-V4 region bacterial 16S rRNA gene. Amplicon libraries were prepared and sequenced using Illumina MiSeq technology. Metabarcoding analysis revealed diverse bacterial communities associated with *Amblyomma hebraeum*. The cattle, sheep and goat associated ticks from Dihatswane village consisted of the highest operational taxonomic units (OTUs) with the dominant endosymbiotic genera of *Rickettsia* (>90%). The most abundant genera was *Rickettsia* detected in 17% of the tick DNAs from sheep, followed by 55% and 31% from goat and cattle, respectively. The high abundance of *Rickettsia* spp. suggests its potential role in tick physiology and pathogen transmission. *Coxiella* spp. was found in 99% of all tick samples. Zoonotically important taxa like *Coxiellaceae* identified in this study emphasize the importance of further research into their implications for animal health and disease management.

FRIDAY, 11:30

Bacillus anthracis in South Africa, 1975-2013: are some lineages vanishing?

Kgaugelo Lekota^{1, 2*}, Ayesha Hassim¹, Maphuti Betty Ledwaba¹, Barbra Glover¹, Edgar Dekker³, Louis Ockert van Schalkwyk³, Jennifer Rossouw⁴, Wolfgang Beyer⁵, Gilles Vergnaud⁶ and Henriette van Heerden¹

¹University of Pretoria, Faculty of Veterinary Science, Department of Veterinary Tropical diseases, Onderstepoort, 0110, South Africa

²Unit for Environmental Sciences and Management: Microbiology, North-West University, Potchefstroom campus, Private Bag X6001, Potchefstroom 2520, South Africa

³Department of Agriculture Land Reform and Rural Development, Office of the State Veterinarian Skukuza 1350, Mpumalanga, South Africa

⁴Centre for Emerging Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases a Division of the National Health Laboratory Services, Johannesburg, South Africa

⁵University of Hohenheim, Institute of Environmental and Animal Hygiene, Stuttgart, Germany

⁶Université Paris-Saclay, CEA, CNRS, Institute for Integrative Biology of the Cell (I2BC), 91198, Gif-sur-Yvette, France

The anthrax-causing bacterium *Bacillus anthracis* comprises the genetic clades A, B, and C. In the northernmost part (Pafuri) of Kruger National Park (KNP), South Africa, both the common A- and B-strain clades occur. The rare B-clade strains were reported to be dominant in Pafuri before 1991, while the A-clade strains occurred towards the central parts of KNP. The prevalence of B-clade strains is currently much lower, as only A-clade strains have been isolated from 1992 onwards in KNP. In this study, 319 *B. anthracis* strains were characterized with 31-loci multiple-locus variable-number tandem repeat analysis (MLVA-31). B clade strains from soil (n = 9) and a *Tragelaphus strepsiceros* carcass (n = 1) were further characterised by whole genome sequencing and compared to publicly available genomes. The KNP strains clustered in the B clade before 1991 into two dominant genotypes. South



African strains cluster into a dominant genotype, A.Br.005/006, consisting of KNP as well as the other anthrax endemic region, the Northern Cape Province (NCP), South Africa. A few A. Br.001/002 strains from both endemic areas were also identified. Subclade A.Br.101 belonging to the A. Br. Aust94 lineage was reported in the NCP. The B-clade strains seem to be vanishing, while outbreaks in South Africa are caused mainly by the A.Br.005/006 genotypes as well as a few minor clades such as A. Br. 001/002 and A.Br.101 present in the NCP. This work confirmed the existence of the rare and vanishing B-clade strains that group in the B.Br.001 branch with KrugerB and A0991 KNP strains.

FRIDAY, 11:50

Temporal and Serotypic Dynamics of *Actinobacillus pleuropneumoniae* in South African Porcine Populations: A Retrospective Study from 1985 to 2023

Emmanuel Seakamela

Actinobacillus pleuropneumoniae is a major bacterial pathogen causing porcine pleuropneumoniae, a disease of notable economic impact and high fatality rates among pigs worldwide. It has been reported that 19 distinct serotypes of this bacterium exist. Despite its global prominence, there exists a scarcity of information regarding its prevalence and distribution in South Africa. Thus, this study used laboratory records to investigate the serotype diversity, temporal distribution, and seasonal patterns of *A. pleuropneumoniae* isolated from porcine samples spanning from 1985 to 2023 within South Africa. Data from laboratory registries of 354 cases, obtained from three veterinary laboratories in South Africa, were analysed. The data was categorized into two-time frames: term 1, covering 1985 to 2001, and term 2, spanning from 2002 to 2023. The dataset identified 11 different serotypes, with serotype 7 being the most prevalent at 22.7% (n = 62), followed by serotype 5 at 13.8% (n = 42). The study highlighted variations in the prevalence of serotypes among diseased animals over a 38-year period. Serotypes 3, 5, 7 and 8 were commonly observed during this time, while serotype 4 was absent from 1985 to 2001, and serotypes 1, 6, and 10 were absent from 2002 to 2023. The distribution of serotypes showed a diverse variation in age of affected animals, clinical manifestation, and seasonal occurrence. The information collected during this study will serve as a baseline for future epidemiological studies as well as to inform control strategies.

FRIDAY, 12:10

Rift Valley fever: questioning dogma and debunking myths

Peter Thompson BVSc, MMedVet, PhD¹

Co-author: Melinda K. Rostal, DVM, MPVM, PhD²

¹Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Onderstepoort, 0110, peter.thompson@up.ac.za

²EcoHealth Alliance, 520 Eighth Ave, Ste. 1200, New York, NY 10018, U.S.A., rostal@ecohealthalliance.org

Rift Valley fever (RVF) virus (RVFV) is a zoonotic arbovirus causing periodic epidemics in East, West and southern Africa, and more recently beyond sub-Saharan Africa, with significant ruminant livestock and human morbidity and mortality. Its wide range of known and potential hosts and vectors and its sporadic and often unexpected emergence present challenges to understanding its ecology and epidemiology. Although some aspects of these have been elucidated, many questions remain unanswered. However, certain assumptions and speculations have become entrenched in the literature and need to be critically evaluated. This presentation addresses two of these.

A widely-cited assumption is that the primary mechanism for long-term RVFV survival during interepidemic periods is via transovarial transmission (TOT) in floodwater-breeding *Aedes* spp. mosquitoes in temporary wetlands. This is based on a single publication from Kenya in 1985 which has never since been confirmed, despite numerous attempts. Whereas TOT likely plays some role in RVFV maintenance, particularly in arid areas, recent evidence strongly suggests that continuous vector-host circulation, sometimes combined with host movement and possibly vector dispersal, can explain RVFV dynamics in the absence of TOT.

Another popular theory, perpetuated in many publications, is that there may exist a cryptic wildlife reservoir for RVFV. However, current knowledge of arthropod-borne RNA arboviruses suggest that this is highly unlikely, mainly due to the very short viraemic period in vertebrate hosts and the absence of a carrier state. Instead, the “reservoir” for RVFV is likely to comprise a system involving one or more wildlife and/or livestock populations and their associated blood-feeding mosquitoes, with or without a contribution from TOT.

Recent findings from South Africa and across the continent will be discussed which challenge these two popular theories regarding RVFV epidemiology, and a more likely hypothesis for RVFV maintenance in a reservoir system will be presented.

Veterinary antibiotic traces in formal and informal red meat slaughtered food animals in the West Coast District of the Western Cape

FRIDAY, 14:00

Retrospective Analysis of Serotype Distribution in *Mannheimia haemolytica*, *Pasteurella multocida*, and *Bibersteinia trehalosi* Isolates: Insights from 50 Years of Specimen Data at Onderstepoort Veterinary Research Laboratory.

Itumeleng Matle¹, Moloko Seakamela², Skhumbuzo Mbizeni³

¹*Bacteriology Division, Agricultural Research Council: Onderstepoort Veterinary Research, Onderstepoort, Pretoria, South Africa*

²*Department of Agriculture and Rural Development Lephalale Veterinary Laboratory, Veterinary Services, Department of Agriculture and Rural Development, South Africa*

³*Department of Agriculture and Animal Health, University of South Africa, Pretoria, South Africa*

Respiratory diseases caused by *Mannheimia haemolytica*, *Pasteurella multocida* and *Bibersteinia trehalosi* have been known to result in a considerable loss due to mortality and reduced production in animal. This study utilizes laboratory records to explore the serotype diversity, temporal trends, and seasonal variations of Pasteurellaceae isolates spanning the period 1970 to 2020 in South Africa. Analysis was conducted on 3379 laboratory cases of Pasteurellaceae isolated from diverse animal species, including both clinically healthy animals and those exhibiting respiratory disease symptoms. However, 562 cases, not accounted for in the main species categories, resulted in a total of n=2817 cases. The dataset revealed 15 distinct species within the Pasteurellaceae family, with *M. haemolytica* (46.8%; n = 1318) emerging as the predominant species, followed by *P. multocida* (22.3%; n= 627) and *B. trehalosi* (11.0%; n=310). The prevalence of individual serotypes of *M. haemolytica* revealed that serotype A1 exhibited the highest prevalence at 10.2%, followed by A2 (9.8%), and A6 (7.9). *M. haemolytica* serotypes were identified most often in animals with signs of respiratory disease, but 14% of serotypes were isolated from apparently healthy animals. Five different serotypes of *P. multocida* identified with serotype A being the most prevalent (26.6%) and was exclusively associated with animals with respiratory disease. The distribution of serotype showed a diverse variation in different animal species with ovine and poultry accounting accounts for majority of cases, geographical location (Gauteng recording the highest number of positive cases), and seasonal occurrence. Investigation of temporal patterns of Matle serotypes over the 50-year period showed *M. haemolytica* peak in isolation between 1984-1998, whereas *P. multocida* emerged as a prevalent strain between 1998-2010, with a significant surge continuing into 2011-2023 for *B. trehalosi*. This study provides a comprehensive baseline of



M. haemolytica, *P. multocida*, and *B. trehalosi* associated with respiratory disease across different animal species, informing future epidemiological studies and control strategies.

Keywords: Respiratory disease, Pasteurellaceae, Ovine, Poultry, Porcine, Wildlife, domestic animal

FRIDAY, 14:20

THEME: Wildlife Epidemiology

Tuberculosis in a Skukuza vervet monkey troop – a monkey on the back of the One Health concept?

Lin-Mari de Klerk-Lorist

Introduction: Tuberculosis (TB) in vervet monkeys (*Chlorocebus pygerythrus*) often mirrors the epidemiological patterns seen in human populations. Factors such as population density, contact rates, and environmental conditions can influence the spread of the disease among vervet monkey populations. This disease control exercise sought to determine the prevalence within a habituated vervet monkey troop while preventing spill-over to neighbouring troops and tourists alike.

Methods: Vervet monkeys with clinical signs were captured, euthanised and necropsied. Confirmation of TB infection necessitated further disease control measures and strategic trapping of the exposed vervet monkey troop was implemented. All trapped monkeys were tested for TB with a range of available diagnostic tests including the ante-mortem intrapalpebral tuberculin test and the Quantiferon assay

Results: Confirmation of bovine tuberculosis (bTB) in the index case was surprising, given the human habitat the monkeys frequented (restaurants, shop, camping sites). Disease was severe in all clinically diseased monkeys with tuberculous granulomas present in the lungs, spleen and various lymph nodes. Acid-fast counts on Ziehl-Neelsen impression smears were excessive compared to other species.

Discussion: Previous outbreaks of tuberculosis in monkey populations in Africa were associated with *M. tuberculosis*, especially in zoos and research centres. Given the zoonotic potential of bTB, efforts to control the disease in vervet monkeys can have broader implications for public health. A One Health approach, which emphasizes the interconnectedness of human, animal, and environmental health, especially within a conservation area where there is an increased rate of contact and spill-over risk between humans and primates, is crucial for effective bTB control in non-human primate populations.

Conclusion: Continued research into bTB and TB in vervet monkeys is essential for better understanding the disease dynamics, developing improved diagnostic tools and treatment strategies, and ultimately mitigating the impact of TB on both primate conservation and public health.

FRIDAY, 14:40

Species composition of ticks (Acari: Ixodidae) infesting selected wild ungulates from two protected wildlife management areas in Northern Botswana

Obuile Owen Raboloko^{1*}, Kemolatlhe ON¹, Kgathi V¹, Lele L¹, Thlolwane OI¹, Mogwera K², Gwafila M¹, Ponego, L¹

¹Department of Veterinary Services, Ministry of Agriculture, Gaborone, Botswana

²National Agricultural Research and Development Institute

*Author to whom correspondence should be addressed

Abstract

Introduction: Ticks transmit a variety of pathogens and are considered primary vectors of diseases of wildlife, livestock and public health importance. Little is known on ticks infesting wildlife animals in two protected wildlife management areas in northern Botswana.

Method: To address this gap, a convenience survey was conducted to determine the species composition of ixodid ticks infesting selected wildlife animals namely: Giraffe, Giraffa (*Camelopardalis*); African buffalo, (*Syncerus caffer*); Kudu (*Tragelaphus strepsiceros*); Impala (*Aepyceros melampus*), waterbuck (*Kopus ellipsiprymnus*), Red lechwe (*Kobus leche*) at the two protected wildlife areas in northern Botswana. To this end, hundred and twenty (120) adult animals were each opportunistically sampled on a single occasion from June 2020 to June 2021. A total of eighty six (86) ixodid ticks belonging to three tick genera and five species were found to be parasitizing wildlife animals.

Results: Of the recovered ticks, *R. evertsi evertsi* (51%) was found to be the most prevalent followed by *A. variegatum* (20%). *R. evertsi evertsi* had the highest host richness followed by *R. (B.) decoloratus*. African buffalo was the major host of tick species identified. Notably, large animals were significantly infected with ticks compared to small animals. **Conclusion:** Our work provides invaluable insight on ticks infesting wildlife animals at the two protected management areas in northern Botswana, thus, highlight the need for further epidemiological investigations on ticks and TBDs at the wildlife–livestock–human interface in northern Botswana under “One Health” paradigm.

FRIDAY, 15:00

Black-backed jackal-associated rabies case in white rhino from North-West Province, South Africa

Chuene Ernest Ngoepe

Co-presenters: Prof Daniel Qekwana², Prof James W. Oguttu⁴, Prof Claude Taurai Sabeta^{1,3}

¹WOAH Rabies Reference Laboratory, Agricultural Research Council (Onderstepoort Veterinary Institute), Onderstepoort, 0110, Pretoria, South Africa (claude.sabeta@up.ac.za)

²Department of Paraclinical Sciences, Faculty of Veterinary Science, University of Pretoria, Onderstepoort, 0110, Pretoria, Gauteng, South Africa (nenene.qekwana@up.ac.za)

³University of Pretoria, Department of Veterinary Tropical Diseases, Private Bag 04, Onderstepoort, 0110, Pretoria, South Africa (claude.sabeta@up.ac.za).

⁴Department: Agriculture and Animal Health, School of Agriculture and Life Sciences, University of South Africa, Pretoria, 0001, Gauteng, South Africa (joguttu@unisa.ac.za)

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. There are two forms of rabies epidemiological cycles which includes urban and sylvatic. The urban rabies cycle constitutes a dog-to-dog transmission cycle whereas sylvatic rabies is characterized by the involvement of wildlife that maintain stable cycles of transmission over time in particular geographic areas. Recently, North-West province has been shown to have both urban and sylvatic rabies epidemiological cycles respectively. The objective of the study was to identify which rabies cycle resulted in the death of a white rhino in North-West Province. A brain specimen was submitted to ARC-OVR on the 06 August 2022 from Elandslaagte farm for rabies confirmation. The appropriate brain parts were extracted and examined to confirm the diagnosis using the gold standard direct fluorescent antibody test (dFAT) and a partial region of the glycoprotein gene as well as the variable G-L intergenic region of the viral genome was analysed using nucleotide sequences generated from the PCR amplicons. The brain tissue tested positive for rabies on dFAT confirming the white rhino was infected with lyssavirus. The monoclonal antibody typing, and phylogenetic reconstruction demonstrated that the white rhino was infected with canid rabies virus variant. Further, the phylogenetic analysis revealed



that rabies virus sequences obtained from the black-backed jackals had 100% sequence identity with rabies virus sequence obtained from the white rhino. Furthermore, the data suggest a black-backed jackal-associated rabies virus caused infection in the white rhino in the North-West province, South Africa. Therefore, there is a need for greater awareness regarding zoonotic risks such as rabies, prophylactic measures, and the establishment of specific procedures to limit attacks from rabid wildlife in conservation areas especially the endangered species.

FRIDAY, 15:20

Translocation risk assessment model for white rhinoceroses (*Ceratotherium simum*) from wildlife populations infected with tuberculosis, South Africa

Oonagh Pretorius¹, José Pablo Gomez Vazquez¹ & Beatriz Martínez Lopez¹

1.Center for Animal Disease Modeling and Surveillance, University of California Davis

Introduction: In South Africa, rhino conservation is under threat from a range of environmental factors and poaching. Strict movement restrictions imposed on rhino populations inhabiting bovine tuberculosis (bTB) infected free-ranging ecosystems, further constrain biological preservation of the species.

Aim: To develop a tool with which to assess the risk of translocating white rhinoceros from bTB-endemic areas into wildlife populations of negative or unknown tuberculosis status, under a variety of population scenarios, bTB prevalence levels, diagnostic test parameter uncertainty and subsequently quantify the financial requirements of undertaking a test and quarantine procedure.

Method: Analyses were performed using *@RISK* and *R* statistical software. Monte Carlo-type simulations were run using 5000 iterations. The proportion of true infected individuals were sampled from a hypergeometric distribution with a standard bTB prevalence value of 0.18 (0.05; 0.45). The proportion of true positive and true negative reactors were sampled from a binomial distribution. Shipment status simulations were evaluated at various rejection criteria of positive reactors. Quarantine costs were calculated for cohort sizes between one and twenty.

Results & Discussion: Disease transmission risk was minimised when candidates were sourced from populations with bTB prevalence levels of 0.25 or lower; population size did not alter the outcomes; three rounds of screening tests should be performed in series over an extended quarantine period; and cohort rejection criteria should be limited to one individual testing positive. Input costs for a test-out quarantine operation were very high and profit margins were not overly lucrative but were maximised when groups of twenty animals were subdivided into cohorts of four to eight animals.

Conclusion: This model provides a preliminary method with which to quantify the risk of disseminating bTB via white rhino translocations, facilitate decision-making, source optimal quarantine candidates and curb financial losses and could potentially be applied to a range of alternative disease and species scenarios.

FRIDAY, 15:40

-- END ORAL PRESENTATIONS --



Poster Presentations

in order of appearance as on the programme

POSTER SESSION 1 – WEDNESDAY 21 AUGUST 2024, 12:30

4. Prognostic indicators of survival in dogs with clinically suspected canine distemper infection in Harare, Zimbabwe

Takudzwanashe Matiza

Department of Clinical Veterinary Sciences, Faculty of Veterinary Science, University of Zimbabwe, Harare, Zimbabwe.

Department of Companion Animal Clinical Studies, Faculty of Veterinary Science, University of Pretoria, Onderstepoort, South Africa. Department of Clinical Veterinary Sciences, Faculty of Veterinary Science, University of Zimbabwe, Harare, Zimbabwe.

Introduction: Canine distemper (CD) is a highly contagious disease that affects dogs of all ages, with a high mortality. Definitive diagnosis of CD is challenging in clinical practice, and many dogs are diagnosed based on clinical suspicion alone.

Aims: The main objective of this prospective, observational, and descriptive field study was to assess the correlation of clinical suspicion of CD to diagnostic antigen testing for canine distemper virus (CDV). A secondary objective was to determine prognostic indicators of survival in dogs with suspected canine distemper.

Methods: fifty-two client-owned dogs with clinical signs consistent with canine distemper were diagnosed at the University of Zimbabwe Veterinary Teaching Hospital. They were tested with two different commercial immunochromatography (IMC) tests and a reverse transcriptase PCR of conjunctival and nasal swab samples. Clinical, haematological, and biochemical parameters were recorded for patients. Univariate and multivariable logistic regression analyses were performed to evaluate factors associated with survival at 21 days.

Results: Of the study dogs, 9.6% (n = 5/52) and 1.9% (n = 1/52) tested positive with both IMC and RT-PCR tests, respectively. Multivariate analysis showed increased mortality was associated with the presence of neurological signs (OR = 8.61; 95%; P = 0.024), dogs presented longer than 6 days from the development of clinical signs (OR = 8.10; 95%; P = 0.017), and dogs weighing more than 25 kg (OR = 9.93; 95%; P = 0.022).

Conclusion: The study revealed a low correlation between clinical diagnosis and CDV diagnostic testing. This may be due to poor test sensitivity or case selection. As case selection was stringent, findings highlight the low confidence of private veterinarians in the currently available point-of-care tests to diagnose CD. The increased association of mortality with neurological presentations and delayed presentation was expected; however, increased mortality in larger dogs was unexpected.

7. Husbandry practices among peri-urban free-roaming pigs in Gert Sibande District Municipality, Mpumalanga Province, South Africa

Priscilla Makungo^{1, 2, #}, Folorunso Oludayo Fasina^{3, 4}, Christian Anayochukwu Mbajiorgu² and James Wabwire Oguttu²

¹Department of Agriculture, Rural Development, Land and Environmental Affairs, Nooitgedacht Research Farm, Animal Research, Non-Ruminant sub-directorate, Ermelo, 2350; ²Department of Agriculture and Animal Health, College of Agriculture and Environmental Science, University of South Africa; ³Food and Agriculture Organization of the United Nations, 00153 Rome, Italy; ⁴Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, Onderstepoort, 0110, South Africa

Introduction: The aim of this study was to investigate the peri-urban free roaming pig (FRP) production husbandry practices and identify production constraints and risks in Gert Sibande District Municipality of Mpumalanga province.

Methods: A cross sectional study design was adopted in this study. Snowball sampling technique was used to identify farmers keeping pigs on a FRP basis. A total of 124 farmers were identified and agreed to voluntarily participate in the study. Data was summarised using descriptive statistics and presented as tables and figures. Cross-tabulation and correlation analysis were used to assess the relationship between categorical variables. The data was analysed using SPSS V28.0, and statistical significant was set at $\alpha = 0.05$ for all analyses.

Results: The overwhelming majority (93.5%) of farmers reared pigs without permission from the local authorities and were not registered for animal identification (72.6%). While 94.35% did not employ disinfection, 87.1% of pig farmers were unaware of transboundary animal diseases and zoonosis. Majority (75.8%), of farmers adopted no weaning protocol to manage their pigs. Most farmers reared exotic breeds or their crosses (72.5%), and most of the sows (51.6%) farrowed 6 - 10 piglets per litter. More farmers who reared exotic breeds or their crosses weaned >11 (large litters) (23.4%) in comparison to farmers who reared the indigenous (17.5%) and crosses of indigenous/exotic breeds (16.7%). Moreover, farmers who reared exotic breeds weaned of the litters at ≤ 60 days (30%) as compared to those who reared other breeds. Rearing pigs on a FRP scavenging basis around residential areas had a significant positive relationship with pigs crossing roads and owners not concerned with where the pigs got their feeds.

Discussions and Conclusion: The widespread poor husbandry practices and production indices observed among FRP farmers presents opportunities to develop customized risk communication and community engagement materials for farmers and the communities. Gert Sibande District Municipal authorities should adopt a fit-for-purpose peri-urban livestock policy, with clear incentives and penalties to promote animal identification and good practices. Given the potential of pigs spreading diseases to humans, good production practices have the potential to reduce risks of spread of diseases from animal-sourced food to humans.

25. Student Voice in the Development of a Pedagogic Model for Integrating Ethnoveterinary Medicine into the Curriculum of Animal Health Education

Rendani Victress Ndou¹ & Amogelang Khule¹ & Nothemba Ndukuya¹

¹Centre of Animal Health Studies, School of Agricultural Studies North West University, Mafikeng Campus, Private Bag X2046, Mmabatho, 2735

Ticks and tick-borne diseases (TBDs) have a major impact on livestock productivity in South Africa. TBDs included economically significant diseases such as heartwater, babesiosis, and anaplasmosis. Therefore, this study was conducted to evaluate the knowledge and practices of communal livestock farmers regarding ticks and TBDs in Mafikeng Local Municipality. Data was collected from 305 farmers (110 cattle, 95 goats, and 100 sheep) using a structured questionnaire. The data was analyzed for descriptive and inferential statistics using SPSS version 29. The findings revealed that a majority of cattle farmers had some knowledge of ticks and TBDs diseases. However, when shown pictures, only 45.44% of them were able to identify *Hyalomma* tick and 29.99% identified *Amblyomma* tick. Among goat farmers, 50% had sufficient knowledge of tick-borne diseases, but the majority could only identify *Amblyomma* tick, while none of them were able to identify *Rhipicephalus* tick. Surprisingly, 12% of sheep farmers did not believe that sheep can contract diseases from ticks, and a staggering 84% of them were unable to identify the *Amblyomma* tick from a picture. The most common tick control method used across all three enterprises was acaricides, with manual removal and ethnoveterinary medicine also being used. The Chi-Square test for independence with values $\chi^2=55,516a$, $df = 30$, and $p=0.003$ revealed that the level of education of farmers had a significant association with their knowledge of ticks and TBDs. The study concluded that farmers need more extension services on ticks and TBDs. Additionally, effective, affordable, sustainable, and environmentally friendly tick management strategies including those presented by ethnoveterinary medicine should be investigated, developed, and promoted. The study recommends that stakeholders collaborate and coordinate their efforts to address the challenges associated with ticks and TBDs in livestock production.

28. Systematic review on traditional medicinal plants used for the treatment of livestock diseases in the Eastern Cape Province

Siza Mthi N. Nongauza & Z. Dubeni

Dohne Agricultural Development Institute, Private Bag x 15, Stutterheim 4930, Eastern Cape, South Africa, Department of Rural Development and Agrarian Reform, Private Bag X9032, East London, 5200, Department of Botany and Zoology, Faculty of Science, University of Fort Hare, Private Bag x 1314, Alice 5700, South Africa.

Majority of people in South Africa rely on traditional medicinal plants to treat several diseases including livestock. However, few studies conducted to document medicinal plants used for the treatment of livestock diseases in the province.

This systematic review was aimed to examine and synthesize available evidence focusing on medicinal plants used for the treatment of livestock diseases in the Eastern Cape Province.

Data for this review were generated from published peer reviewed journals, conference proceedings and theses. There was no restriction on the period of publications and no discriminations were made in relation to methodologies applied when collecting data. Focus was only on flora found in the Eastern Cape Province. Data were analysed using descriptive statistics and to calculate frequencies, percentages and generate graphs Microsoft Excel (2016) was used. This search produced 19 articles. Most studies were done within the radius of 200 km around Fort Hare University.

From a total of 75 research articles use of medicinal plants to treat livestock diseases belonging to 56 plant species and 33 families were identified in the Eastern Cape Province. The most used plant families were *Asphodelaceae* 10.7%, *Fabaceae* 8.9%, *Lamiaceae* 8.9%, *Rubiaceae* 5.4%, *Rutaceae* 5.4%, *Asteraceae* 3.6%, *Apiaceae* 3.6%, *Hypoxidaceae* 3.6% and *Asparagaceae* 3.6%. *Aloe ferox*, *Acokanthera oppositifolia* and *Elephantorrhiza elephantina* were the most often mentioned medicinal plants to treat livestock disease in the Eastern Cape Province. Trees were the most dominant growth form while leaves (38.7%), and roots (24.2%) were frequently used plant parts for treatment preparation. Oral (72.3%) administration was the favourable route of administration and prepared through fresh plant materials.

Medicinal plants have been used to treat various livestock diseases in the Eastern Cape Province. Information obtained from this review will serve as a guide to discover novel agents from plants. Therefore, there is an urgent need to conduct further research to identify and document plants used to treat livestock diseases in the Eastern Cape Province.

30. Prevalence and associated risk factors of *Cryptosporidium* in domesticated ruminants in the Rust de Winter area, Gauteng Province, South Africa

Tebogo Atlivia Seanego^a, M.C. Marufu^{a*}, C. Byaruhanga^a, L. Korsten^b

^a*Department of Veterinary Tropical Diseases, University of Pretoria, Private Bag X4 Onderstepoort, 0110, South Africa;*

^b*Department of Plant and Soil Sciences, Department of Science and Innovation National Research Foundation Centre of Excellence Food Security, University of Pretoria, Pretoria, 0002, South Africa*

Cryptosporidiosis, an emerging enteropathogenic disease with negative implications for public and livestock health, remains poorly investigated in Africa, necessitating focused epidemiological studies. To determine the prevalence and risk factors associated with *Cryptosporidium* infections in domesticated ruminants, a longitudinal study was conducted on seven farms in Rust de Winter, Gauteng Province, South Africa. During winter (2022) and summer (2023), 370 faecal samples were collected from cattle (n=146), sheep (n=105), and goats (n=119). Microscopic analysis using the gold standard Modified Ziehl Neelsen (MZN) test was

employed, followed by screening of the positive samples for *Cryptosporidium parvum* using quantitative real-time PCR (qPCR). Microscopy identified *Cryptosporidium* oocysts in 57 (15.4%) of the 370 faecal samples. However, the qPCR detected *Cryptosporidium* DNA in only one (1.8%) of the 57 MZN-positive samples. Despite the limitations associated with the qPCR method, this research provides valuable insights into the epidemiology of *Cryptosporidium* infections in ruminants in Gauteng Province. Further investigation involving more animal farms and assessment of the occurrence of infections in humans will contribute to more understanding of *Cryptosporidium* infections. There is also a need to evaluate clinical vs sub-clinical cases on farms with regards to the detection limit of nucleic acid-based methods.

34. Evaluation of the qualitative economic impact of African swine fever virus outbreaks using the Outcost tool in the Mpumalanga Province, South Africa

Taelo Sibi^{1,2}, Folorunso Oludayo Fasina², Japhta Mokoel³

¹Department of Agriculture, Rural Development, Land and Environmental Affairs, Mpumalanga Provincial Veterinary Services, Veterinary Diagnostic Services, Ermelo, 2350, South Africa

²Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, Onderstepoort, 0110, South Africa

³Department of Agriculture and Animal Health, College of Agriculture and Environmental Science, Florida, University of South Africa

Background: African swine fever virus (ASFV) is a DNA virus that causes high fatalities of domestic pigs. Since 2019, ASFV outbreaks outside the endemic areas of the MP have been recurring. A novel approach to conduct economic evaluation and analysis has been developed called the Outbreak COSTing Tool (OutCosT). ASFV can have devastating impacts on pig farmers and value chain actors. Socioeconomic articulations with attribution to ASF outbreaks are desirable within the province, particularly as it impacts on smallholder farmers. Reliable statistics based on ground level surveys are scarce, making traceability and planning difficult. The OutCosT tool will allow the opportunity to conduct quantitative economic impact-evaluations of ASFV outbreaks in Mpumalanga.

Aim: To determine the quantitative economic impacts and cost implications of limited and widespread outbreaks of ASFV in the Mpumalanga Province South Africa.

Material and methods: The OutCosT cost input items will be used. Surveys are designed to meet subcategory outputs: Direct cost of the disease; control and eradication measures in affected farms; cost of the disease and measures in neighbor and contact farms; prevention and surveillance activities in non-affected farms; coordination and other control measures; awareness and training campaigns. The skip-logic and snowball approaches are used to cater for ASFV real directly affected outbreak sites; 3km quarantine and 10km surveillance zones; scenario cases; State Veterinary Services (SVS) and other stakeholders surveys are conducted.

Results: Results have demonstrated that farmers that are directly impacted by ASFV suffer between 60-85% in direct livestock losses. While indirectly affected farmers suffer economic losses mainly due to loss of sales opportunities. The SVS incurred the most significant losses of stakeholders that deal with the ASFV disease outbreaks.

Discussion: Affected smallholder pig farmers suffer significant socio-economic losses due to ASFV-outbreaks. SVS experiences significant financial expenditure attempting to control the ASFV-outbreaks, while endeavouring to achieve food safety and security objectives.

Conclusion: The OutCosT tool has the potential to quantify the impact of ASFV outbreaks within the Mpumalanga Province.

44. Detection of *Theileria haneyi* in South African equids using a newly developed quantitative real-time PCR assay.

Tshenolo Mbaba¹, NE Collins¹, RV Bhoora¹

¹Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, Private Bag X04, Onderstepoort, 0110, South Africa.

Theileria haneyi is an apicomplexan parasite that is closely related to *Theileria equi*, a known causative agent of equine piroplasmiasis. *Theileria equi* genotypes A, B, C, and D have been reported to occur in South African equids. Preliminary studies in South Africa indicated an association between *T. equi* genotype C and *T. haneyi* infections. The molecular distinction between these parasites is reliant on a nested PCR assay, which has been reported to be unreliable. A recently reported indirect ELISA based on the equi merozoite antigen (*ThEMA-11*) of *T. haneyi* can detect geographically diverse *T. haneyi* strains. Based on the exclusivity of the *ema-11* gene to *T. haneyi*, we developed a TaqMan minor groove binder (MGB™) quantitative real-time PCR (qPCR) assay to amplify and detect the *ema-11* gene. Published *Thema-11* gene sequences were used to design primers for the amplification of the *ema-11* gene from South African samples. *Thema-11* amplicons were cloned and sequenced. An alignment of the South African *ema-11* gene sequences with published sequences enabled the identification of a conserved region for the design of the qPCR assay. The *T. haneyi ema-11* (*Thema-11*) qPCR assay was shown to be rapid, specific, and sensitive in detecting *T. haneyi* infections. The diagnostic utility of the *Thema-11*-specific qPCR assay was evaluated together with a *T. equi ema-1*-specific qPCR assay. *Theileria haneyi* was detected in 75% of the South African field samples screened, while the occurrence of *T. equi* based on the quantitative amplification of the *ema-1* gene was much higher (100%). These results suggest that used in combination, the *Thema-11*-specific qPCR assay, and the *T. equi ema-1*-specific qPCR assay could detect and differentiate between *T. haneyi* and *T. equi* infections.

46. Knowledge, attitude and practices: an investigation and assessment of the medicinal plants' potential to heal wounds in communal cattle at Ephraim Mogale Municipality, Limpopo Province

Malebo Lekgethisho

Introduction: Plant based therapy is widely used in different parts of the world to treat animals and human ailments due to their accessibility, affordability and effectiveness. Ethno veterinary medicine is based on beliefs, knowledge, skills and practices to safeguard the health and welfare of humans and animals. In the Ephraim Mogale municipality, animal wounds represent some of the major burdens to animal production as they cause severe economic losses, impaired health, damaged hides, weight loss, loss of fertility and death through wound infections and septicemia which may lead to loss of commercial value. Due to lack of financial resources, farmers often resort to medicinal plants to treat animal wounds. However, there is no data on the efficacy, formulation and guidelines on these medicinal plants in the municipality. Therefore, this study seeks to (1) investigate and analyze the efficacy of commonly used plants in treating animal wound (2) investigate the livestock practices in communal areas of the Ephraim Mogale Municipality and (3) to isolate the compounds from selected plants

Material and Methods: Quantitative and qualitative research methods will both be used in this study. Qualitative data will be collected using a semi-structured interviews to assess knowledge, attitudes and perceptions of farmers in the municipality. Structured questionnaires will be developed to obtain data related to plants used for the treatment of cattle wound. Samples of commonly used plants will be collected and transported to the laboratory, for analysis. The Statistical analysis will be performed using Prism software (GraphPad), Thematic software & SPSS V28.0 (IBM Corp, 2021)

Discussion and conclusion: This study will be the first of its kind around Ephraim Mogale Municipality communal livestock farmers to investigate and analyse the medicinal plants having potential to wounds healing and to document the practices used. The study will also validate the efficacy, safety precautions of the traditional medicines used in wound healing treatment potential in livestock.

60. Comparison of the Bionote NSP Ab ELISA and Priocheck FMDV NS ELISA

Khomotso Moabelo¹, Angelika Loots¹, Sven Parsons^{2,3}, Melvyn Quan¹

¹University of Pretoria, Department of Veterinary Tropical Diseases, Pretoria, South Africa.

²Deltamune, Roodeplaas, Pretoria, South Africa.

³University of Pretoria, Department of Anatomy and Physiology, Pretoria, South Africa.

Foot and mouth disease (FMD) is a highly contagious viral disease that causes devastating economic losses due to decreased productivity, trade restrictions and control measures. Accurate and timely diagnostics are crucial for effective disease management, including early detection, control, and prevention. The detection of antibodies against non-structural proteins (NSP) of the FMD virus (FMDV) is one of the best tools to determine natural FMDV infection and can be used to differentiate infected from vaccinated animals. The purpose of the study was to evaluate the diagnostic agreement between the Bionote NSP Ab ELISA and PrioCheck FMDV NS ELISA. Four hundred and one serum samples were obtained from the Agricultural Research Council-Onderstepoort Veterinary Institute, Transboundary Animal Disease (ARC-OVR, TAD) Biobank. Results indicated that 257 (64 %) samples were negative on both the Bionote and PrioCheck ELISAs, 132 (33 %) serum samples tested positive on both ELISAs, and 38 (9 %) and 12 (3 %) samples tested positive on the Bionote and PrioCheck ELISAs, respectively. Cohen's Kappa coefficient for the two tests was calculated to be 0.7, depicting moderate to substantial agreement between the two ELISAs. Based on these findings, it was concluded that both the Bionote and PrioCheck ELISAs demonstrate effectiveness in detecting FMDV NSPs. It also suggests a degree of confidence in their ability to identify positive samples. However, the disparity in the number of samples testing positive on each test suggests that there may be variations in sensitivity or specificity between the two ELISAs. Further investigations are warranted to identify the factors contributing to these differences and to determine the optimal circumstances in which each test should be used. Overall, the evaluation provides valuable insights into the performance of the Bionote NSP Ab ELISA and PrioCheck FMDV NS ELISA and highlights their potential applications in FMD diagnostics.

61. Construction of three foot-and-mouth disease virus peptide phage display libraries as a tool for the identification of important epitopes

Naledi Sekgobela^{1,2}, Pamela A. Opperman^{1,3}, Jeanni Fehrsen^{1,2} and Melanie Chitray^{1,2}

¹Agricultural Research Council, Onderstepoort Veterinary Research Institute, Vaccines and Diagnostic Development Programme, Onderstepoort, Pretoria, South Africa,

²Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, South Africa.

³Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, South Africa.

Foot-and-mouth disease (FMD) is a transboundary animal disease affecting cloven hoofed animals where outbreaks significantly impact livestock production, particularly in the endemic sub-Saharan African region, where five of the seven FMD virus (FMDV) serotypes exist. In South Africa, the African buffalo is the FMDV wildlife maintenance host deeming eradication near impossible. Thus, emphasis is mainly placed on control by vaccination and animal movement restriction. The FMD virus exhibits high antigenic variation where vaccination against one serotype does not confer protection against another, mainly due to variations on the capsid coding (P1) region of the FMDV genome. Knowledge of FMDV antigenic sites can be useful to produce recombinant FMD vaccines with broad and long-lasting immunological responses, therefore improving FMD control. Towards this end, three FMDV phage display peptide libraries were constructed using the fragmented P1 regions of FMD serotype SAT1, SAT2 and SAT3 viruses and biopanned against purified IgGs obtained from FMDV infected bovine sera samples. Through biopanning, a 36-mer peptide sequence *i.e.*, SAT3 ϕ 1 was identified, potentially forming part of a FMDV SAT3 epitope. The SAT3 ϕ 1 sequence aligned with the FMDV VP1 C-terminus, overlapping the 2A N-terminus. Further analysis revealed nine potential SAT3 antigenic sites, with four potential sites suggesting novel antigenic sites. The FMDV

peptide phage libraries are novel and the study has added value to our understanding of FMDV SAT3 antigenic sites, contributing to FMD research and potentially leading to improved vaccines, reduced livestock vaccination frequency, enhanced trade and livestock productivity, while alleviating poverty through strengthening food security.

68. Conservation and economic benefits of medicinal plants used to treat livestock ailments in the Eastern Cape Province, South Africa

Nwabisa Nongauza^{1#}, S. Mthi² and Z. Dubeni³

^aDepartment of Rural Development and Agrarian Reform, Private Bag X9032, Amathole District Office, East London, 5200. South Africa, ^bDepartment of Rural Development and Agrarian Reform, P.O. Box 112, Queenstown, 5320, ^cDepartment of Botany and Zoology, Faculty of Science, University of Fort Hare, Private Bag x 1314, Alice 5700, South Africa.

Medicinal plants play an important role on socioeconomic and health benefits in most rural areas across Africa especially areas with limited veterinary health facilities. High utilisation of medicinal plants for various human and animal diseases without proper conservation strategies can lead to the extinct of these plants. This study was conducted to assess the economic benefits and conservation status of medicinal plants in the Eastern Cape Province, South Africa. Pre-tested semi structured questionnaires and transect walks were used to collect data from 56 respondents with focus on their socio-demographic characteristics, medicinal plants used and plant parts used to treat diseases in the communities, preparation and administration of these remedies, availability trend of medicinal plants, drivers of loss of medicinal plants, contribution of medicinal plants to gross incomes and conservation strategies. Results showed fourteen plants species belonging to 6 families were used to treat 10 livestock diseases. The mostly highly cited plant family was Fabaceae. Furthermore, these medicinal plants contributed more than 30% of household gross annual income. Age, level of education, gender, culture was the most determining factor for the use of medicinal plants for family income. Over-harvesting and knowledge limitations were found to be the major constraints that could lead to the scarcity of medicinal plants in these areas. There is a need for increased awareness on various conservation strategies to be identified. The increase in awareness on conservation and protection of medicinal can contribute towards policy development and economic spinoff towards rural development strategies.

70. The effect of the COVID-19 pandemic on vaccination of domestic dogs and incidence of canine parvoviral disease in Pretoria, South Africa

Josef Hanekom and Dr Robert Boyes

Companion Animal Clinical Studies, Faculty of Veterinary Science, University of Pretoria

In South Africa, the pandemic caused by COVID-19 prompted a strict national lockdown with restrictions on movement and social interactions. A rise in vaccine hesitancy and changes in disease incidence were anecdotally observed in veterinary clinics. In this study, we examined the incidence of canine parvoviral disease (CPV) and vaccination against CPV from hospital records of the Outpatients section of the Onderstepoort Veterinary Academic Hospital for the years 2017 to 2021. The study examined incidence between February 19th to June 8th corresponding to the before, during and after the initial 36-day lockdown (26th March 2020) period.

Compared to 2017, the incidence of dogs presenting for vaccination was significantly increased in 2019 (OR = 1.617; 95% CI = 1.445 - 1.809) but reduced in 2020 (OR = 0.541; 95%CI = 0.462 - 0.634) and 2021 (OR = 0.518; 95% CI = 0.447 - 0.601). Compared to 2017, the incidence of dogs presenting for canine parvovirus was increased in 2018 (OR = 1.621; 95% CI = 1.043 - 2.520) and 2021 (OR = 2.375; 95% CI = 1.546 - 3.650).

During the observed time and population, there was a substantial reduction in vaccinations in 2020 and 2021 and this was followed by a significant increase in the incidence of CPV treated at the OVAH. The reduction in dog vaccinations coincided with and persisted after the institution of COVID-19 control measures. Reduced vaccination could have contributed to the substantially increased incidence of CPV observed in 2021. Many factors including climatic and economic factors influence vaccination uptake and canine parvovirus in dogs and more studies are needed to evaluate the effect of vaccine hesitancy on animal health.

78. Comparing udder health status in cattle belonging to small-scale farmers in Eastern Cape and Gauteng provinces, South Africa

Nyeleti Manganyi^{1*}, Dr. Moerane Rebone¹ and Prof. Petzer Inge-Marié¹

¹ *Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Private Bag X04, Onderstepoort 0110, South Africa*

Udder Health is globally known to significantly contribute to calf rearing and food security. Factors such as mastitis and tick burden on udders continue to pose a challenge in South Africa. This study aimed to investigate the prevalence of udder health challenges in cattle belonging to small-scale farmers in two South African districts, Amathole in Eastern Cape province (a rural coastal area) and Sedibeng in Gauteng province (a semi-urban inland area), and compare these findings.

The study comprised three parts of data collection: namely farmer survey, farm visit, and milk sample collection from lactating cows for California Milk Cell Test (a cow side test) and laboratory analysis. The farmer survey was conducted to collect background information such as the farmer's age, farming reason, and cattle herd size; while udder tick burden, udder lesions, and conformation data were determined during the farm visit. Data was analysed using JASP 2020 statistical software version 0.14.1.0.

Cattle results are reflected in Table 1 below. The prevalence of subclinical mastitis was higher in Amathole 73.9% (17/23) than in Sedibeng 42.1% (8/19). The proportion of bacteria positive was higher in Amathole (58.3%) than in Sedibeng (25.0%), n=7 and n=5 respectively.

Table 1. Representation of results

Variable	Eastern Cape (n=69)	Gauteng (n=79)	p-value
Udder lesions	65.2%	27.7%	<0.001
Inactive quarters	15.3%	3.9%	0.0061
Udder tick burden	78.3%	34.2%	<0.001
Poor udder suspension	34.2%	13.0%	<0.001

Farmers in Sedibeng farmed more for economic benefits and seemed to have a better understanding of udder health by dipping their cattle, hence they had fewer udder health challenges.

This study concluded that udder health problems in cows were more prevalent in Amathole district and that ticks were the major contributor to udder damage. Extension services that can educate and motivate farmers regarding udder health management to improve production should be prioritised.

POSTER SESSION 2 – THURSDAY 22 AUGUST 2024, 12:30

1. Knowledge, attitudes and practices of communal goat farmers towards the control of gastrointestinal nematodes

Khanyisani Ndwandwe^{1*}, Michael Chimonyo², Ana Tsotetsi-Khambule³, Munyaradzi Christopher Marufu¹

¹Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, Private Bag X4, Onderstepoort, 0110, South Africa.

²Department of Agricultural and Rural Engineering University Road Thohoyandou, Limpopo, 0950

³Department of Life and Consumer Sciences, University of South Africa, Florida Campus, Roodepoort, 1709, South Africa

*Presenting author: Ndwandwekc@gmail.com; Telephone: +27 78 749 5755

Abstract

Gastrointestinal nematodes (GIN) are a significant impediment to communal goat production, causing considerable economic losses, making their control imperative. However, substantial gaps persist in understanding farmers' perceived knowledge regarding GIN prevalence and control. This study investigated farmers' knowledge, attitudes, and practices on the prevalence and control of GIN in communal goat flocks. A structured close-ended questionnaire was used to interview communal goat farmers (n = 384) across four local municipalities in uMkhanyakude District Municipality of northern KwaZulu Natal, namely: Jozini, Hluhluwe Big 5, Mtubatuba and uMhlabuyalingana. Descriptive statistics, chi-square tests and ordinal logistic regression analyses were conducted using SPSS. Most respondents were male (75%), household heads (67%), aged above 40 years old (69%), and possessed primary or no formal education (66%). While more than 80% of farmers (P < 0.05) were aware of GIN, only 8% were aware of control measures. Logistic regression showed a significant association (P < 0.05) between age and underdosing, with older farmers being 1.4 times likely to underdose compared to younger farmers (P < 0.05). Diarrhoea and emaciation were the most reported clinical signs observed in goat flocks. Poor attitudes among communal goat farmers regarding GIN prevalence and control were observed in the present study. Farmers appeared to be aware of GIN infections on their farms. However, their attitudes and practices are not fulfilling the expectations of successfully controlling GINs. These stemmed from demographic factors such as old age, low education levels and poor-socioeconomic status and contributed to ineffective management and worsened GIN impacts. Targeted programs to improve farmers' veterinary knowledge and more in-depth study of the prevalence of GIN in goats owned by communal goat farmers, are recommended.

10. Dog - mediated Human Rabies Elimination in Kenya: Status, and assessment of knowledge, attitude, and practices of Rabies Elimination Strategy implementation in Selected Counties

Ruphline Anyango¹, Claude Sabeta¹, Joseph Kamau²

¹ Department of Veterinary Tropical Sciences, University of Pretoria

² Kenya Institute of Primate Research.

Dog-mediated human rabies is an important one health threat and is targeted for global elimination by 2030 (Abela-Ridder et al., 2016). There is evidence for success stories from North America and Europe and more recently Namibia to suggest that elimination of dog-mediated human rabies is feasible (Lembo et al., 2010); (Cleaveland et al., 2014). This research seeks to determine the status of rabies elimination in selected counties of Kenya by establishing number of reported cases between 2013 and 2023 and assessing how the Strategic Plan for Elimination of Human Rabies 2014-2030 is being implemented.

This is a mixed study that will be conducted in 5 Counties of Kenya and will entail retrieving records of confirmed cases of rabies in dogs from Kenya Animal Biosurveillance Application (KABS) and dog bites in humans from Kenya Health Information System (KHIS) between 2013 and 2023. Interviews will be conducted to identified stakeholders involved in prevention and control of dog- mediated rabies to assess



the Knowledge, Attitude and Practices on implementation of Strategic Plan for Elimination of Human Rabies 2014 – 2030. The proposal will be submitted to the Research Ethics Committee of University of Pretoria for review and subsequent Ethical Approval. Once granted, an application will be submitted to National Commission for Science, Technology, and Innovation (NACOSTI) in Kenya for a research permit. Authorizations to retrieve data will be sought from the Director of Veterinary Services and Director of Health of each County. All interview respondents will be provided with written consent before interviews.

The findings from this study will provide information on the incidences and spatial distribution, seasonality and cyclicity of dog-mediated rabies in selected Counties of Kenya. The challenges will offer insights on what can be done to ensure policies are better implemented.

12. Histology of the gizzard and proventriculus of indigenous chickens fed wheat offal-based diet supplemented with maxigrain and polyzyme

Babatunde Falana^{1*}; O.O Alabi²; E.M Okon³ and A.J Shoyombo²

¹*Department of Life Sciences, Faculty of Bioengineering, King Fahd University of Petroleum and Minerals, Dhahran, Saudi Arabia.*

²*Department of Animal Science, Faculty of Agriculture, Landmark University, P.M.B. 1001 Omu-Aran, Kwara State, Nigeria*

³*Department of Animal Sciences and Aquatic Ecology, Faculty of Bioscience Engineering, Ghent University, Ghent, Belgium.*

The poultry industry has become a rapidly developing project among the other sectors of meat industries in Nigeria, hence the need to improve the productivity of poultry farming. This study was carried out to determine the effect of maxigrain and polyzyme on indigenous birds. Maxigrain and polyzyme are important enzymes that helps to improve performance, breakdown and absorption of nutrients in poultry birds. Forty-eight domestic birds were raised for eight weeks; water and food were provided *ad libitum* with all management practices. Two dietary treatments with three replicates were used. Treatment 1 was poultry feed without enzyme supplementation, while Treatment 2 was supplemented with enzymes (maxigrain and polyzyme). At the end of the experiment, the organs from the birds (proventriculus and gizzard) were collected and taken for histological analysis. Poultry fed without enzyme supplementation showed marked differences in their gizzard and proventriculus. Poultry fed with enzyme supplementation showed differences in the histology of the gizzard and proventriculus, indicating no positive effect due to enzyme supplementation. Animals fed without enzymes mild sloughing off of the proventricular tubular glands. However, animals fed with supplemented enzymes showed normal proventricular tubular glands, except for the second treatment under this group, which showed visible lesions. Poultry fed without enzyme supplementation showed degenerated subcuticular region for the gizzard, while poultry fed with enzyme supplementation showed inflammatory heterophils, necrosis, marked degeneration of the subcuticular layer, and thick cuticle. This study showed that enzyme supplementation had no positive effect on the gizzard and proventriculus of the indigenous birds.

29. In the light of one health approach, a general overview of zoonotic impacts of West Nile virus in Africa

Ahmed Ibrahim^{a,b*}, Zafer Yazici^c

^a*Department of Preventive Medicine and Clinical Studies, Faculty of Veterinary Sciences, University of Gadarif, P. O. Box. 449, 32211 Al Qadarif, Sudan*

^b*Institute of Biochemistry and Biophysics, Polish Academy of Science, 02-106 Warsaw, Poland*

^c*Department of Virology, Faculty of Veterinary Medicine, Ondokuz Mayıs University, 55139 Samsun, Turkey*

Abstract:

When scrutinizing emerging pandemics from the past to the present, it becomes evident that zoonotic pathogens have played a significant role, particularly in today's context. Zoonotic viruses transmitted via arthropod vectors, such as insects and ticks, are recognized by the World Health Organization (WHO), the World Organisation for Animal Health (OIE), and the Food and Agriculture Organization (FAO) as primary public health concerns. From this perspective, West Nile Virus (WNV), a member of the Flaviviridae family, holds considerable importance among zoonotic pathogens. It is transmitted by blood-sucking mosquitoes (an arbovirus) and can infect humans, horses, and birds, leading to neurological disorders and even death. WNV is also part of the Japanese Encephalitis virus (JEV) sero-complex group, which includes other viruses such as St. Louis Encephalitis virus (SLEV), Murray Valley Encephalitis virus (MVEV), Usutu virus (USUV), and Kunjin virus (KUNV), distributed globally. In recent years, its morbidity, incidence, and case fatality rates have risen in many countries, even outside Africa, due to climate change, exhibiting more frequent seasonality. WNV infection is a transboundary disease of One Health concern, and there are several possibilities for its introduction into non-endemic areas. This situation may necessitate implementing more effective control measures and applying comprehensive field investigations alongside mass sentinel surveillance to minimize the risk of this arthropod-borne disease. Through this presentation, we aim to shed light on this disease, which is considered an endemic in our region, by reviewing and analyzing published works related to its epidemiology, phylogenetic relationships, transmission criteria, species barriers, vaccination, and control implementations within the One Health approach to this crucial zoonotic infection.

32. Tick control measures and tick infestation levels on communal cattle: a case study of Sinthumule – Kutama Area, Limpopo Province

Makhado Sedina M.P¹. Oguttu, J.W.¹

¹.*Department of Agriculture and Animal Health, Florida Campus, UNISA, South Africa.*

Background. Ticks are external parasites responsible for tick-borne diseases in the livestock industry. The lack of information on the level of tick infestation makes it hard to determine their effects on a countrywide scale. Establishing tick infestation levels helps to determine effective tick control strategy while preventing tick-borne diseases. However, there is no evidence of studies that have investigated tick infestation levels on cattle and the status of tick control measures in the study area. Therefore, this study investigated the tick control measures and tick infestation levels on communal cattle of Sinthumule – Kutama area.

Methodology. A cross-sectional study design of a quantitative nature was employed to realise the objectives of this study. Semi-structured face to face interviews and checklist were used to collect farm and animal level data. Randomly selected farmers (n=168) within the 17 villages of the study area were interviewed. Tick counts on different predilection sites of randomly selected cattle (n=788) was conducted. Data was analysed using STATA (Version 17).

Results. Most cattle farmers were males (67.26%) and married (57.74 %). The dominant age group was over >60 of age and had attained secondary level (60.21%). Most respondents kept mixed herd (97.02%). Most cattle (49.62 %) were old (>8 years old). Cattle with a body score condition of 4 were the majority (74.62%). Average tick count was highest on the lower perineum (M =37.5; IQR =43). Over 94% of respondents indicated that there were no dipping tanks available in their areas, while dipping facilities were not in good condition (96.43%). Over half of farmers (54.76%) indicated that dipping was rarely conducted. Pour-on method (61.31%) was the most practiced strategy.

DISCUSSION. Cattle keeping is still a male dominated industry. The results confirm that the lower perineum tend to carry the highest tick infestation levels.

CONCLUSION

High tick challenge observed in this study, can be attributed to the disruption of tick control services as reported by the participant, incorrect preparation and application of acaricides.

33. Temporal changes in the prevalence of *Staphylococcus aureus* colonisation among humans in South Africa: Retrospective study from 2013 to 2017

Onalenna Mabalane¹, Themba Sigudu²

¹.Department of Virology, School of Pathology, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg, South Africa

².Department of Health and Society, School of Public Health, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg, South Africa

Introduction: *Staphylococcus aureus*, a Gram-positive bacterium, commonly inhabits in the skin and upper respiratory tract of humans and can lead to various infections in both community and hospital environments. This study aimed to describe the prevalence of *S. aureus* isolates obtained from samples isolated from humans that have undergone diagnostic testing in South African laboratories.

Methods: The research analysed a dataset comprising 16,543 positive *S. aureus* isolates from diagnostic laboratories in the province between 2013 and 2017. Crude and factor-specific proportions for categorical variables along with their corresponding 95% confidence intervals (95% CI) were computed. Temporal graphs were used to depict the annual variation in the proportion of *S. aureus*.

Results: The results indicated that 52.4% of isolates were attributed to males, 46.0% to females, and the least proportion were from unspecified sex (1.6%). The majority of isolates originated from individuals with unspecified age (16.1%), followed by those aged 30-34 years (9.6%), while individuals aged 60-64 years contributed the least (3.1%). Gauteng province had the highest proportion of isolates (37.4%), followed by KZN (21.9%) and the Western Cape (10.8%). Throughout the study duration, there was a consistent increase in isolates, rising from 10.9% in 2013 to 26.1% in 2016, with a sharp increase between 2014 and 2015. Nevertheless, seasonal variations in isolate numbers were minimal, with autumn (22.5%), winter (29.0%), spring (28.0%), and summer (20.5%) making relatively similar contributions. A somewhat noteworthy association between age and specimen type was detected ($p = 0.085$), with individuals of unspecified age contributing the highest proportion of specimens (16.1%).

Conclusion: The study provides valuable insights into the demographic and temporal patterns of *Staphylococcus aureus* prevalence in South Africa. The findings highlight the need for continued surveillance and targeted interventions to mitigate the burden of the pathogen, particularly in regions with higher prevalence and among specific demographic groups.

37. Coagulase Positive *Staphylococcus aureus* Isolated between 2010 and 2014 from specimens submitted to diagnostic laboratories in Mpumalanga Province, South Africa

Mojaki Nyabela¹, Molefi Rakometsi¹, Akuphelo Klaas¹, Themba Sigudu²

¹.School of Public Health, University of the Witwatersrand, Johannesburg, South Africa.

².Department of Health and Society, School of Public Health, University of the Witwatersrand, Johannesburg, South Africa.

Introduction: *Staphylococcus aureus*, a significant human pathogen with potential zoonotic implications, poses risks to both human and animal populations. This study aimed to characterise the distribution of *S. aureus* isolates obtained from human specimens submitted to diagnostic laboratories in Mpumalanga Province between 2010 and 2014.

Methods: The study examined data of 11 465 *Staphylococcus aureus* isolates obtained from diagnostic laboratories in the province between 2010 and 2014. Crude and factor-specific proportions for categorical variables with corresponding 95% confidence intervals (95% CI) were computed. Temporal graphs were used to depict the annual variation in the proportion of *S. aureus*.

Results: Results indicated a male predominance (52.7%) in *S. aureus* isolates compared to females (45.6%), with the least proportion from individuals with unknown sex (1.7%). Patients of unspecified age contributed

the highest proportion of isolates (19.4%), followed by the 0-4 age group (12.5%), while those aged 60-64 years contributed the least (2.5%). Isolates predominantly came from the Ehlanzeni district (63.6%), followed by Nkangala (22.4%) and Gert Sibande (13.9%) districts. The proportion of isolates increased steadily from 16.8% in 2010 to 25.1% in 2014, with a sharp increase from (18.2%) in 2012 to (23.1%) in 2013. Seasonal variation was minimal, with autumn, winter, spring, and summer each contributing approximately a quarter of the isolates (25.8%, 27.3%, 24.2%, and 22.7%, respectively). A marginally significant association ($p = 0.085$) between age and specimen type was observed, with patients of unknown age contributing the most specimens (19.4%).

Results indicated a male predominance (52.7%) in *S. aureus* isolates compared to females (45.6%), with a smaller proportion from individuals with unknown sex. Patients of unspecified age contributed the highest proportion of isolates (19.4%), followed by the 0-4 age group (12.5%), while those aged 60-64 years contributed the least (2.5%). Isolates were predominantly sourced from the Ehlanzeni district (63.6%), followed by Nkangala (22.4%) and Gert Sibande (13.9%) districts. The proportion of isolates increased steadily from 16.8% in 2010 to 25.1% in 2014, with a sharp rise from an unspecified percentage in 2012 to an unspecified percentage in 2013. Seasonal variation was minimal, with each season contributing relatively evenly. Results indicated a male predominance (52.7%) in *S. aureus* isolates compared to females (45.6%), with a smaller proportion from individuals with unknown sex. Patients of unspecified age contributed the highest proportion of isolates (19.4%), followed by the 0-4 age group (12.5%), while those aged 60-64 years contributed the least (2.5%). Isolates were predominantly sourced from the Ehlanzeni district (63.6%), followed by Nkangala (22.4%) and Gert Sibande (13.9%) districts. The proportion of isolates increased steadily from 16.8% in 2010 to 25.1% in 2014, with a sharp rise from an unspecified percentage in 2012 to an unspecified percentage in 2013. Seasonal variation was minimal, with each season contributing relatively evenly. Results indicated a male predominance (52.7%) in *S. aureus* isolates compared to females (45.6%), with a smaller proportion from individuals with unknown sex. Patients of unspecified age contributed the highest proportion of isolates (19.4%), followed by the 0-4 age group (12.5%), while those aged 60-64 years contributed the least (2.5%). Isolates were predominantly sourced from the Ehlanzeni district (63.6%), followed by Nkangala (22.4%) and Gert Sibande (13.9%) districts. The proportion of isolates increased steadily from 16.8% in 2010 to 25.1% in 2014, with a sharp rise from an unspecified percentage in 2012 to an unspecified percentage in 2013. Seasonal variation was minimal, with each season contributing relatively evenly.

Conclusion

The study highlights variations in *S. aureus* distribution by sex, age, district, and specimen type, with insignificant seasonal influences. Further investigation into district-specific disparities and drivers behind the observed increase in isolates is warranted to enhance our understanding of *S. aureus* transmission dynamics and inform infection, prevention and control strategies across human and animal populations.

38. Tuberculosis at the wildlife/livestock/human interface in southern Bushbuckridge, Mpumalanga, South Africa

Oupa Rikhotso

Introduction

Study aim was to investigate presence of infection in cattle and farmers at the selected diptanks at the wildlife/livestock/human interface, if found to be present the prevalence using the intradermal comparative skin test. Re-train Animal Health Technicians on intradermal tuberculin test. Bovine tuberculosis transmission risk factors between cattle and buffaloes were investigated by using a questionnaire. The study site of Bushbuckridge south state veterinary area was chosen because it borders the KNP.

Objectives

1. Determine *M. bovis* infection presence in cattle at each of the 8 study diptanks, if present to estimate its prevalence by using the intradermal comparative skin test and
2. Determination whether it occurs in humans in the study area through collaboration with department of health
3. Re-train AHTs in TST, assess their skills improvement
4. Estimate frequency, location of buffalo break-outs using questionnaire interview with the local farmers and veterinary officials.

Materials and Methods: Study Area: Bushbuckridge South State Veterinary area, at the interface with the KNP. 8/44 diptanks abutting the wildlife-livestock interface were selected for this study, close to KNP and history of buffalo breakouts into those dip tank areas.

Results: 0.006% cattle tested positive for BTB on TST, awaiting Bovigam results. Clinic samples are being cultured, results should be available July. 25 AHTs enrolled for TB testing training. 24/25 in the pre-training assessment test. Five passed, 20,8%. 18/24 passed post-training test ,75%. The older AHTs under-performed. There was a 54.2% difference between pre-training and post-training. 9/21 saw buffaloes moving through these breaks and grazed with cattle.

Discussion: Gap in AHT rpractical training. Fence broken mainly in winter. 7-21 hours to repair break in the fence.

Conclusion: NTMs in cattle herders/owners indicates the predisposition of BTB. Theoretical, practical, meta-cognitive learning at AHT training institutions should be encouraged. Fence permeability worrying and needs addressing.

41. Seroprevalence of bovine brucellosis and risk factors associated with occurrence of the disease in cattle in Dr. Kenneth Kaunda District of North West Province

Eunice Matome^{1,2}, Alex Chako¹, Tsepo Ramatla^{2,3}, Oriel Thekiso², Kgauelo Lekota²

¹Potchefstroom Veterinary Provincial Laboratory, North West Department of Agriculture and Rural Development, Potchefstroom, 2520

²Unit for Environmental Sciences and Management, North-West University, Potchefstroom, 2531

³Centre for Applied Food Sustainability and Biotechnology, Department of Life Sciences, Central University of Technology, Bloemfontein, 9300 Bovine brucellosis is a significant livestock disease that causes reproductive problems in cattle, including abortion, stillbirth, and decreased fertility. In the Dr Kenneth Kauda region of the North West province, there is currently no scientifically analysed data available to evaluate the progress made towards the elimination of brucellosis.

This study analysed laboratory test results from all cattle serum samples from the Dr Kenneth Kaunda district farms that were submitted to the Potchefstroom Veterinary Provincial Laboratory between 2016 and 2023. The samples were tested using the Rose Bengal test, which was further confirmed by the complement fixation test. Furthermore, we interviewed several of the farmers owners whose animals tested positive for the disease in an effort to find risk factors linked to its incidence.

The total herd prevalence of brucellosis among the 204425 cattle serum samples that were reported between 2016 and 2023 was 2.4 % (4903/204425). Higher seroprevalence of 5, 2% was observed in 2020 as compared to 1, 3% in 2017. For Matlosana, JB Marks, and Maquassi Hills, the relative seroprevalences were 3.0% (1839/66517), 2.0% (2167/115065), and 3.5% (792/22843) per municipality. A higher seroprevalence of 3.5% was observed in for Maquassi hills and 3.0% for Matlosana as compared to JB Marks (2.0%) municipality. The overall seroprevalence in beef was 2.60%, which was significantly higher than in dairy (0.36%). Lack of vaccination (75%), history of abortions (100%) and poor handling of aborted materials (15%) were identified as primary risk factors associated with the occurrence of the disease.

43. The impact of comorbidities and physiological conditions on the burden of food-borne disease: A case study of rural Eastern Cape, South Africa

Nandisa Ndlame N.N.¹, Oguttu, J.W.¹¹, Mbombo-Dweba, T. P.¹¹

¹*Department of Agriculture and Animal Health, University of South Africa*

Introduction

There is limited understanding of the burden of FBDs within the rural areas of South Africa. Furthermore, there is no evidence of studies that have assessed the impact of co-morbidities among patients presenting with symptoms of food-borne diseases (FBDs) on the health care system.

Objective(s): The study investigated the source of FBDs among patients patronizing the hospital that supplied the data, and the role of comorbidities and physiological conditions with potential to compromise the immune status of patients, on the burden on FBDs in a rural setting in South Africa.

Methods: Retrospective data of 419 patients from a rural hospital that services the study participants was used in this study. Only data collected between January 2016 and December 2020 was included in this study. The type of food eaten by the patient, the type of comorbidities that patient had, and whether the patient was admitted or not were extracted from the data. Data was analysed using descriptive statistics and by computing marginal probabilities of being admitted.

Results & Discussion: The distribution of comorbidities and other conditions with potential to alter the immune status of the patients was as follows: 5.25% (n=22) had hypertension, 3.34% (n=14) were HIV positive, 6.44% (n=27) had diabetes, 2.15% (n=9) were positive for tuberculosis and 3.10% (n= 13) were pregnant. Most patients contracted foodborne illness after eating meat from a cow that had been treated (42%; n=176), followed by eating of dead cattle meat (26.25%; n=110), cattle bitten by a snake (12.89%; n=54), dead sheep (4.30%; n=18), dead goat (0.24%; n=1) and sick chicken (0.72%; n=3). Patients with comorbidities such as diabetes (Marginal Effects (ME) = 0.64), TB positive (ME = 0.66) and HIV positive (ME=0.64) as well as pregnant patients (M=0.61) had high probabilities of being admitted.

Conclusion: People eating meat that should otherwise be condemned was the most common cause of FBDs. A one-health approach involving environmental health officials, the veterinary team, medical practitioners plus the local authority, is needed to design interventions strategies and education awareness programmes about food safety to help reduce the burden of FBDs in the study area. Comorbidities and conditions such as pregnancy heighten the severity of FBDs, thereby increasing the likelihood of patients with such conditions being hospitalization. This increases the burden of FBDs on the health care system.

63. Evaluation of a commercial probiotic on the biological performance of Nile tilapia (*Oreochromis Niloticus*) during sex-reversal and extended nursing in Kenya

Gugulethu Moyoa, Francis Murrayb, Will Leschenb, Patricia Muendoc

a – Gauteng Department of Agriculture and Rural Development, 56 Eloff Street, Umnotho House, Johannesburg, 2000, South Africa

b – Institute of Aquaculture, University of Stirling, Stirling FK9 4LA, Scotland, UK

c – Machakos University, P.O. BOX 136 – 90100, Machakos County, Kenya, EA

Intensification of aquaculture production is associated with increased incidence of diseases. The use of antibiotics to control diseases has been curtailed. Probiotics have been proposed and are already being used as alternatives as they increase growth of and resistance of aquatic animals to diseases. However studies have shown that they do not always work in different culture conditions. The objective of this trial was to evaluate if a limited duration application of an 'in-feed' commercial probiotic, alternating treatments between sex reversal and juvenile tilapia nursing phase can enhance health and production performance compared to a negative ('no-treatment') control. Sex reversal Nile tilapia fry of sample average weight of 0.014g were randomly allocated into eight replicates of control and of probiotic treatments in 2m² hapas at stocking densities of 5000 fish m² and raised for 22 days in the same pond. At the end of this stage the treatments were reallocated resulting in the establishment of four treatments each with four replicates which were stocked in 5m² hapas and later, 20m² hapas, during an extended nursing phase of 28 days. At the end of both stages sample average weights, individual weights and bulk weights were obtained from each of the replicate treatments. Specific growth rates, Fultons condition factor, economic feed conversion ratio and percentage survival were calculated from these data. There were no significant differences between the sample average weights, specific growth rates and Fulton's condition factor ($p > 0.05$) for the different treatments at all stages of the trial.

73. Genome Sequences of the Fifteen Bluetongue Virus Vaccine Strains Incorporated in the South African Live-Attenuated Vaccine

Tendai Mlingo

Bluetongue virus (BTV) is the prototype member of the Orbivirus genus (Sedoreoviridae family) that causes disease in wild and domestic ruminants. The genome comprises 10 linear double-stranded RNA segments encapsidated by three protein layers. The most effective control strategy against Bluetongue disease is vaccination. The live-attenuated vaccine (LAV) supplied by Onderstepoort Biological Products (OBP) comprises 15 serotypes equally distributed in bottles A, B and C. Sequencing of plaque-purified vaccine strains has been reported. However, legislation for veterinary biologicals stipulates a maximum of five passages from the master seed antigen during vaccine production. We describe the genome sequences of master seed antigens used in the OBP LAV. Whole genome sequencing of the 15 strains was completed using next-generation sequencing on the Ion Torrent and Illumina sequencing platforms. Clonal amplification of the complementary DNA (cDNA) library was achieved on Ion Sphere Particles and sequencing completed using the Ion Torrent PGM System. Paired-end sequencing was performed on the Illumina MiSeq and NextSeq sequencing platforms. The read quality was assessed using FastQC and the Trimmomatic tool. Genome assembly was carried out on CLC Genomics Workbench by mapping reads to reference strains. A pairwise alignment of the open reading frames of the 15 vaccine sequences with South African reference genomes was carried out using BioEdit to determine nucleotide identities. The nucleotide identities of bottle A serotypes were $\geq 82.97\%$ for all segments. Bottles B and C serotypes had nucleotide identities of $\geq 99.49\%$ and $\geq 92\%$, respectively. A phylogenetic analysis of segment 2 grouped the 15 vaccine strains into 8 nucleotypes. The data is of importance for continuous evaluation of the efficacy of the vaccine against circulating strains.

83. Evaluation of overdose safety of Lumpy Skin disease vaccine

Sbahlle Zuma^{1,2}, Leeann Naicker², Vusi Dibakwane² and Nobalanda Mokoena²

¹Department of Biochemistry, School of Life Sciences, University of KwaZulu-Natal (Pietermaritzburg campus), Scottsville, 3209,

²Onderstepoort Biological Products (SOC. Ltd), 100, Old, Soutpan Road, Onderstepoort, 0110, Pretoria, South Africa

Introduction: Lumpy skin disease (LSD) is a viral disease that affects cattle of all ages and breeds with younger and lactating calves being more susceptible. The disease is characterized by mild to severe symptoms resulting in financial losses in affected cattle industries due to reduced productivity in milk and beef production. LSD has rapidly spread and is considered transboundary following outbreaks in Europe, Russia, the Middle East, and Asia, previously considered disease-free regions. Vaccination is marked as the most effective control and the vaccine supplied by Onderstepoort Biological Products (OBP) has been successfully used for prophylactic immunization of animals against LSD. The safety of the OBP LSD vaccine has been demonstrated in the field at the recommended dosage. Herein we evaluated vaccine overdose safety under controlled clinical conditions.

Methods: Calves with no previous exposure to LSDV were grouped into three treatment groups. Animals in the first group were administered with the recommended (1X); the second group received a 10X LSD vaccine overdose and the third group was used as a placebo injected with vaccine diluent. Rectal temperatures and clinical reactions were monitored for 14 days post-infection.

Results: All animals remained healthy and no temperature reactions were detected. Both the recommended 1X and 10X overdose had a temperature profile of 38-40°C while the placebo group had a similar range of 38,3-40,6°C. Minor skin lesion at the site of injection was observed with both the recommended 1X and 10X overdose which is typical following vaccination with the commercial LSD vaccine. No clinical signs of LSD were observed in the placebo group.

Discussion: The lesions observed in the vaccinated groups are characteristic of LSD vaccination with the Neethling strain of LSDV.

Conclusion: The commercial LSD vaccine supplied by OBP is considered safe in cattle when administered up to ten times the recommended dosage.

POSTER SESSION 3 – FRIDAY 23 AUGUST 2024, 12:30

2. Safety and Immunogenicity of the serotype-reduced Bluetongue vaccine in sheep

Ntombikayise Nkomo¹; Boitumelo Moetlhoa¹; Tendai Mlingo¹ and Nobalanda Mokoena¹

¹ Onderstepoort Biological Products (SOC. Ltd), 100, Old, Soutpan Road, Onderstepoort, 0110, Pretoria, South Africa

Introduction: Bluetongue virus (BTV) is the prototype member of Orbivirus genus belonging to the *Reoviridae* family which causes haemorrhagic disease in ruminants. BTV is endemic throughout most of South Africa and 22 of the 29 known serotypes have been detected in the field. Every vector season sees the emergence of several serotypes, with the variety of serotypes primarily relying on herd immunity. Vaccination plays a crucial role controlling the spread of BT. The aim of the current project is to evaluate the safety and immunogenicity of the improved BT vaccine at two doses.

Methods: The animals were grouped into three treatment groups. The first group was subcutaneously vaccinated with 1 ml of the improved bluetongue vaccine (two doses). The negative and control groups included the vaccine diluent and the commercial BT vaccine, respectively. Rectal temperatures were recorded every day for 14 days following vaccination and animals were monitored for local or systemic reactions. Blood samples were collected every 7 days from day 0 to day 70 for serology.

Results: None of the vaccinated animals showed any local or systemic reactions during the study period. Animals in the vaccinated groups induced neutralising antibodies at high levels from day 14 and remained above threshold for the duration of the trial. Animals injected with vaccine diluent induced no immune response.



Discussion: The improved bluetongue vaccine was found to be safe as evidenced by absence of adverse reactions. Additionally, the BT vaccine was also found to be immunogenic in eliciting adequate immune response in sheep.

Conclusion: The improved BT vaccine will provide protection against the BT disease.

11. Antimicrobial use and practice in aquaculture production systems in Nairobi, Kenya

Elvis Waga,¹ Gabriel O. Aboge,¹ Nduhiu Gitahi,¹ Claire Heffernan,² and Lorna Benton²

¹University of Nairobi, Nairobi/00100, Kenya

²London International Development Centre, London/WC1A 2NS, United Kingdom.

Link to the publication.

https://researchonline.lshtm.ac.uk/id/eprint/4668057/1/Madara_Heffernan_Benton_2022_ANTIMICROBIAL-USE-AND-PRACTICE-IN-AQUACULTURE.pdf

Introduction: Inappropriate use of antibiotics in aquaculture, livestock and agriculture contributes significantly to development of antimicrobial resistance (AMR). Consequently, antimicrobial residue deposition in the food chain may result, posing a risk to food safety. This study assessed Knowledge, Attitudes and Practices (KAP) on use of antimicrobials amongst aquaculture farmers and antimicrobial residues in fishponds' fish, water and sediments within Nairobi County, Kenya.

Methods: A prospective list of 24 aquaculture farmers was provided by the Fisheries authority and only 18 farmers were surveyed. A semi- structured questionnaire was administered using Kobo Toolbox from ODK-collect. Water (17), fish (11) and sediment (9) samples were collected, and antimicrobial residues analysed using LC-MS/MS. Microsoft Excel and Stata/IC 16.1 for Mac were used for data cleaning and processing. Responses were scored to create composite KAP variables for univariate analysis by Chi2 test.

Results: Only two farmers were reported to be using antibiotics (Tetracyclines and colistin in combination) in their aquaculture farms. 88.89% and 72.22% reported having sufficient knowledge and favourable attitude towards prudent antibiotic use respectively, while 66.67% demonstrated inadequate practice around antibiotic use. Thirteen antimicrobial residues tested were at least detected in all the 3 sample types. Sediments recorded highest residue concentrations followed by fish and water respectively.

Discussion: The ongoing national awareness AMR campaigns in Kenya may explain the sufficient knowledge of AMR and favourable attitudes to prudent use of antibiotics reported. The varying concentrations in the 3 sample types may be attributed to residue deposition into the bottom layer of pond, bioaccumulation in fish tissues and fortnight replacement of fishpond water respectively.

Conclusion: The low reported antibiotics usage does not equate to prudent antibiotics use in aquaculture farming within Nairobi County, Kenya. There's a need to strengthen antimicrobial stewardship amongst aquaculture farmers.

18. Bacterial pathogens associated with bovine mastitis and their antimicrobial resistance profiles in the JB Marks Municipality of North West Province, South Africa

Cecilia Sizana-Kgaje^{1,2}, Alex Chako¹, Tsepo Ramatla^{2,3}, Oriël Thekisoë², Kgaugeto E. Lekota²

¹Potchefstroom Veterinary Laboratory, Agriculture Centre, Chris Hani Street, Potchefstroom, 2531

²Unit for Environmental Sciences and Management, North-West University, Potchefstroom, 2531

³Centre for Applied Food Sustainability and Biotechnology, Department of Life Sciences, Central University of Technology, Bloemfontein, 9300

Bovine mastitis is caused by various bacterial mastitis pathogens and has an impact on milk quality and production. Understanding these pathogens and their basic epidemiology is crucial to implementing

appropriate control programs and proactive management of dairy herds. This study investigated the prevalence of bacterial mastitis pathogens and their antimicrobial profiles among dairy farms within the JB Marks municipality. A total of 1014 quarter milk samples were collected from different dairy herds in the JB Marks municipality. The isolates were identified using an automated Sensititre™ Aris 2X ID/AST system and further confirmed using RapID™ Systems. The antimicrobial susceptibility test was determined using the Kirby-Bauer Disk-diffusion assay. Of the 1014 milk samples investigated, 94.8% tested positive for contagious and environmental mastitis pathogens. The non-coagulase *Staphylococcus* species was the most prevalent at 49,4%; followed by 22,8% *Bacillus cereus*; 12,6% *Escherichia coli*; 12,5% *Corynebacterium* spp.; 12,5% *Streptococcus uberis*; 9,3% *S. agalactiae*; 8,8% *Staphylococcus aureus*; 4,8% *Pseudomonas aeruginosa*; 4,5% *Enterobacter cloacae*; 2,9% *Micrococcus luteus*; 0,6% *S. dysagalactiae*; 0,6% other *Streptococcus* species; 0,5% *Klebsiella pneumoniae*; 0,3% *Rhodococcus equi*; and 0,1% *Trueperella pyogenes*. Antimicrobial-resistant profiles showed that 46,7% of *Staphylococcus* spp. showed resistance to Beta-lactam antibiotics. Some *Pseudomonas aeruginosa*, *Escherichia coli*, *Enterobacter cloacae*, and *Klebsiella pneumoniae* isolates showed multidrug resistance. *Rhodococcus equi* isolates were resistant to Pirlimycin. The high prevalence of *Staphylococci* spp. is a main concern due to resistance to beta-lactams, which are the most commonly used antibiotics. Data generated in this study highlights that it is necessary to improve milk hygiene and implement proper intervention strategies to control mastitis pathogens in dairy herds.

24. Antibiotic resistance patterns, virulence gene profiles, and genetic diversity of *Salmonella enterica* subsp *enterica* serovar Typhimurium isolated from the environment, animal and food products in South Africa (1999-2021)

Nkagiseng Moatshe^{1,2}, Khanyisile R. Mbatha¹, Nombasa Ntushelo³, Itumeleng Matle⁴

¹Department of Life and Consumer Sciences, College of Agriculture and Environmental Sciences, University of South Africa, Pretoria, South Africa

²Biotechnology Division, Onderstepoort Veterinary Research, Agricultural Research Council, Pretoria, South Africa

³Department of Biometry, Infruitec, Agricultural Research Council, Cape Town, South Africa

⁴Bacteriology Division, Onderstepoort Veterinary Research, Agricultural Research Council, Pretoria, South Africa

Introduction: *Salmonella* Typhimurium is a leading serovar responsible for human and animal salmonellosis, substantially impacting global socioeconomic factors. This study investigates the antibiotic resistance patterns, virulence genes, resistance genes, and plasmids within *S. Typhimurium* isolates across nine provinces in South Africa (S.A) from 1999 to 2021.

Method: A total of 180 isolates were randomly selected for this study. Only 129 isolates were confirmed as *S. Typhimurium* through conventional PCR. These isolates were obtained from various sources: animals (n=94), food (n=16), environment (n=7), and feed (n=12). Phenotypic antibiotic resistance was assessed against 13 antibiotics. PCR assays were performed to screen for resistance genes, virulence genes and integrons. Enterobacterial Repetitive Intergenic Consensus Polymerase Chain Reaction (ERIC-PCR) was used for genetic relationship evaluation of isolates.

Results: This study revealed alarming levels of antibiotic resistance, with 86.8% of isolates resistant to ciprofloxacin, 69.0% to ceftriaxone, and 65.1% to piperacillin. Several isolates exhibited multi-drug resistance, with one isolate exhibiting resistance to eleven antibiotics. Genetic analysis revealed the presence of various resistance genes, including *bla*CMY-2 (44.9%), *bla*PSE (32.6%), *tetA* (24.0%), and *qnrB* (21.7%). Class 1 integrons were identified in 47.4% of isolates. The study uncovered the presence of virulence genes within the isolates, including *sopB* (95.3%), *sspH1* (82.9%), *sifA* (83.0%), *pefA* (79.8%), and *spvC* (79.1%). ERIC-PCR yielded 44 clusters (A–RR). In Cluster R, two isolates indicated 100% similarity.

Discussion: Over the years, an increase in antibiotic resistance to commonly used antibiotics has been observed in *S. Typhimurium*. Notably, our research has unveiled resistance among *S. Typhimurium* isolates to antibiotics commonly employed for livestock growth promotion in S.A.

Conclusion: The findings of this study underscore the urgent need for increased surveillance and intervention strategies to combat the spread of antibiotic resistance and virulence factors of *S. Typhimurium* in S.A, emphasizing the importance of monitoring and controlling this public health concern.

36. Prevalence of *Staphylococcus pseudintermedius* species isolated from canine specimens submitted to a veterinary diagnostic laboratory in South Africa, 2012 – 2017

Themba Sigudu^{1,2*}, Daniel N. Qekwana³, James W. Oguttu¹

¹Department of Agriculture and Animal Health, College of Agriculture and Environmental Sciences, University of South Africa, Johannesburg, South Africa

²Department of Health and Society, School of Public Health, Faculty of Health Sciences, University of Witwatersrand, Johannesburg, South Africa

³Section Veterinary Public Health, Department of Paraclinical Sciences, Faculty of Veterinary Science, University of Pretoria, Pretoria, South Africa

Introduction: *Staphylococcus pseudintermedius*, a commensal bacterium of canine skin and mucous membranes, has emerged as a significant opportunistic pathogen in dogs. The objective of this study was describe the distribution of *S. pseudintermedius* isolates obtained from samples collected from dogs submitted to a veterinary diagnostic laboratory in South Africa.

Methods: The study utilised a dataset comprising 1,392 positive *S. pseudintermedius* isolates obtained from a South African veterinary diagnostic laboratory between 2012 and 2017. Crude and factor-specific proportions with corresponding 95% confidence intervals were calculated for categorical variables. Temporal graphs illustrated the annual variation in *S. pseudintermedius* proportions.

Results and discussion: Between 2012 and 2017, a total of 1,392 *S. pseudintermedius* positive isolates were identified, with male dogs accounting for 53.3% and female dogs 46.7%. Dogs aged 2 to 4 years contributed the highest proportion (26.5%) of isolates, while those under 2 years had the lowest (10.2%). KwaZulu-Natal Province yielded the most isolates (44.4%), whereas the Northern Cape Province contributed the least (0.1%). Skin specimens predominated (51.1%), while respiratory samples were least common (4.5%). Isolate numbers increased steadily over the study period, from 125 (9.0%) in 2012 to 372 (26.7%) in 2017, notably spiking from 2015 (18.1%) to 2017 (26.7%). However, isolates exhibited minimal seasonal variation, with proportions across autumn (23.6%), winter (26.3%), spring (25.4%), and summer (24.7%) remaining relatively consistent.

Conclusion: The findings suggest a variation in the distribution of *S. pseudintermedius* based on sex, province and specimen type. Season does not seem to have a significant influence on the occurrence of *S. pseudintermedius*. Further that probe the observed difference in the distribution between the provinces particularly, and the observed consistent increase in the number of isolates over the study period are recommended.

53. Ticks population dynamics (Acari: Ixodidae) on and of bovine hosts

Mandla Yawa¹ & Nkululeko Nyangiwe²

¹Dohne Agricultural Development Institute, South Africa, and ²Department of Agriculture and Animal Health, University of South Africa, Florida, South Africa.

Background: Ticks are the most important external parasites of cattle and are known to transmit more pathogens than any other group of arthropods worldwide. About 80% of the world's cattle population is at risk of ticks and tick-borne diseases, causing a global annual loss of \$US22–30 billion. In Africa, the impact of ticks is ranked high, and they transmit diseases such as cowdriosis, anaplasmosis, bovine babesiosis and theileriosis.

Method: A total of 31,425 ticks were collected from 10 cattle and also from six drag samples during the 12-month study period. Adult ticks were removed from the right-hand side of each animal and all instars of ticks were placed in containers filled with 70% ethanol.

Results: Based on morphological traits, 10 tick species were identified: *Rhipicephalus (Boophilus) decoloratus* (32.5%), *R. evertsi evertsi* (18.8%), *R. appendiculatus* (17.3%), *Amblyomma hebraeum* (16.3%), *R. simus* (7.7%), *Ixodes pilosus* (3.8%), *Hyalomma rufpes* (3.5%), *R. follis* (0.08%), *Haemaphysalis elliptica*

(0.04%), *H. silacea* (0.02%). The southern African yellow dog tick, *H. elliptica*, was only found on vegetation. The agroecological zones differ significantly in tick species and their distribution. The *A. hebraeum* and *R. evertsi evertsi* counts were higher in Kowie Thicket (KT) during the summer season (2.05 ± 0.01 and 1.00 ± 0.09 , respectively) compared to Bedford Dry Grassland (BDG) and Bhisho Thornveld (BT) veld types. In all vegetation types, *R. appendiculatus* had higher counts in KT in spring (0.91 ± 0.08), summer (0.78 ± 0.08) and winter (0.78 ± 0.08). *Rhipicephalus (Boophilus) decoloratus* was more frequent in the BT (1.78 ± 0.11) during the summer season. BDG had lower tick infestation with *R. evertsi evertsi* being the most frequent species in summer. No *H. rufpes* was collected in the KT.

Conclusions: Of epidemiological interest, *R. (B.) microplus* was absent in the study area which needs further investigation. Within the context of this study, we found agroecological differences and seasonal variations to influence tick species distribution.

54. Genomic insight into multidrug resistant *Klebsiella* species from sheep and goat faeces as well as water sources in Matlwang, Potchefstroom

Tshepang Motlhaping, T.I¹, Ramatla, T.^{1,2}, Thekiso, O¹, Lekota, K.E¹

¹Unit for Environmental Sciences and Management, North-West University, Potchefstroom, 2531, South Africa.

²Centre for Applied Food Sustainability and Biotechnology, Department of Life Sciences, Central University of Technology, Bloemfontein, 9300.

Klebsiella species are of significant public health concern due to their increasing resistance to antibiotics. In this study we assessed the antimicrobial resistance (AMR) profiles of *Klebsiella* species isolated from water sources and those infecting sheep and goats. A total of 35 and 17 faecal samples were collected from sheep and goats, respectively, while 10 samples were collected from water sources (stream [n=1], animal drinking water troughs [n=3], and tap water [n=3] and water wells [n=3]). Whole genome sequencing (WGS) was used to determine AMR profiles of *Klebsiella* spp. isolates from sheep (n=2), and water (n=4). Comparative genomics was employed on the 83 and 2 *K. pneumoniae* strains from GenBank and the current study, respectively by investigating multilocus sequence typing (MLST), antibiotic resistance genes (ARGs), and plasmid types. A total of 11 and 5 isolates were identified as *Klebsiella* spp. from sheep and goats, respectively, whilst 27 were isolated from water. The *K. pneumoniae* was identified from goats (n=3), sheep (n=7) and water (n=2), whilst *K. variicola* (n=2) and *K. michiganensis* (n=2) were from water identified by WGS. Phenotypic AMR profiles showed that 94% and 91% of the isolates from animals and the environment, respectively were resistant to ampicillin. Two new sequence types of *K. pneumoniae* strains, both consisted of plasmid AB595 that encodes for tetracycline (*tetA*), sulphonamide (*sul*), and aminoglycoside (*aph(3')-Ia*) resistance. Genomes of *K. variicola* and *K. michiganensis* contained fosfomycin (*fosA*), nalidixic acid (*oqxAB*) and beta-lactamase (*blaLEN* or *blaOX-1-3*) ARGs. Whilst *K. michiganensis* strains additionally contained aminoglycoside (*aph(3')-Ia*) gene. The sequenced *Klebsiella* spp. genomes present novel sequence types with distinct genetic diversity. This study demonstrated that sheep and goats as well as water sources in Potchefstroom carry the multi-drug resistant *K. pneumoniae*, *K. variicola* and *K. michiganensis* which are pathogens of "One Health" importance with public health impact for farmers, farm workers, veterinary employees.

55. Molecular detection of *Coxiella* species from sheep ticks in Matlwang, Potchefstroom

Jody Howard¹, Ramatla T.^{1,2}, Lekota, K.E.¹ & Thekiso, O.¹

¹Unit for Environmental Sciences and Management, North-West University, Potchefstroom. 2531, South Africa.

²Department of Life Sciences, Centre for Applied Food Sustainability and Biotechnology, Central University of Technology, Bloemfontein, 9300, South Africa.

Coxiella burnetii is a small Gram-negative intracellular bacterium that causes a disease called coxiellosis in animals and Q- fever in humans. It is transmitted by ticks of the genera *Haemaphysalis*, *Rhipicephalus*, *Hyalomma* and *Amblyomma* during blood feeding. Ticks can carry both *C. burnetii* and genetically different but closely related *Coxiella*-like endosymbionts (CLEs). Both *Coxiella* species can be found in the placenta, amniotic fluid, urine, faeces, and milk of infected animals with goats, cattle, and sheep serving as their main reservoirs. The aim of this study was to detect *Coxiella* species from sheep ticks in Matlwang village of Potchefstroom. Molecular identification and characterization of sheep ticks was conducted using *cytochrome C oxidase subunit 1 (CO1)* gene sequences, while *C. burnetii* and CLEs were detected and characterized from sheep ticks using PCR, sequencing and phylogenetics with use of the *16S rRNA* and *IS1111* gene respectively.

A total of 192 ticks were collected from sheep in the small communal farming village of Matlwang, Potchefstroom. In total, 77 pooled ticks were further characterized i.e., 39 being engorged females and 38 being pooled males. The ticks were identified as *Rhipicephalus evertsi evertsi* using both morphological and genetic analysis. Phylogenetic analysis using the *CO1* gene supported the respective taxon in comparison to sequences available in NCBI GenBank. A total of 66.23% (51/77) and 10.39% (8/77) tested positive for CLEs and *C. burnetii*, respectively. In this study the CLEs were more prevalent than *C. burnetii*. This study demonstrated that sheep ticks carry *C. burnetii*, an important zoonotic bacterium which is of public health importance for agricultural workers, veterinarians and abattoir employees.

Introduction: Plant based therapy is widely used in different parts of the world to treat animals and human ailments due to their accessibility, affordability and effectiveness. Ethno veterinary medicine is based on beliefs, knowledge, skills and practices to safeguard the health and welfare of humans and animals. In the Ephraim Mogale municipality, animal wounds represent some of the major burdens to animal production as they cause severe economic losses, impaired health, damaged hides, weight loss, loss of fertility and death through wound infections and septicemia which may lead to loss of commercial value. Due to lack of financial resources, farmers often resort to medicinal plants to treat animal wounds. However, there is no data on the efficacy, formulation and guidelines on these medicinal plants in the municipality. Therefore, this study seeks to (1) investigate and analyze the efficacy of commonly used plants in treating animal wound (2) investigate the livestock practices in communal areas of the Ephraim Mogale Municipality and (3) to isolate the compounds from selected plants

Material and Methods: Quantitative and qualitative research methods will both be used in this study. Qualitative data will be collected using a semi-structured interviews to assess knowledge, attitudes and perceptions of farmers in the municipality. Structured questionnaires will be developed to obtain data related to plants used for the treatment of cattle wound. Samples of commonly used plants will be collected and transported to the laboratory, for analysis. The Statistical analysis will be performed using Prism software (GraphPad), Thematic software & SPSS V28.0 (IBM Corp, 2021)

Discussion and conclusion: This study will be the first of its kind around Ephraim Mogale Municipality communal livestock farmers to investigate and analyse the medicinal plants having potential to wounds healing and to document the practices used. The study will also validate the efficacy, safety precautions of the traditional medicines used in wound healing treatment potential in livestock.

56. Antimicrobial sensitivity testing of preserved *S. enterica* and *E. coli* isolates from 2000 to 2021 in the agricultural sector

Masabata Motaung Annah^{1,2}, Matle Itumeleng², Kayoka-Kabongo Prudence Ngalula¹

¹Agricultural Research Council - Onderstepoort Veterinary Research, Pretoria, South Africa

²Department of Agriculture and Animal Health, College of Agriculture and Environmental Science, University of South Africa, Florida, South Africa.

Over time, the antimicrobial susceptibility pattern of bacteria isolates has shifted toward resistance, which could be attributed to antimicrobial drug misuse. This is a cause for concern because antimicrobial resistance has emerged in important zoonotic pathogens. The study aimed to monitor antimicrobial sensitivity patterns for stored South African bacterial isolates over 20 years. This study investigated the antimicrobial sensitivity of seventy-five bacterial isolates comprising *Salmonella enterica* (n=53) and *Escherichia coli* (n=22) using disc diffusion assay, MIC, and PCR. The disc diffusion test and MIC revealed that all tested *S. enterica* and *E. coli* isolates were sensitive to ten antibiotics except tetracyclines. The study also discovered that the resistance genes *tetA* (38%), *tetB* (32%), *blaPSE* (15%), and *blaTEM* (4%) were prevalent in *S. enterica*, while in *E. coli*, only *blaPSE* (38%) was detected. Other resistance genes found in the genome were *tetB*, *cat1*, *flo*, *cm1*, *qnrA*, *qnrB*, and *qnrS*. Despite low antimicrobial resistance levels in *S. enterica* and *E. coli*, susceptibility values were shifting towards resistance. Between 2000 and 2004, the isolates were sensitive to chloramphenicol, but then showed a sensitivity shift towards resistance to the same antibiotic at 8 mg/L in subsequent years. This shift necessitates action to alter farmers' knowledge and practices regarding antibiotic use. This retrospective study determined the antimicrobial sensitivity profile of significant zoonotic and foodborne pathogens, as well as their resistance patterns over time.

69. Molecular identification and characterization of selected food-borne pathogens in imported dried fish sold in informal markets around Gauteng province in South Africa

Rendy Nkosi

Dried fish highly contributes to the demand for nutritional protein in our daily diet. In recent years, dried fish has become more popular in informal market and it plays an important role in providing low-cost, easily accessible, and nutritious food to the urban populace. The examination of microbiological quality is therefore needed to ensure health of the general public. The purpose of this study was to assess the microbiological quality of different types of dried fish sold in Pretoria and Johannesburg, South Africa. A total of 12 markets were visited, and 140 samples were collected. Three types of dried fish were obtained, which were smoked (40), sun-dried (80), salted (20). During that collection of samples, hygienic measures applied by vender were observed and recorded in a checklist and the results revealed that sellers were not adhering to the most basic hygienic practices and not using proper storage of dried fish. All the sellers did not wash hands before touching the samples, and 83.3% exposed to air outside. The mean total bacterial count, sun-dried fish recorded 2.91×10^7 cfu/g, smoked fish 2.71×10^7 cfu/g, and salted fish 2.13×10^7 cfu/g respectively. According to the standard guideline of bacterial load in seafood, the values obtained in this study reveal that the dried fish sold in the informal markets are not suitable for human consumption as it's above the standard guideline. Some of these bacteria are important human pathogens responsible to for serious illness. *Staphylococcus aureus*, *Staphylococcus sciuri*, *Klebsiella pneumonia* are among the food-borne pathogens. The disc diffusion technique was used to test the antibiotic susceptibility of the isolated bacteria, and the results were interpreted using the Clinical Laboratory Standards Institute (CLSI). *Staphylococcus aureus* (100%), *Staphylococcus xylosus* (100%), *Staphylococcus sciuri* (100%), were all susceptible to Chloramphenicol, according to the findings. There is a need to emphasize more caution on microbial hygiene quality of dried fish and more evaluation for public health must be taken into consideration.

76. The occurrence of gastrointestinal parasitic infections in sheep and goats in the Eastern Cape, South Africa

Mlungisi Jansen, Yawa, M¹, Nyangiwe, N²

¹Döhne Agricultural Development Institute, Private Bag X 15, Stutterheim 4930, South Africa.

²Department of Agriculture and Animal Health, University of South Africa, Florida, South Africa

Background: Gastrointestinal parasites are a worldwide problem in sheep and goats. The most serious economic consequences of gastrointestinal parasites are based on the overall number of worms, number of genera and species present.

Objective(s): The study aimed to determine the occurrence of gastrointestinal parasites in sheep and goats in the humid zone of the Eastern Cape Province, South Africa.

Methodology Faecal samples were collected from sheep and goats between January 2012 and December 2015 in Waartburg in the Eastern Cape Province between different seasons. All collected data were analysed using the Statistical Analysis System version 9.1 (SAS, 2003). Statistical significance was tested at 95 % level, with all results with $P < 0.05$ considered statistically significant.

Results: A total of 4391 faecal samples were collected from sheep and 3241 samples were collected from goats between January 2012 and December 2015. Of the collected roundworm species (faecal eggs and faecal cultures), *Haemonchus contortus* was the only species found. The prevalence of gastrointestinal parasites was significantly higher in sheep (*H. contortus* 81% and coccidia 37%) and lower in goats (*H. contortus* 75% and coccidia 22%). *Haemonchus contortus* had significantly higher faecal egg counts (FEC) during spring (1465.73 ± 143.56) and summer (1418.73 ± 160.73) and the lowest during autumn (496.67 ± 219.13) and winter (352.05 ± 164.44). This study confirms that helminths and coccidia are major causative agents.

Discussion and Recommendations: Animals can be treated for parasitic infections using anthelmintics. Furthermore, resting heavily infected pastures by ploughing, reseeding, haying or grazing with another species (cattle) can reduce parasite loads and level of pasture contamination.

77. Distribution of slaughtered of bush and warthog pigs in Gert Sibande District and disease spread risks

Mpendulo Xashimba

BACKGROUND: The project was triggered by the approval stamp impounded on a tree slaughter. The tree slaughter meat circulated on the butcheries with no-one noticing, as the carcasses had approval stamps. These suspicious stamped carcasses were found in butcheries and traced back to the original farm "slaughter pole" and the approval stamp was found and impounded by Veterinary Public Health officers and handed over to the SAPS, a court case was then opened. The butchery has been selling the unsafe stamped meat for more than 5 years upon enquiry.

Approval stamp: Slaughter pole where the approval stamp was found

OBJECTIVES: To evaluate the manufacturing, procurement, handling, control, and also evaluate the court judgement on pass stamp.

MATERIAL AND METHODS: Questionnaires were implemented to meat inspectors, operating and closed abattoir owners, VPH officials, stamp shops, SAMIC (manufacturers) and the court judgement was also scrutinised.

DISCUSSION: Illegally slaughtered carcasses are mostly consumed by the low income community members as it attracts those who cannot afford, it is affordable. There is high risk of spreading zoonotic and food borne diseases, also promotes the stock theft. Competition with illegal slaughter leads to some abattoir owners to quit the industry as the tree slaughter cuts corners and as such their meat is so cheap.

This court case has taught us that there are approval stamps used in the meat industry on uninspected meat. On a positive note this court case has led to improved communication between abattoir owners & VPH regarding approval stamps, and the slaughter figures have also increased in the nearby abattoirs resulting to consumption of safe meat. The old stamps (the stamps complying to old regulations).



80. Systematic Reviews of Epidemiology of Porcine Cysticercosis in South Africa from 2003 to 2023

Naomi Masango: Dr Rendani Victress Ndou¹

¹Centre of Animal Health Studies, School of Agricultural Studies North West University, Mafikeng Campus, Private Bag X2046, Mmabatho, 2735

ABSTRACT

Taenia solium, the pig tapeworm, causes cysticercosis in its larval form. In humans, cysticercosis can result in neurologic problems such as seizures, epilepsy, and even death; it presents serious public health risks. It is prevalent in regions with limited access to health and poor sanitation, such as Latin America, Asia, and sub-Saharan Africa. This review aimed to systematically compile and synthesize data on the prevalence of porcine cysticercosis in South Africa. Comprehensive search strategies were used to retrieve South African studies published between 2003 and 2023 from WorldCat Discovery and Google Scholar databases. The search indicated that various diagnostic tests, including Enzyme-linked Immunosorbent Assay (ELISA), Enzyme-linked Immuno-electro Transfer Blot (EITB), full carcass dissection, lingual examination, meat inspection, and molecular techniques were employed to detect cysticercosis in pigs. Furthermore, each test was reported to have its own set of benefits and drawbacks. This review exposed a South African country-wide pooled frequency of 33% of porcine cysticercosis, which is a serious public health hazard. Risk factors associated with porcine cysticercosis include pig farming methods (particularly the traditional free-range system), unprotected water sources, aging pigs, open defecation, and the absence of latrines in homes. Some of the studies also reported information gaps among farmers and the public, including the inability to recognize cysts and a lack of awareness of the condition. These results highlight the complex interactions between socioeconomic, environmental, and public health factors that affect the prevalence of porcine cysticercosis in the area. Thus, highlighting the necessity of all-encompassing strategies to combat this significant zoonotic illness through focused interventions and control measures, including education and provision of proper sanitation methods in impoverished areas.

-- END POSTER PRESENTATIONS --

Thank you for joining us for the 21st Annual SASVEPM Congress

