19th ANNUAL SASVEPM CONGRESS 2022
24-26 August 2022 • East London ICC

one

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PROGRAMME

SOUTHERN
AFRICAN
SOCIETY FOR
VETERINARY
EPIDEMIOLOGY &
PREVENTIVE
MEDICINE

in partnership with

USDA United States Department of Agriculture

BTRP Biological Threat Reduction Program

ABOUT SASVEPM

The Southern African Society for Veterinary Epidemiology and Preventive Medicine (SASVEPM) was formed at the end of 2000, with the objective of promoting veterinary epidemiology and preventive medicine in the Southern African region. One of the reasons for starting a regional society was the realisation that we have unique problems and circumstances in Africa that require us to formulate a unique brand of epidemiology that can be applied in the region.

The best people to do this are the Africans themselves. For too long resources had been wasted on disease surveillance and control because of a lack of understanding about epidemiology or because of the application of methodology that is inadequate for our region.

Our biggest problem was the lack of capacity in the discipline. We therefore needed a forum that would enable those with some expertise, or an interest, to cross pollinate expertise and ideas, with the objective of building capacity in the region, but also of creating a unique methodology applicable to our region.

The Society also aims to enhance communication between epidemiologists in the region. With the weakness of the currencies in the region it is also becoming increasingly difficult to attend conferences or continuing education courses overseas; a regional society thus allows local veterinarians to attain these goals at an affordable cost.

SASVEPM now has a multi-national membership of over 200, including private vets, state vets, vets in industry and others in academia and research. To date the Society has held eighteen Annual Congresses, which have been a highly successful blend of scientific papers, posters, and continuing education (CE) sessions. SASVEPM also hosted the twelfth International Symposium for Veterinary Epidemiology and Economics (ISVEE XII) during August 2009 at the ICC in Durban. We are also very proud to announce that we have won the bid to host the next ISVEE in Cape Town during 2027.


SASVEPM EXECUTIVE COMMITTEE, 2021

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MESSAGE FROM THE PRESIDENT

Dear SASVEPM Members

On behalf of the Southern African Society for Veterinary Epidemiology & Preventive Medicine EXCO it is with great pleasure to greet and welcome you all. SASVEPM is again ready to host the 19th Annual SASVEPM Congress at the East London International Convention Centre in East London, Eastern Cape from 24-26 August 2022. We are promising a platform that will continue to provide opportunities for interesting attendee engagements.

Africa has her unique problems with the sub-Saharan Africa, on many occasions, identified as one of the least developed regions of the world. The region has been inundated by several notifiable disease outbreaks. We must acknowledge that outbreaks do not occur in a vacuum. Aside from the interaction of the host/agent/environment, critical to the emergence, spread and containment of diseases are social, economic, and behavioural factors which are key determinants of the duration and outcomes of disease outbreaks. Thus, it is important to understand what is already being done in the communities, as well as the beliefs surrounding the causes of both disease and transmission. Social dynamics and behaviours are essential to understanding disease transmission, they also present potential barriers and opportunities for intervention. This is demonstrated by the spread of diseases like Rabies, African swine fever and Ebola in some parts of the African continent.

In 2017, the OIE adopted a Global Animal welfare Strategy which was developed with the objective of achieving "*A world where the welfare of animals is respected, promoted and advanced, in ways that complement the pursuit of animal health, human well-being, socio-economic development and environmental sustainability*". This is a critical area which presents a wide spectrum of interpretations from diverse cultural and religious groups. The need for harmonizing critical aspects of animal welfare with animal/public health, not ignoring the entire objective, is becoming more urgent. Hence the need for increased awareness.

The 19th SASVEPM congress is offering a forum for authors to present research, as oral or poster presentations, to the SASVEPM audience under the theme ***"One Africa, One Health, One Welfare"*** with three subthemes. SASVEPM is further looking forward to hosting some of the World's renown scientists as guest speakers to unpack the subthemes and beyond.

SASVEPM 2022 is honoured to have Prof. Brian Perry (Visiting Professor, Nuffield College of Clinical Medicine, University of Oxford), Dr Tenzin Tenzin (Programme Office for the World Organisation for Animal Health) and Mr Tennyson Williams (Director for Africa, World Animal Protection).

Time, effort, and commitment from fellow SASVEPM executive committee members and the SAVETCON team, together with the generous support from our partners and sponsors have made it possible to organise this congress. Lastly, we would like to thank all the speakers, presenters and congress participants for their contributions which are the foundation of this congress.

I thank you for choosing to participate in the 19th Annual SASVEM Congress. May you enjoy your time at the congress.

Dr Noluvuyo Magadla
President, SASVEPM

PROGRAMME

Wednesday, 24 August 2022

Time	Theme	Title	Speaker
07h30	**Registration opens - arrival coffee and tea / Industry Networking**		
		Session Chair: Dr Mohamed Sirdar	
08h00	Opening	Welcome and Opening: SASVEPM President	Noluvuyo Magadla
08h15	Keynote 1	The quest for one health and one welfare in contrasting global livestock systems and market demands	Prof. Brian Perry
09h15	Integrating social dynamics in disease control & outbreaks	A descriptive exploration of livestock movement within the FMD protection zone of Bushbuckridge, Mpumalanga South Africa	David D. Lazarus
09h35		Prioritisation of provinces for African swine fever intervention in South Africa through Decision Matrix Analysis	Leana Janse van Rensburg
09h55		Farmer's knowledge, perceptions, and attitudes of FMD in the control zone of Limpopo Province	Kibambe K. Daddy
10h15	Sponsor - OBP		Aubrey Dladla
10h25	**Mid-morning refreshments/Posters/Industry networking**		
		Session Chair: Dr Sikhumbuzo Mbizeni	
11h00	Integrating social dynamics in disease control & outbreaks	Attitude towards dog bites among residents of two communities in eThekwini District, KwaZulu Natal Province, South Africa	Mohube T. Letsoalo
11h20		Assembling value chain and trade networks as a basis for cost effective surveillance in rural chickens in the Eastern Cape Province of South Africa	Vincent Simbizi
11h40		Spatio-temporal epidemiology of animal and human rabies in northern South Africa in 1998-2017	Kgaogelo Mogano
12h00		Awareness and risk factors of zoonotic infections among abattoir workers in the Eastern Cape, South Africa	Koketso D. Mazwi
12h20		Investigations into Middle East Respiratory Syndrome coronavirus in camels and humans in Sudan	Khalid A. Enan (virtual)
12h40	Sponsor - BTRP		Alex Robinson
12h50	**Lunch**		
		Session Chair: Dr Wonderful Shumba	
14h00	Integrating social dynamics in disease control & outbreaks	Zero human deaths from dog-mediated rabies by 2030– How far are we from the target? – experiences from Limpopo Province	Unarine B. Makungo
14h20		In-Vitro Potential of Crude Extracts of Selected Garden Herbs for Mastitis Management in Zambia	Joshua Ngwisha
14h40		Knowledge, attitudes and practices of farmers and veterinary officials regarding bovine brucellosis and tuberculosis control at the livestock-wildlife interface in Northern KwaZulu-Natal, South Africa	Alfred T. Kgasi
15h00	Epidemiological Network for SADC		Sihle Mdluli
15h10	**Mid-afternoon refreshments/Posters/Industry networking**		
15h40	Integrating social dynamics in disease control & outbreaks	Rabies epidemiology in South Africa, 1993-2021: Can molecular epidemiological analysis provide additional insights?	Natalie Viljoen
15h50		Does gender play an integral role in disease control & outbreaks? Narratives of Smallholder farmers in two provinces of South Africa	Zimbini Mdlulwa
16h10		Designing a minimum- intervention strategy for the control of Neurocysticercosis in the Eastern Cape province of South Africa	Caryn Shacklock (virtual)
16h30	End of Day 1		
18h00	**Welcome Reception**		

Thursday, 25 August 2022

Time	Theme	Title	Speaker
Session Chair: Dr Noluvuyo Magadla			
08h00	Keynote 2	Rabies elimination strategies and the WOAH procedures for endorsements of official control programmes for dogmediated rabies and self-declaring freedom from a canine mediated rabies	Dr Tenzin Tenzin
09h00	Adaptive Epidemiology for healthy communities	Characterization of *Brucella* species and biovars in South Africa between 2008 and 2018 using laboratory diagnostic data	Itumeleng Matle
09h20		Post-outbreak African horse sickness surveillance: a scenario tree evaluation in South Africa's controlled area	John D. Grewar
09h40		Persistent NTM exposure results in false positive bovine tuberculosis diagnosis and reduced Interferon-ɣ production in BCG vaccinated calves	Akinbowale Jenkins (virtual)

Time	Theme	Title	Speaker
10h00	Adaptive Epidemiology for healthy communities	Seroprevalence and associated risk factors of toxoplasma gondii in commercial and communal sheep and goats in the North-West province	Mthokozisi Masombuka
10h20	Epidemiology for healthy communities	Laboratory-based surveillance of Malignant Catarrhal Fever in Lephalale municipality in Limpopo province, South Africa	Emmanuel Moloko Seakamela
10h20	**Mid-morning refreshments/Posters/Industry networking**		
Session Chair: Dr Liesl De Boni			
10h50	Keynote 3	Integrating Animal Welfare into World Welfare	Mr Tennyson Williams
11h50	World of Welfare	Animal welfare knowledge, attitudes and practices of stock people in Zimbabwe's large-scale dairy farms	Zivanayi Matore
12h10		Socioeconomics and traction animals in a peri-urban area of the Vaal Triangle, Gauteng	Dimakatso B. Molapo
12h30		Identification of animal welfare hazards during and around stunning and bleeding of ostriches (Struthio camelus) at a high-throughput abattoir in South Africa: A retrospective study	Mussett Dube
12h50	**Lunch**		
Session Chair: Dr John Grewar			
14h00	Adaptive Epidemiology for healthy communities	Surveillance of Avian Influenza virus in environmental faecal samples from wild birds in Gauteng Province	Gerbrand A. van der Zel
14h20		Enterotoxigenic *Escherichia coli:* prevalence in South African piglets	Thierry Y. Fonkui
14h40		Genetic characterization, virulence and detection of antimicrobial resistance genes of *campylobacter jejuni* from slaughter age broiler chickens	Tsepo Ramatla
15h00		Occurrence of *Cryptosporidium* spp. and *Giradia* spp. infections from sheep and goats in Potchefstroom, South Africa	Mpho Tawana
15h20		Distribution and genetic diversity of cystic echinococcosis in a non-endemic region: a one health approach	Titus Mutwiri
15h40	**Mid-afternoon refreshments/Posters/Industry networking**		
16h00	SASVEPM AGM		
19h00	**Gala Dinner – "African Chique"**		

Friday, 26 August 2022

Time	Theme	Title	Speaker
Session Chair: Dr Pamela Woods			
08h00	Round Table Discussion		Brian Perry, Tenzin Tenzin & Tennyson Williams
09h00	Adaptive Epidemiology for healthy communities	Isolation and antibiotic sensitivity of Campylobacter species from fecal samples of broiler chickens in North-West Province, South Africa	Kealeboga Mileng
09h20		Improved safety profile of Inactivated Neethling strain of the Lumpy Skin Disease Vaccine	Matome Matsiela
09h40		Prevalence and characterization of Shiga toxin-producing *Escherichia coli* in dairy cattle in South Africa	Alaba S. Olawole
10h00		Immunological Evidence of Variation in Exposure and Immune Response to *Bacillus anthracis* in Herbivores of Kruger and Etosha National Parks	Sunday O. Ochai
10h20		ILRI One Health Initiatives in Africa: Concepts and Applications	Amos Lucky Mhone (virtual)

10h40	**Mid-morning refreshments/Posters/Industry networking**		
		Session Chair: Dr Japhta Mokoele	
11h00	Adaptive Epidemiology for healthy communities	Serotyping and resistance profiling of non-typhoidal *Salmonella* isolates from poultry in South Africa	Elly Masitha
11h20		Porcine mycobacteriosis in slaughter pigs from South Africa: Mycobacterial species diversity, MAH genotypes and Potential public health implications	Nomakorinte Gcebe
11h40		Species richness and the encroachment of the invasive cattle tick, *Rhipicephalus microplus* (Acari: Ixodidae) on camps grazed by sheep in the Eastern Cape Province, South Africa	Nkululeko Nyangiwe
12h00		Genomic Sequencing of *Bacillus cereus* Sensu Lato Strains Isolated from Meat and Poultry Products in South Africa Enables Inter- and Intranational Surveillance and Source Tracking	Itumeleng Matle
12h20		Preliminary validation of a single-spot solid-phase competition ELISA for the diagnosis of southern African territories 1 foot-and-mouth disease serotype exposure in goats	Moses Gobiye
12h40	Awards & Closure of Congress 2022		Noluvuyo Magadla
13h15	**Lunch & Departure**		

Posters

Theme	Title	Speaker
Integrating social dynamics in disease control & outbreaks	1. A serological assessment of rabies-neutralising antibodies in wildlife species to facilitate international movement	Mmantshuruge J. Miyen
	2. Cattle trade networks in the foot-and-mouth disease (FMD) Protection Zone of Limpopo Province	Kholofelo Kenneth Malatji
	3. Investigating microbiological quality of broiler chicken carcass slaughtered informally and in registered abattoir from emerging small-scale farms in the Gauteng province, South Africa	Thabiso P. Nxumalo
	4. Assessment of risk factors for African swine fever in Gauteng province	Keneiloe Malokotsa
	5. The Livestock-foods-Humans-environment interface of Klebsiella pneumoniae in South Africa: a review study on virulence, resistance, and diagnosis methods for control strategies	Katlego L. Ndlovu
	6. Post African swine fever outbreak biosecurity investigation in North-West Province, Dr Kenneth Kaunda District in Potchefstroom	Lebo Mnisi
	7. Factors that are correlated with knowledge of African Swine Fever among emerging pig farmers in uThukela District, KwaZulu Natal Province, South Africa	Nicol Mbali Thusi
	8. Cattle management factors related to the incidences of reproductive disorders in communal farms of Mafikeng	Keitiretse Molefe
	9. The outbreak of Aflatoxicosis: Cases in Africa	Kgomotso Galian Setsetse
	10. The “One Health” concept as a potential key driver of job creation in the Eastern Cape Province, South Africa	Ivan Lwanga-Iga
Adaptive Epidemiology for healthy communities	11. Characterisation and antimicrobial resistance profile of Staphylococcus spp. isolated from canine specimens submitted to a diagnostic laboratory in South Africa, 2012 - 2017	Themba T Sigudu
	12. A preliminary report: prevalence of ecto- and endo-parasites in the free-roaming pigs in peri-urban areas of Gert Sibande District Municipality of Mpumalanga province, South Africa	Priscilla Munzhelele
	13. Wirevax' one health approach one health approach to reduce antimicrobial resistance	Mantetikwe N.Maphalala
	14. Genomic Characterisation and antimicrobial resistance profiles of Listeria monocytogenes isolated from pig farms	Puseletso M Masemola
	15. Quantitative risk assessment of the likelihood of importing mechanically recovered poultry meat contaminated with Salmonella into South Africa	Tandile N Ndobeni
	16. Antimicrobial Resistance of foodborne pathogens in South Africa	Mpinda Edoaurd Tshipamba
	17. Surveillance of West Nile Virus in horses and humans in South Africa for 2021	Carla Lourens
	18. Preliminary findings of a descriptive epidemiological study of food-borne diseases recorded at a hospital in O.R. Tambo District, Eastern Cape Province, South Africa	Nandisa N. Ndlame
	19. Prevalence and risk factors of Coxiella burnetii infection in cattle on farms in Limpopo province, South Africa	Vhahangwele Sadiki
	20. Q fever: Seroprevalence, Risk Factors in Slaughter Livestock and Genotypes of Coxiella burnetii in South Africa	Maruping Mangena
	21. Efficacy of plant species from the Celastraceae family on multidrug-resistant Staphylococcus aureus isolated from subclinical bovine mastitis cases	Dikeledi C. Sebola
	22. Efficacy of deltamethrin against ticks on goats at Makhuduthamaga rural areas and detection of Ehrlichia ruminantium in Amblyomma hebraeum	Mashifane Mamaje Kgaogelo

	23. Investigation of orthobunyaviruses in animals with unsolved febrile and neurological disease in South Africa	Miné van der Walt
	24. Contagious Ecthyma (CE) Infection in Eastern Africa: A Constant Threat to Livestock Productivity	Ahmed Eisa Elhag Ibrahim
	25. Health screening of tilapia (Oreochromis species) populations held at a tropical aquarium with particular focus on two specific pathogens: Mycobacteria spp. and Tilapia Lake Virus	Nelson Matekwe
	26. Molecular and serological investigation of Shuni virus in South Africa	Matshepo Elizabeth Rakaki
	27. Effects of dietary protein supplementation on body weight gain and reproduction in female boer goats	Mpho S. Tsheole
	28. Epidemiology research at ILRI to support the control of zoonotic diseases	James Akoko
	29. Capacitating One Health in Eastern and Southern Africa (COHESA)	Amos Lucky Mhone

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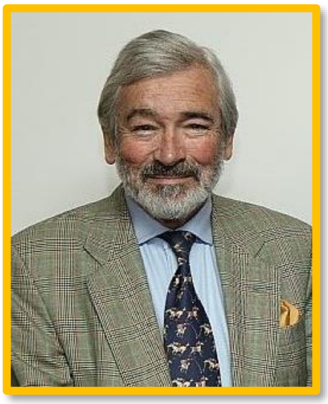
KEYNOTE SPEAKERS

Prof. Brian Perry



Brian Perry, a British citizen, is an international development scientist, a veterinarian by profession and an epidemiologist by specialization. He holds academic positions of Honorary Professor at the College of Medicine and Veterinary Medicine, University of Edinburgh, and Visiting Professor of Tropical Veterinary Medicine at the University of Oxford, UK.

Since 2010 he has chaired the Scientific Advisory Board of Afrique One Aspire, a Wellcome Trust-funded African Research Consortium for Ecosystem and Population Health comprising 11 universities and research institutes in eastern and western Africa. He is member of the Technical Committee of the Global Alliance for Livestock Veterinary Medicine (GALVmed)-administered AgResults Foot-and-Mouth Disease Vaccine Challenge Project and sits on the judging panel of the Global Alliance for Livestock Veterinary Medicine (GALVmed)-administered AgResults Brucellosis vaccine prize competition. Prof Perry is also member of the Management Board of the Medical Research Council (MRC)- funded International Veterinary Vaccinology Network and a member of the International Committee of World Horse Welfare.

He has published more than 300 scientific articles in refereed journals, books and proceedings as author and co-author.

Presentation: Wednesday 24 August, 08h15-09h15

The quest for one health and one welfare in contrasting global livestock systems and market demands

Dr Tenzin Tenzin

Dr. Tenzin Tenzin joined the OIE Sub-Regional Representation for Southern Africa on 1 May 2019 as programme officer and coordinator for the "Technical Support for Namibia in Eliminating Rabies in Dogs" project, which is being funded by the German Federal Ministry of Food and Agriculture (BMEL).

Tenzin is a Bhutanese veterinarian who joins us at the OIE from the Bhutan National Centre for Animal Health. Besides his veterinary medicine degree from Kerala Agriculture University, India,
Tenzin also holds a Master of Science (MSc) degree in Veterinary Epidemiology and Animal Health Economics from the University of Utrecht, the Netherlands.

He also has a Doctor of Philosophy (PhD) degree in epidemiology and control of rabies from the Sydney School of Veterinary Science, University of Sydney, Australia.

He developed technical expertise in rabies epidemiology and control, veterinary epidemiology, public health, zoonoses, one health, geographic information systems, data analysis and scientific writing during his PhD programme and post PhD field experiences.

Tenzin initiated mass dog vaccination campaigns against rabies and post vaccination monitoring along Bhutan-India border to create an immune buffer and cordon sanitaire, which resulted in reduced rabies outbreaks in dogs and human rabies deaths in Bhutan. As a result, Bhutan is now well on right track towards achieving zero human deaths due to dog-mediated rabies by 2030.

Tenzin took part in the revision of WHO Expert Consultation on Rabies (third edition) and was also involved in the WHO Rabies Modelling Consortium to synthesize evidence on access to rabies post-exposure vaccines and coordinated community-based dog bite and rabies contact tracing studies to support the GAVI Learning Agenda on Rabies.

Presentation: Thursday 25 August, 08h00-09h15

Rabies elimination strategies and the WOAH procedures for endorsements of official control programmes for dogmediated rabies and self-declaring freedom from a canine mediated rabies

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Mr Tennyson Williams

Hi, I'm Tennyson J. C. Williams, Country Director for World Animal Protection Africa.

My goal is to enhance and establish World Animal Protection's reach, influence and credibility as a leading animal welfare organization. In Africa, we work with governments, communities and partners to adopt solutions that include developing policies and encouraging responsible animal welfare practices.

Having grown up with animals all my life and studied Zoology, I've always endeared to see a world where they live free from suffering. Animals are sentient beings that play a critical role in sustaining the livelihoods of communities hence why we need to take more responsibility for them.

My blog will unfold our milestones, experiences and lessons and how you can support our cause in Africa. We can only achieve a better future for our animals when we work together.

Presentation: Thursday 25 August, 10h50-11h50

Integrating Animal Welfare into World Welfare

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LIFETIME ACHIEVEMENT

Dr Lubabalo Mrwebi: Honouring his contribution to South Africa's veterinary science and disease control

The Southern African Society for Veterinary Epidemiology and Preventative Medicine would like to honour the retired Dr Lubabalo Mrwebi, former Chief Director at Eastern Cape Department of Agriculture - Veterinary Services, for his support to SASVEPM and his contribution to disease control.

I, Lubabalo Mrwebi, qualified as a veterinarian in 1991 from the erstwhile Medical University of Southern Africa (MEDUNSA). I spent my entire professional life, spanning 37 years, in the public service, based in the Eastern Cape Province.

From 1991 - 2000 I was hands on in state veterinary work. During that period, I had the onerous, but wonderful opportunity to provide clinical services to the underprivileged livestock owners of various municipalities, including Mnquma LM, Mbashe LM, Alfred Nzo DM, Chris Hani DM and Joe Gqabi DM.

I also had a singular honour of heading the Eastern Cape state veterinary services from 2000 until my retirement in April 2017. It was during my stint as the Director of Veterinary Services that I managed to convince the Eastern Cape provincial government to institutionalize the control of sheepscab in the province. It is a project that I look back at with pride. During this period there has been a very significant improvement in both the quality and the quantity of wool that has come from the communal areas of the province.

A similar dispensation was extended to the control of anthrax. Like sheepscab, cattle vaccination against anthrax remains the responsibility of the State in the Eastern Cape province. This incentivized service allowed the veterinary professionals unfettered access to the livestock community. The opportunity has been taken advantage of to extend veterinary education widely, and as a result, we have a relatively well-informed livestock owning community.

I was at the centre of the control of three major animal disease outbreaks: foot-and-mouth disease outbreak that broke out in KwaZulu-Natal in 2001; the avian influenza (H5N5) outbreak in Somerset East in 2004 and the classical swine fever outbreak in 2005. The latter was controlled successfully, after a two-year struggle.

I also take pride in the knowledge that I facilitated a conducive environment for many veterinarians who qualified abroad to come and work in the Eastern Cape. Many other provinces followed suit. A significant number of those veterinarians have since made Eastern Cape their second home.

I retired from the public veterinary service at the end of April 2017.

ORAL PRESENTATIONS

Theme: Integrating social dynamics in disease control & outbreaks

A descriptive exploration of livestock movement within the FMD protection zone of Bushbuckridge, Mpumalanga South Africa

David D. Lazarus, Pamela A. Opperman, Mohamed M. Sirdar, Tanja E. Wolf, Ilana van Wyk, Oupa B. RIkhotso, Geoffrey T. Fosgate

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Background

Livestock movement is one of the most prominent ways of spreading infectious diseases including FMD between infected and susceptible animals. Many livestock diseases are transmitted through direct contact between animals, and thus between herds and flocks through animal movements. In this study, we described the pattern of livestock movements among smallholder farmers within a communal farming area in South Africa.

Objectives

The objective of this study was to evaluate movement patterns of livestock within the FMD protection zone with vaccination of Bushbuckridge, Mpumalanga, South Africa.

Methods and Analysis

A cross-sectional survey using a semi-structured questionnaire was administered to 116 respondents, and 13 focus group discussions employing participatory mapping and semi-structured interviews were conducted among smallholder farmers.

Results

Data from the study reported 37 nodes and 78 ties with an overall network density of 0.059 (SD 0.235) for goats, and 42 nodes and 90 ties with an overall network density of 0.052 (SD 0.223) for cattle across the study area. The study identified several high-risk locations to prioritise for FMD vaccination control programmes for cattle and targeted disease surveillance. Four locations within the (former) FMD-free zone of the country were identified to have connections with movement of goats from the study area.

Discussion and Recommendations

Findings from this study further demonstrated that goats are moved without official movement permits to the FMD free zone of the country, with most farmers being unaware of the need to obtain official veterinary movement permits. These animal movements put the country at risk of FMD outbreaks within the free zone. We recommend that risk-based control measures be considered to reduce the spread of FMD and other infectious diseases of livestock in the country.

Prioritisation of provinces for African swine fever intervention in South Africa through Decision Matrix Analysis

Leana Janse van Rensburg, Mary-Louise Penrith (1) Eric M.C. Etter (2, 3, 4)

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(2)Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria. (3) CIRAD, Montpellier, France. (4) ASTRE, Univ Montpe - marylouise@vodamail.co.za; eric.etter@cirad.fr

Background

South Africa has unfortunately experienced an increase in the number of African swine fever (ASF) outbreaks in domestic pigs in the last ten years. Intervention will be needed in the form of control and prevention strategies to minimise the impact of this disease in the country.

Objectives

The aim of this study was to prioritise which provinces resources should be allocated to for ASF intervention strategies, based on the risk factors identified to be pertinent in South Africa.

Methods and Analysis

Data for this study was collected from 2018 to 2020. A multi-criteria decision analysis approach was followed using an analytic hierarchy process (AHP) method to determine the perceived risk of ASF outbreaks in domestic pigs per province. Nine risk factors applicable to the South African context were identified from literature. Data on the presence of these risk factors per province were collected from records and by means of a questionnaire administered by veterinary officials and the South African Pork Producers' Organisation. The risk factors were weighted by means of an AHP, with pairwise comparison of risk factors performed by members of the South African ASF working group.

Results

The decision matrix determined that ASF intervention and prevention resources should be focused on Mpumalanga, Free State and Gauteng provinces in South Africa.

Discussion and Recommendations

Specific intervention strategies should be focused on confinement of pigs, swill-feeding of pigs and selling/buying of pigs at auctions through a participatory approach with stakeholders.

References

Janse van Rensburg, L.; Penrith, M.-L.; Etter, E.M.C. Prioritisation of Provinces for African Swine Fever Intervention in South Africa through Decision Matrix Analysis. Pathogens 2022, 11, 135. https://doi.org/10.3390/pathogens11020135

Farmer's knowledge, perceptions, and attitudes of FMD in the control zone of Limpopo Province

Kibambe K. Daddy(1), Eric Etter (1),(2), Petronella Chaminuku (3), Alexis Delabouglise (4) and Geoffrey Fosgate (1)

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Background

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

Objectives

Assess the level of knowledge, attitudes, and perception of FMD among small-scale, communal cattle producers with vaccination using

Methods and Analysis

The study area was Vhembe and Mopane districts in Limpopo Province and a total of 12 dip-tanks were randomly selected and a cross-sectional study was performed to assess the level of knowledge, attitudes, and perception of FMD among small-scale, communal cattle producers with vaccination using a structured questionnaire and a two-stage interview process.

Results

A total of 275 interviews were conducted at dip-tanks and 110 at homesteads. Most (75%) interviewed farmers were male and the majority (67%) were 60 years of age or older. Forty-five percent of interviewed farmers were involved in livestock farming as the main activity and 38% did not have a formal education. Sixty percent of interviewed farmers knew the name of FMD in local language and 35% reported that the cause of the disease was buffalo. The majority described the clinical signs of FMD in their animals including lameness (34%), salivation (24%), weight loss (8%), death of calves (2%). According to interviewed farmers, co-grazing with infected cattle (32%), contact with buffalo (12%) and transporting cattle (1%) were among the main causes of FMD spread. Thirty-one percent of farmers believed that the injection of antibiotic such as oxytetracycline is an effective treatment for FMD in cattle. Also, forty-six percent of farmers strongly agreed that FMD vaccine is effective in preventing outbreaks in cattle

Discussion and Recommendations

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

Attitude towards dog bites among residents of two communities in eThekwini District, KwaZulu Natal Province, South Africa

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Background

KwaZulu-Natal has recorded more cases of canine rabies compared to other provinces in South Africa.

Objectives

This study investigated the attitude towards dog bites in two selected communities in eThekwini, South Africa.

Methods and Analysis

A cross-sectional questionnaire based study design was used to collect data on a random sample of 768 participants. A score was computed for the attitude towards dog bites for each respondent, and respondents who scored over 60% were considered to have a good attitude towards dog bites. A Chi-Square test was used to assess for associations and significance was set at $\alpha<0.05$.

Results

Age was associated with a good attitude towards dog bites ($p<0.012$). Respondents aged 36-53 years (62.15%) were more likely to have a good attitude towards dog bites compare to respondents aged 54 -71 (57.81%), 18-35 (50.12%) and >71 (57.81%) years. Male respondents (61.79%) were significantly ($p=0.0055$) more likely to have a good attitude towards dog bites compared to female (51.43%). No significant ($p=0.384$) difference in the attitude towards dog bites was observed between Verulam (56.77%) and Embo (53,65%). Religion was significantly associated ($p=0.0001$) with a good attitude towards dog bites, with Muslims (67.74%) more likely to have a good attitude towards dog bites as compared to Christians (59.49%), Hindus (58.33%) and followers of African religion (46.43%). Respondents who owned pets (75.31%) were significantly ($p=0.001$) more likely to have a good attitude towards dog bites compared to those who did not (1.44%). Education attained by the respondents was significantly (p=0.001) associated with a good attitude towards dog bites. Respondents who had attained tertiary education (66.96%) were more likely to have a good attitude towards dog bites as compared to those with secondary education (61.82%), no formal education (53.49%), completed matric (48.72%) or completed primary (39.60%).

Discussion and Recommendations

This study shows the attitude towards dog bites differs based on the demographic characteristics of the respondents. However, there was no difference in the attitude of respondents based on the community of origin. Therefore, education programmes for the control of canine rabies must take into consideration the demographic profile of community members and their attitude towards dog bites

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Assembling value chain and trade networks as a basis for cost effective surveillance in rural chickens in the Eastern Cape Province of South Africa

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Background

Despite the benefits of rural chickens in the Eastern Cape Province (ECP) of South Africa, this sector is still underdeveloped and poorly surveyed for poultry diseases. The lack of a sustainable disease surveillance system coupled with communities and practices where the interactions between birds are high, emphasize the need for targeted surveillance.

Objectives

To evaluate the possibility of combining rural chicken value chain and social network analysis (SNA) for informing targeted surveillance within rural ECP where scarce resources constitute a big challenge. To use the value chain analysis (VCA) to understand the barriers to market entry for rural chicken farmers.

Methods and Analysis

A survey which involved a rural chicken VCA that also included an assessment of trading practices to identify biosecurity hotspots and an identification of barriers to market entry for rural farmers was conducted. Secondly, a SNA of chicken movements in the province was carried out to identify trade hubs that could be targeted for disease surveillance based on their centrality within the network and their size and influence within their ego networks.

Results

Traders and their transport vehicles were identified as biosecurity risk hotspots that could be targeted for disease surveillance within the chain. SNA identified three municipalities (Umzimvubu, King Sabata Dalindyebo and Enoch Mgijima) as trade hubs where interaction between rural chickens occurs and resources can be focused. The main barriers to market entry included production constraints and current policy.

Discussion and Recommendations

This is the first study to formally describe chicken trade networks within the ECP and the surrounding region. It provides a model for cost effective targeted surveillance in the ECP and similar resource poor regions. It also describes the barriers to market entry for farmers and factors hampering the profitability and expansion of this sector.

Spatio-temporal epidemiology of animal and human rabies in northern South Africa in 1998-2017

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Background

Rabies is a fatal zoonotic disease that is maintained in domestic dogs and wildlife populations in the Republic of South Africa. A retrospective study was conducted to improve understanding of the dynamics of rabies in humans, domestic dogs, and wildlife species, in relation to the ecology for three northern provinces of South Africa (Limpopo, Mpumalanga, and North-West) between 1998 and 2017.

Objectives

The objectives were to (1) examine geographic patterns and characterize rabies trends over the 20-year period; (2) identify spatio-temporal clusters of animal rabies cases; and (3) evaluate the nature and extent of ecological factors that could facilitate such patterns. The ultimate aim of the study was to enhance understanding of the molecular evolutionary dynamics of rabies within the spatio-temporal clusters.

Methods and Analysis

A descriptive epidemiology study was conducted for human and animal rabies. Dog rabies cases were analyzed using spatio-temporal scan statistics. The reproductive number (R0) was estimated for the identified disease clusters. A phylogenetic tree was constructed based on the genome sequences of rabies viruses isolated from dogs, jackals, and an African civet, and Bayesian evolutionary analysis using a strict time clock model. Several ecological and socio-economic variables associated with dog rabies were modeled using univariate analyses with zero-inflated negative binomial regression and multivariable spatial analyses using the integrated nested Laplace approximation for two time periods: 1998-2002 and 2008-2012.

Results

Human rabies cases increased in 2006 following an increase in dog rabies cases; however, the human cases declined in the next year while dog rabies cases fluctuated. Ten disease clusters of dog rabies were identified, and utilizing the phylogenetic tree, the dynamics of animal rabies over 20 years was elucidated. In 2006, a virus strain that re-emerged in eastern Limpopo Province caused the large and persistent dog rabies outbreaks in Limpopo and Mpumalanga Provinces. Several clusters included a rabies virus variant maintained in jackals in Limpopo Province, and the other variant in dogs widely distributed. The widely distributed variant maintained in jackal populations in North-West Province caused an outbreak in dogs in 2014. The R0 was high when the disease clusters were associated with either multiple virus strains or multiple animal species. High-risk areas included Limpopo and Mpumalanga Provinces characterized by woodlands and high temperatures and precipitation.

Discussion and Recommendations

Rabies is a fatal zoonotic disease transmitted primarily via bites by animals infected with the rabies virus. The majority of human cases occur due to the exposure to infected domestic dogs. In the Republic of South Africa, rabies is endemic, and domestic dogs, mongooses, bat-eared foxes, and jackals are the main reservoir hosts. Rabies control efforts typically target domestic dog populations, as it is difficult to monitor and control in wildlife species. Jackals are known to sustain infection cycles with domestic dogs. This study was conducted to improve understanding of the spatial and temporal dynamics of rabies in human, domestic dogs, and wildlife, in relation to ecology and socio-economics in northern South Africa. Human cases occurred where disease clusters in dogs were identified. Large size outbreaks in dogs were caused by dog rabies virus variants, but disease clusters included multiple virus variants in multiple host species. Rural communities in Limpopo and Mpumalanga Provinces, characterized by woodlands and high temperatures and precipitation, were at high risk of canine rabies originating from dogs. Control efforts should be focused on improving the geographical distribution of dog rabies vaccination coverage.

Awareness and risk factors of zoonotic infections among abattoir workers in the Eastern Cape, South Africa

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Background

Exposure to infectious pathogens from apparently healthy animals is a growing concern that warrants urgent attention and regular awareness campaigns especially to those at risk of exposure. The lack of proper use of personal protective equipment (PPE) and knowledge regarding zoonotic infections among abattoir workers can result in zoonotic outbreaks.

Objectives

To evaluate the associated risk factors of infectious diseases and create awareness among abattoir workers in the Eastern Cape province, South Africa.

Methods and Analysis

One hundred and sixteen abattoir workers from five abattoirs in the Eastern Cape were purposely selected for the study. Of these, 40 respondents participated in the questionnaire on microorganisms causing zoonotic diseases, while 76 participated on risk factors of zoonotic diseases.

Results

Of the 40 abattoir workers comprising of butchers, cleaners and health inspectors who participated in the awareness session, 87.5% had some knowledge on germs (microorganisms) of which 22.9% believed that germs can be seen with naked eyes. Of the 76 respondents on the risk factors of zoonotic diseases, 18,4%, 19.2% and 47.4% of abattoir workers had knowledge on Q-fever, toxoplasmosis and brucellosis, respectively whereas 15% had no knowledge on all the diseases. Consumption of undercooked meat was reported in 11,8% of the workers, while 31,6% of the workers drank unpasteurized milk. Most abattoir workers (84%) wore PPE. Abattoir workers (75,3%) also reported hand cut injuries which occurred whilst at work. An awareness session was held to demonstrate the presence of microorganisms (germs) on work surfaces, human body and their clothes using fluorescent glow paint and fluorescent light.

Discussion and Recommendations

Lack of knowledge observed regarding micro-organisms, as well as paucity in understanding the use of PPE raises a concern, since abattoir workers have high exposure potential to different zoonotic infections. This can be transmitted in several ways including inhalation of contaminated aerosols and direct contact with infected carcasses or their secretions. The presence of infectious diseases in apparently healthy animals are of concern and we recommend regular public awareness campaigns and educational activities, which we perceive are essential to mitigate human infections.

Zero human deaths from dog-mediated rabies by 2030– How far are we from the target? – experiences from Limpopo Province

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Background

Rabies is a viral zoonotic disease that can be prevented by vaccination and it still remains a global public health concern. Dogs are the most common source of human rabies, contributing to up to 99% of all cases. As of 20 May 2022, seven laboratory-confirmed human rabies deaths were reported in South Africa. Prevention involves vaccination of dogs and prevention of dog bites, as well as immediate, thorough wound washing with soap and water after contact with a suspected rabid animal and administration of post-exposure prophylaxis.

Objectives

The study's objective was to present an overview of recent dog bites in the last five years and confirmed human rabies cases and share lessons learned in Limpopo Province.

Methods and Analysis

We conducted a retrospective analysis of dog-bite surveillance data from January 2017 to May 2022, laboratory-confirmed human rabies cases for the period January 2008 to May 2022, and reviewed outbreak reports.

Results

A total of 37 771 dog bites were reported between 2017 and May 2022. Majority were reported from Vhembe (n=23 814; 63%) and Mopani district (n = 5229; 14%). A total of 61 laboratory-confirmed 1 probable cases were reported since 2008. The median age of the combined cases was 10 years old; range (2-72) and (n=39;63%) were males. Those less than 10 years accounted for (n=30;48%) of the cases and (n=17;27%) were between 10-19 years. Three of the laboratory-confirmed cases reported in 2022 did not seek medical care prior to the onset of symptoms and one of them had no history of exposure to a dog.

Discussion and Recommendations

Human rabies remains a concern in the Limpopo province and highlights the need to strengthen the One Health approach to meet the goal of eliminating human deaths from dog-mediated rabies by 2030. Children remain at high risk and schools should be targeted to drive health education campaigns. Recent cases highlight the knowledge gap in the community regarding the disease and anti-rabies post-exposure prophylaxis. Vaccinating the animals in their community provides the best rabies prevention. The coordination of efforts among stakeholders is inadequate, and stakeholders must work together to improve response coordination. Actions in the field The Department of Health in collaboration with the National Institute for Communicable Diseases (NICD) plans to train the veterinary doctors and technologists on the Notifiable Medical Conditions Surveillance System (NMCSS) surveillance system in order to improve notification of zoonotic conditions. In addition, the province intends to re-establish the provincial rabies advisory committee and embark on a Rabies awareness drive in high-risk areas.

Investigations into Middle East Respiratory Syndrome coronavirus in camels and humans in Sudan

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Background

The Middle East respiratory syndrome coronavirus (MERS-CoV) is a zoonotic human pathogen associated with severe respiratory symptoms and renal failure, with a fatality rate of up to 35 %. It is thought that MERS CoV is transmitted to humans from infected dromedaries, indeed MERS CoV has been detected in dromedaries in several countries in the Middle East, Africa and South Asia. Human to human transmission of MERS CoV is possible, and has been reported in health care settings as well as more infrequently among family members.

Objectives

We aimed to investigate the circulation of MERS-CoV in camels and humans in Sudan, in order to gain a better understanding of the risk of transmission to humans who live and work in close proximity to camels.

Methods and Analysis

To this end, in 2016 - 2017 both nasal swabs (n=331) and serum samples (n=371) were collected from dromedaries in Kassala, Gezera, and Atbara, as each side we held a one day seminar to explain the purpose of our visit, the importance of MERS-CoV and its relationship with camels and why we are collecting the samples. We assumed them that the results of the survey will be available to anyone interested in obtaining them. Our samples were only collected from people who agreed to donate them.Serum samples only (n=290) were collected from dromedaries in the River Nile and Khartoum states. Dromedary nasal swabs were then analysed for MERS CoV RNA by real time RT-PCR and camel serum samples for anti-MERS CoV IgG antibodies by ELISA. Human serum samples from healthy blood donors in Khartoum (n=92), and from patients presenting with atypical pneumonia in Khartoum (n=41) were analysed for anti MERS CoV IgG antibodies by ELISA, as were serum samples collected from people who worked in close contact with the dromedaries in Kassala (n=120), Gezera (n=92) and Alfaw (n=92).

Results

We report a high prevalence of MERS-CoV antibodies in dromedaries in several states ranging from 78 % in Khartoum to 96 % in Kassala State. MERS CoV RNA was detected in 1/234 nasal swabs (0.4 % prevalence) taken from dromedaries in Gezera and in 10/37 nasal swabs (27 % prevalence) from dromedaries in Atbara. In human samples an anti-MERS-CoV IgG seroprevalence rate of 1.1% was found in both people who worked in close contact with dromedaries in Alfaw and blood donors from Khartoum, however none of the human serum samples from Kassala or Gezera were seropositive. In addition 2/41 patients (5 %) with atypical pneumonia were found to be seropositive for anti-MERS CoV IgG antibodies.

Discussion and Recommendations

This study confirms the circulation of MERS-CoV in Sudan in dromedary populations. The discovery of human serum samples positive for MERS CoV IgG antibodies indicates the possible transmission of MERS CoV from camels to humans in Sudan. However further detailed studies are needed to fully elucidate and then mitigate the risk of MERS CoV transmission to humans in Sudan.

In-Vitro Potential of Crude Extracts of Selected Garden Herbs for Mastitis Management in Zambia

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Background

The advent of bovine mastitis associated antimicrobial resistance has necessitated development of alternative herbal remedies. Some of the herbs of importance that could hold solutions to our challenges are found within our proximal environments such as farms and backyard gardens, yet their potential remains largely untapped.

Objectives

In this study, we set out to test, invitro, the antimicrobial efficacy of three crude extracts [1] aqueous, [2]ethanol and [3] ethyl acetate extracts of Zambian cultivated Aloe barbadensis Miller (Aloe vera) and Curcuma longa (Turmeric) and made comparisons to synthetic anti-mastitis formulations.

Methods and Analysis

The active compounds of these herbs were obtained as crude extracts using the solvents water, ethanol and ethyl acetate. The test microbes comprised of ten recognized controls including Escherichia coli and Pseudomonas aeruginosa and eighty four field isolates (all gram positive bacteria) from clinical and subclinical mastitis milk samples from selected districts of the Southern province of Zambia belonging to the genera Staphylococcus, Streptococcus, Bacillus and Lactobacillus. The agar dilution method was used to determine the antimicrobial activity by observing the susceptibility, which was graded, as susceptible, intermediate or resistant. Commercial synthetic anti-mastitis preparations served as positive controls and their susceptibility was compared to that of the herbal preparations. The Minimum Inhibitory Concentrations (MIC) of the herbal formulation was determined using two-fold serial dilutions.

Results

On average, the agar dilution trials revealed; 41.8 per cent resistance, 13 per cent intermediate and 45.3 per cent susceptibility for the herbal formulation while the synthetic antimicrobials produced 23.5 per cent resistance, 5.2 per cent intermediate and 71.3 per cent susceptibility. The gram negative controls tested were generally resistant. Mean MIC was 11.5mg/ml at the 5 per cent serial dilution for the herbal extract compared to the Cephalexin (semi-synthetic antimicrobial) MIC for S. aureus at 0.5mg/L or 0.0005mg/ml.

Discussion and Recommendations

Ethno-veterinary herbal preparations comprising of Zambian grown Aloe vera and Curcuma longa, possess gram positive antibacterial and antifungal spectrum of activity on bovine mastitis and other pathogenic microorganisms in-vitro and carry the prospect of being utilized as alternatives to locally used synthetic anti-mastitis preparations in Zambia, at an MIC of 5 per cent. This study recommends to policymakers, interest groups and other researchers, the validation of such and other useful local herbs and formulations in Zambia to the benefit of the most affected and resource limited small scale dairy and organic farmers. An intervention impact assessment on the reduction of antimicrobial residues in milk, coupled with mitigating the development of antimicrobial resistant pathogens associated with bovine mastitis, may also be necessary. It is further recommended to academia and policymakers to consider developing a cadre of ethnoveterinary practitioners through the establishment of a postgraduate diploma in ethno-veterinary practices in Zambia, as this may aid in natural resource development, utilization and job creation.

References

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Knowledge, attitudes and practices of farmers and veterinary officials regarding bovine brucellosis and tuberculosis control at the livestock-wildlife interface in Northern KwaZulu-Natal, South Africa

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Background

BR and bTB are zoonotic diseases with economic and public health importance across the world, especially in developing countries where the diseases are endemic (WHO Report, 2005). The diseases remain a worldwide problem and are classified as neglected diseases in developing nations with poor resources despite having been brought under good control in some developed countries (Muma, Syakalima, Munyeme, Zulu, Simuunza & Kurata, 2013). Community participation in animal and public health programmes during investigation, design and implementation creates ownership, enhances acceptability and sustainability. There is a need to always understand farmers' priorities in livestock disease control for a sustainable livestock health policy intervention (Waziri, 2020). Formal and informal consultative mechanisms with clients and stakeholders are required to assist in any successful planning and policy formulation of animal-health programme delivery. The success of public health measures has been found to be directly depended on understanding the social and economic aspects of the targeted communities (Muleme, et al., 2017).

Objectives

The aim of the research is to assess the knowledge, attitudes and practices of small-scale farmers and veterinary officials towards BR and bTB control measures at a livestock-wildlife interface in South Africa.

Methods and Analysis

Quantitative (using a statistical approach) and qualitative method (using focus group discussions), were used to interview small-scale farmers and veterinary officials in Northern Kwa-Zulu Natal Province,, in South Africa.

Results

Majority of small-scale farmers and veterinary officials did not believe that the current methods for control of BR and bTB were effective. Reasons provided were the lack of sufficient resources (people and funding) by the Government. Communal farming infrastructure was stated as a hindrance to effective disease control. Poor training of farmers and unrestricted animal movement had negative effect on disease control. Factors such as difficulty in isolating/separating animals (biosecurity) in communal areas, provincialization of disease control strategies, lack of enforcement, lack of compensation for farmers, were raised by stakeholders.

Discussion and Recommendations

It is recommended that the current structure of the South African veterinary services' delivery model be revised to enable coherent disease control co-ordination between National Department and Provinces. Resource allocation and enforcement by veterinary officials is necessary to ensure effective disease control. Compulsory vaccination for BR is recommended, and further research is required into possible bTB vaccination. Rural infrastructure should be improved, particularly fences, to ensure separation of livestock from wildlife. A comprehensive compensation system needs to be put in place during test-and-slaughter interventions. Effective movement control of animals and education of farmers is critical. The outcome of the study should serve as guide for policy development and implementation for both BR and bTB control measures in South Africa

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Rabies epidemiology in South Africa, 1993-2021: Can molecular epidemiological analysis provide additional insights?

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Background

In South Africa, rabies control is complicated by the presence of wildlife and dog rabies cycles that can be maintained independently or insect. Given the global goal of zero canine-mediated human rabies deaths by 2030, understanding rabies epidemiology is crucial to allow the implementation of effective, targeted rabies control strategies.

Objectives

To analyze rabies data for South Africa from 1993-2021 and review existing rabies molecular epidemiological literature.

Methods and Analysis

Rabies data was obtained from the Department of Agriculture, Land Reform and Rural Development database for 1993-2021 and was sorted based on the province, date, animal species and the number of rabies cases per year was collated. District-level analysis was performed for 2010-2021. Published and unpublished rabies epidemiological studies were reviewed to identify key areas for future research.

Results

From 1993-2021, 12879 animal rabies cases were reported. The two provinces with the highest burden of animal rabies, KwaZulu Natal (44.6%, 5739/12879) and the Eastern Cape (13.9%, 1787/12879), have well-established dog rabies cycles and cases in domestic dogs contributed to 85.8% (4925/5739) and 57.6% (1030/1787) of cases reported from these provinces, respectively. In KwaZulu Natal, an emerging wildlife rabies cycle resulted in 40 wildlife rabies cases identified in the uMgungundlovu district between 2015-2016. Dog rabies has emerged in the Mpumalanga, Limpopo and Free State provinces over the last two decades, which was accompanied by a significant decline in rabies reported in the wildlife species that were previously considered to be the most prominent maintenance hosts. In Mpumalanga, mongoose rabies is reported from the central and western districts, while dog rabies is reported from the eastern and southeastern districts suggesting two contrasting epidemiological profiles in this province. While bat-eared fox rabies predominated in the Northern Cape, between 2014-2016, a significant increase in dog and aardwolf rabies was reported. Elucidation of the role of the aardwolf in rabies epidemiology using molecular analysis is warranted.

Discussion and Recommendations

Between 1993-2021, significant changes in rabies epidemiology has been noted, particularly the expansion various of wildlife rabies cycles. Molecular epidemiological analysis may provide insights into the connection between these wildlife cycles and emerging or existing dog rabies cycles.

Does gender play an integral role in disease control & outbreaks? Narratives of Smallholder farmers in two provinces of South Africa

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Background

Globally, livestock production is recognized to alleviate poverty, secure livelihoods, and improve food security in rural communities. This paper presents findings from 149 male and 84 female smallholder farmers (SHF) from North West and Eastern Cape provinces of South Africa.

Objectives

The purpose was to determine SHF application of biosecurity measures and prioritization of resources on primary animal health care (PAHC) towards disease control and outbreaks.

Methods and Analysis

Thirteen focus group discussions (FGDs) were conducted. Farmers were organized into five female and eight male groups. Collected quality data was analyzed thematically.

Results

FGDs revealed that except for the state controlled animal diseases, SHF buy vaccines, drugs and medicines from the cooperatives and pharmaceutical companies. However, SHF lamented about the high cost of vaccines and other related animal health supplies. Discussions from women groups revealed that female headed households spend more on animal health as they also pay for livestock herders. According to these women, a herder is not just about taking livestock for grazing but also observes the animals which they believe forms part of animal health. While male SHF reported that they spend more than women, because they pride in good quality animals. SHF were asked about the handling of abortions and dead animals. Women reported that they wear plastics to hold the foetus and dig a hole to bury it while male SHF reported that they hold it by hand, throw it away or cook it for dogs. In handling of dead animals, female SHF reported that men slaughter the animal and advise them on whether to cook the carcass for human consumption. Male SHF indicated that if not injected, its grave is a human stomach.

Discussion and Recommendations

The study revealed a knowledge gap in terms of animal production and animal health related matters between male and female SHF. Interventions to improve PAHC should be gender sensitive to facilitate better inclusion of female SHF in livestock development programmes for improved productivity, sustainable development and economic growth.

Designing a minimum- intervention strategy for the control of Neurocysticercosis in the Eastern Cape province of South Africa

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Background

Neurocysticercosis (NCC) is a human neurological disease caused by the tapeworm, Taenia solium. The natural life cycle of Taenia solium includes humans as final hosts (known as taeniasis) and pigs as intermediate hosts (cysticercosis). The transmission from pig to human is through the ingestion of encysted larvae in undercooked pig meat; however, NCC develops when humans become accidental intermediate hosts through the ingestion of eggs via a faecal-oral route or from a contaminated environment, allowing the larval stage to develop and migrate to the nervous system. This is a disease of resource-poor, rural communities and the Eastern Cape Province of South Africa has a high number of clinical cases presenting as epilepsy in children and adults. (1)

Objectives

Afrivet, a South African animal health company, initiated and funded a pilot intervention project to tackle cysticercosis and NCC in an Eastern Cape village, with the objective that the region’s state veterinary services continue with the protocol in the long term.

Methods and Analysis

A population of free-ranging pigs was identified in the Upper Gxulu community in the Keiskammahoek region of the Eastern Cape Province of South Africa. A number of community-engagement meetings were held to educate the pig owners and obtain their consent for the proposed intervention project (2), and to provide feedback and recommendations afterwards. A team, which included Afrivet representatives, the state veterinarian and animal health technicians from the local state vet office as well as members of the Upper Gxulu village, embarked on an NCC- intervention program in June of 2021. 105 pigs that met the criteria for eligibility for vaccinations (2) were given a 1ml of Cysvax via deep intra-muscular injection and subjected to lingual palpation to inspect for the presence of T. solium cysts. 5 weeks later, in August 2021, the team returned to the village to administer a second dose of Cysvax to the pigs, as well as a single dose of Paranthic, which is an oxfendazole product effective against the encysted larvae of T. solium, at an oral dose of 30mg/kg. (3) The pigs were marked with an ear tag at each treatment so that fully vaccinated pigs were easily identifiable. A further 76 pigs had reached the age of eligibility for the first vaccination while the team was in the community in August 2021, so this was administered and the state veterinarian committed to return to the village to follow up with the second dose of vaccine and the dewormer. In June 2021, before the program commenced, ten pigs were selected at random from willing sellers and purchased by Afrivet for slaughter at the East London abattoir. The carcases were inspected on the slaughter line using routine meat inspection protocols. This was repeated in February 2022 with 9 pigs that were marked with 2 ear tags each- indicating that they had received both doses of vaccine plus the deworming dose. It should be noted that the gold standard for diagnosing cysticercosis in pigs is necropsy, with multiple incisions throughout the musculature of the carcass. (4) Logistics prevented the use of this technique at the time of the project.

Results

During lingual inspection of the 181 pigs that received the first vaccination, 7 of the pigs each had a single, viable cysticercus on the tongue. 1 carcass from the unvaccinated group that was slaughtered at East London abattoir before the commencement of the program in June 2021, was condemned with focal cysticerci in the tongue and triceps muscles. Incidentally, all but 1 of these unvaccinated pigs had multiple hydatid cysts in the livers and lungs from Echinococcus granulosus and Taenia hydatigena infections. In February 2022, 9 treated pigs were purchased for slaughter and meat inspection. There were no T solium cysts noted in the vaccinated pig carcasses inspected, and only a small number of non-viable hydatid cysts in the livers and lungs of 5 of the pigs.

Discussion and Recommendations

Between 4% and 10% of the pig population that was subjected to lingual or meat inspection was positive for cysticercosis.. It can be concluded that Taenia solium is a problem in the pigs in this community. It has been proposed that an animal health strategy aimed at treating only cysticercosis in the pig population- if carried out responsibly and consistently- can effectively eliminate the associated human NCC disease in a community in 3 years. (5) The apparent reduction in viable cysts in pigs treated with the vaccine and oxfendazole product confirm the efficacy of the proposed protocol, and, if the Eastern Cape veterinary services are able to incorporate this protocol into a primary animal health care program, a positive impact on human health can be expected in the near future.

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Characterization of Brucella species and biovars in South Africa between 2008 and 2018 using laboratory diagnostic data

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Background

Brucellosis is an infectious zoonotic bacterial disease of humans and other animals. In the Republic of South Africa (RSA), animal brucellosis is widespread and the current available data on the prevalence of this disease rely solely on serological testing. The primary limitation of brucellosis serology is the lack of discriminatory powers to differentiate between Brucella species and biovars as well as the cross-reactivity observed with other Gram-negative bacteria.

Objectives

The aim of this study was to conduct a retrospective laboratory-based survey on Brucella species and biovars isolated from various animal species in SA between 2008 and 2018.

Methods and Analysis

The isolation of Brucella species and biovar typing was performed using conventional microbiological techniques

Results

A total of 963 strains of Brucella species were included in this study with a frequency of detection for B. abortus (n = 883; 91.6%) followed by B. melitensis (n = 42; 4.4%), B. ovis (n = 29; 3.0%) and B. canis (n = 9; 0.9%). Of the 883 strains of B. abortus, 90.1% were typed as B. abortus biovar-1 while 5.7% as B. abortus biovar-2, and 3.3% and 0.5% were B. abortus S19 and B. abortus RB51 vaccine strains, respectively. Among the 42 B. melitensis strains, 71.4% were reported as B. melitensis biovar-1 and 26.2% as B. melitensis biovar-3 while 2.4% was B. melitensis biovar-2.

Discussion and Recommendations

A retrospective study, such as this one, provides useful information that can be critical in formulating policies and strategies for the control and eradication of brucellosis in animal populations in RSA.

Post-outbreak African horse sickness surveillance: a scenario tree evaluation in South Africa's controlled area

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Background

An African horse sickness (AHS) outbreak occurred in March and April 2016 in the controlled area of South Africa. This extended an existing trade suspension of live equids from South Africa to the European Union. In the post-outbreak period ongoing passive and active surveillance, the latter in the form of monthly sentinel surveillance and a stand-alone freedom from disease survey in March 2017, took place.

Objectives

We describe a stochastic scenario tree analysis of these surveillance components for 24 months, starting July 2016, in three distinct geographic areas of the controlled area.

Methods and Analysis

The stochastic scenario tree model establishes surveillance component sensitivity and the subsequent probability of freedom from disease accounting for multiple surveillance components. Sensitivity and probability of freedom outputs are reported as median probabilities with 95% probability intervals (PI) following 10000 iterations. The individual animal was considered the primary surveillance unit and the data were aggregated monthly for analysis (surveillance period).

Results

Our results show that, if AHS virus was circulating at a minimum prevalence of 1 infected animal in 1% of herds, the median probability of freedom from AHS in all three areas was between 98.3% - 99.8%. This high level of freedom probability had been attained in all three areas within the first 9 months of the two–year period. The primary driver of surveillance outcomes was the passive surveillance component. Active surveillance components contributed minimally (less than 0.2%) to the final probability of freedom. Sensitivity analysis showed that the probability of infected horses showing clinical signs was an important parameter influencing the system surveillance sensitivity. The monthly probability of disease introduction needed to be increased to 20% and greater to decrease the overall probability of freedom to below 90%.

Discussion and Recommendations

Current global standards require a two-year post-incursion period of AHS freedom before re-evaluation of free zone status. Our findings show that the length of this period could be decreased if adequately sensitive surveillance is performed. To comply with international standards, active surveillance will remain a component of AHS surveillance in South Africa. Passive surveillance, however, can provide substantial evidence supporting AHS freedom status declarations, and further investment in this surveillance activity would be beneficial.

Persistent NTM exposure results in false positive bovine tuberculosis diagnosis and reduced Interferon-ɣ production in BCG vaccinated calves

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Background

Pre-exposure to non-tuberculous mycobacteria (NTM) have been implicated in a reduced efficacy of BCG vaccination and false positive bovine tuberculosis diagnosis. This is due to anamnestic responses to shared antigens between NTM and *Mycobacterium tuberculosis* complex.

Objective(s)

To determine the effect of Original Mycobacterial Sin in the instance of experimental and natural NTM exposure on BCG vaccination in cattle model.

Method and Materials

Our model investigated Original Antigenic Sin phenomenon and the effect of “persistent” pre-exposure to two commonly isolated NTM (*M. malmesburyense* and *M. nonchromogenicum*) in two age groups of cattle i.e. less than 6 months and greater than 6 months. Interferon-γ responses [invitro (bovigam) and invivo (skin test)] to 5 NTM derived purified protein derivatives as well as humoral immune responses to PPD-A, PPD-B, MPB-83 and MPB70 were measured.

Results

We observed that all the treatment groups were strongly responsive to PPD-B by week 4 of the NTM exposure (despite not being responsive to PPD-B prior to the start and end of the experiment). This heightened PPD-B responsiveness in all treatment groups corresponded to approximately one week after the animals had NTM sensitization via multiple routes of exposure. Furthermore, we observed that there was a decline in IFN-γ responses post-BCG vaccination, which is suggestive of a negative impact of NTM on BCG vaccination.

Discussion and Recommendations

In conclusion, persistent NTM exposure results in false positive bTB diagnosis in animals recently exposed to NTM. Similarly, if BCG vaccination is carried out immediately after persistent NTM exposure, it may have negative effects on the efficacy of BCG vaccination in cattle.

Seroprevalence and associated risk factors of Toxoplasma gondii in commercial and communal sheep and goats in the North-West province

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Background

Toxoplasmosis is one of the most widespread parasitic zoonotic diseases arising from Toxoplasma gondii infection. Sheep and goats are susceptible to Toxoplasma gondii infections and may play a key role in the zoonotic parasite's transmission to humans.

Objectives

To determine the seroprevalence and identify risk factors associated with Toxoplasma gondii infection in the commercial and communal sheep and goats of the North West province

Methods and Analysis

Blood sera from 439 animals (164 sheep and 285 goats) were tested for Toxoplasma gondii IgG antibodies using Enzyme-Linked Immunosorbent Assay technique (ELISA). Furthermore, potential risk factors in the farms were assessed in relation to seropositivity using a questionnaire.

Results

Of the 439 sera tested, 13.9% (95% CI: 0.00-1.00%) were positive for antibodies against T. gondii. The seroprevalence in sheep and goats was determined to be 20.7% (34/164) and 9.5% (27/285) respectively. Using the Chi-Squared test or odds ratio confirmed by the Fisher's exact test, the main risk factors associated with Toxoplasma gondii infections were found to be breed, species, animal origin, history of abortion, disposal of aborted material, district, municipality, feeding system, feed storage, and presence of cats on farms.

Discussion and Recommendations

The seroprevalence found in this study suggests that Toxoplasma gondii infection poses a risk of transmission within the animal population and possibly humans. Knowledge of toxoplasmosis prevalence and risk factors in sheep and goats could aid in the adoption of strategies to lessen the disease's burden within their population.

Laboratory-based surveillance of Malignant Catarrhal Fever in Lephalale municipality in Limpopo province, South Africa

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Background

Malignant catarrhal fever (MCF) is a fatal viral disease of domestic cattle, pigs, buffaloes and many species of wild ruminants. This disease is primarily caused by alcelaphine herpesvirus 1 (AlHV-1) and herpesvirus 2 (OvHV-2), and has a serious economic impact for cattle farmers located close to the wildebeest game parks. However, the occurrence of MCF and its related contribution to mortalities has been poorly studied in the livestock farmers from Lephalale district municipality of Limpopo province where cattle and wildebeests cohabit.

Objectives

The aim of this study was to provide a laboratory-based surveillance data that describes the occurrence of malignant catarrhal fever in Lephalale district municipality for a period of 20 years.

Methods and Analysis

Laboratory registry data for a total of 394 samples was analysed. The data included the year of sampling, sample type, animal species, seasonal variation, location and the MCF test result (PCR and/or Histopathology) on samples collected between 2001 and 2021.

Results

Altogether, 56.4% (n = 222) of the samples were positive with a frequency of detection for 65.2% (n = 257) for sample tested using PCR and 37.8% (n = 137) for histopathology. Of the PCR positive samples, 99.0% belonged to AIHV-1 and 1.0% to OvHV-2 serotypes. Serotype AIHV-1 was recorded across various seasons throughout the two decades while OvHV-2 was only reported in summer and spring of the year 2010. Moreover, AIHV-1 was detected only in cattle with a high frequency of detection in blood (57.2%), brain (19.4%) and organ (9%) samples across different areas within the municipality. The OvHV-2 was reported in blood (0.78%) and brain (2.33%) samples from cattle and buffalo.

Discussion and Recommendations

A retrospective study, such as this one, provides useful information on the occurrence of MCF in Lephalale. Data from this study suggest that MCF particularly serotype AIHV-1 is endemic in Lephalale district municipality and affect cattle population. Therefore, there is a need to formulate policies and strategies for the control and possibly eradication of MCF in animal populations in Lephalale.

Surveillance of Avian Influenza virus in environmental faecal samples from wild birds in Gauteng Province

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Background

Various wild bird species act as reservoirs of type A avian influenza viruses (AIV), which may spill over to infect domestic poultry. Highly pathogenic AIV (HPAI) is associated with H5 and H7 subtypes. The aim of this study was to estimate the prevalence of circulating AIVs in wild bird faecal samples in Gauteng Province.

Objectives

Extracted RNA was screened for type A AIV using VetMaX AI Gold test kit. The positive specimens were tested for H5 and H9 antigen using real-time reverse transcriptase PCR assays (rRT-PCR) with the EU-recommended primers. Full genome sequencing was performed on selected samples with low rRT-PCR cycle threshold values.

Methods and Analysis

A total of 222 pooled faecal samples were collected February-May 2022 at open water sources frequented by wild birds. Pools of five faecal swabs were placed into virus transport medium, and transported on ice to the Poultry Research Laboratory, University of Pretoria (non-SANAS accredited and non-DAH approved laboratory)

Results

The pooled samples were positive for type A AIV by PCR in 45% (99/222) of cases. Subtype H5 and H9 was detected in 3% (7/222) and 5% (11/222) of pooled samples respectively. Four samples were confirmed to contain H5N1 AIV by whole/partial genome sequencing and complete genomes for H9N2 lineage K.3 viruses were obtained from five samples.

Discussion and Recommendations

In this study, type A AIV was frequently detected in environmental faecal samples from wild birds in Gauteng Province in the late summer-autumn period. Low prevalence of H5N1 AIV and wild bird lineage H9N2 AIV were also found. H9N2 virus has not caused any illness in South African poultry. Continued surveillance for AIVs in wild birds could serve as an early warning system for poultry producers who suffered major losses during the 2017 and 2021 HPAI H5N1 outbreaks. Such findings may be useful as part of an integrated official surveillance program for informed prevention strategies.

Enterotoxigenic Escherichia coli: prevalence in South African piglets

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Background

Enterotoxigenic Escherichia coli are bacteria that inhabit the small intestine, responsible for neonatal diarrhea, postweaning diarrhea, and severe dehydration in pigs. Beyond its burden in endemic countries, ETEC is the leading cause of diarrhea in travelers from developed regions returning from vacation in low resource countries

Objectives

Characterization and screening for virulence factors in pig samples

Methods and Analysis

Microbiological culture and molecular characterization (PCR)

Results

All the samples investigated (138) under this study were ETEC positive. Each sample carried at least one of the four genes associated with the disease. Serotyping of 302 ETEC isolates shown 56 distinct serogroups with O-138 detected in 49.3% (68/138) followed by O-132 found in12.3 % (17/158) of piglets. Twenty-three of the 56 serogroups were previously associated with diarrhea and oedema disease in pigs. Toxins producing ETEC were found in different proportion as follows: stb, 92% (279/302); stap, 59.6% (180/302); ltb, 49% (148/302); stx2e, 4.3% (13/302).

Discussion and Recommendations

These findings suggest that pigs and associated products in South Africa could be an important reservoir and houses of various ETEC with significant health implication. However, additional study and characterization are needed to fully assess the risk factors associated with these ETEC isolates.

Genetic characterization, virulence and detection of antimicrobial resistance genes of campylobacter jejuni from slaughter age broiler chickens

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Background

Campylobacter is a major cause of food-borne human gastroenteritis worldwide and is designated as a high priority antimicrobial resistant pathogen by the World Health Organization (WHO).

Objectives

The aim of this study was to investigate the presence of the virulence genes profile and antimicrobial resistance genes in C. jejuni isolates.

Methods and Analysis

In this study, a total of 26 C. jejuni isolates from broiler chickens were screened for presence of virulence and antimicrobial resistance genes by PCR.

Results

As a result, the study detected 11/26 (42.3%), 9/26 (34.6%), 8/26 (30.8%), 7/26 (26.9%), 6/26 (23.1%), and 6/26 (23.1%) of cdtC, pldA, cdtB, cdtA, cadF and ciaB virulence genes respectively, with seven of the isolates carrying more than two virulence genes. Majority of the isolates n= 25 (96.1%) were resistant to nalidixic acid, followed by n = 21 (80.7%), n = 22 (84.6%) and n = 5 (19.2%) for tetracycline, erythromycin and ciprofloxacin respectively. Most isolates were habouring catI (n = 16; 84.2%), catII (n = 15; 78.9%), catIII (n = 10; 52.6 %), catIV (n = 2; 10.5%), floR (n = 10; 52.6%), ermB (n = 14; 73.7%), tetO (n = 13; 68.4%), tetA (n = 9; 47.4%), mcr-4 (n = 8; 42.1%) and ampC (n = 2; 10.5%). Class I and Class II integrons were detected in 92.3% (n = 24) and 65.4% (n = 17) isolates, respectively. About 31% (8 out of 26 isolates) isolates were carrying more than two resistance genes.

Discussion and Recommendations

. According to our knowledge, this is the first study to detect class II integrons in C. jejuni. The high prevalence of cdtA, A, cdtB, cdtC, cadF, pldA, and ciaB genes and antibiotic resistance genes in C. jejuni in this study indicates the pathogenic potential of these isolates. Majority of the isolates demonstrated resistance to nalidixic acid, tetracycline (tet), and erythromycin (ermB), which are the drugs of choice for treating Campylobacter infections.

Occurrence of Cryptosporidium spp. and Giradia spp. infections from sheep and goats in Potchefstroom, South Africa

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Background

Diarrheal diseases are the leading cause of death and illness for small animals in developing countries. Cryptosporidium spp. and Giardia spp. are pathogens that cause diarrhoeal diseases of “One Health” importance.

Objectives

The aim of the present study was to determine the occurrence of Cryptosporidium spp. and Giardia spp. infections from sheep and goats in Matlwang village of Potchefstroom using microscopic examination and molecular methods.

Methods and Analysis

A total of 48 faecal samples were collected from sheep (n=24) and goats (n=24). Oocysts were harvested using purification of the concentrated oocysts technique, followed by microscopic observation. DNA was extracted from oocysts for amplification by PCR.

Results

The overall occurrence of Cryptosporidium spp. 22/24 (91.6%) and 5/24 (20.8%) in sheep and goats and 11/24 (45.8%) and 7/24 (29.2%) for Giardia spp. in sheep and goats respectively by PCR. Three different types of occysts were identified by microscopy although they could not be identified to species level.

Discussion and Recommendations

This is the first report of Cryptosporidium spp. and Giardia spp. infections detected sheep and goats in Matlwang village of Potchefstroom, South African. These are zoonotic pathogens known to infect humans and animals and their causing diseases of "One Health" importance. This is preliminary data and further studies will characterize the detected genera to species level. Ultimately, scientific information generated in this study will aid formulation of effective control strategies for zoonotic diseases by the veterinary and human health sectors.

Distribution and genetic diversity of cystic echinococcosis in a non-endemic region: a one health approach

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Background

Cystic echinococcosis (CE), caused by Echinococcus granulosus sensu lato (s. l.) is an endemic zoonosis in pastoral communities in Kenya. However, the spread of CE to non-endemic areas is possible due to livestock trade, dogs' roaming behaviour and limited knowledge on CE transmission.

Objectives

This study determined the presence of CE in humans, the genetic variability of the parasite in livestock and the role of dogs in the establishment of lifecycle in a non-endemic region.

Methods and Analysis

Screening of human CE in Bungoma County was performed using a portable ultrasound scanner, while livestock cysts were collected during meat inspection in Busia and Bungoma slaughterhouses. Around each slaughterhouse, ten dog-keeping homesteads were selected and from each homestead a dog faecal sample was collected for microscopic examination of taeniid eggs and other helminths. Copro-ELISA was performed on the dog faecal samples for detection of E. granulosus s. l. Polymerase chain reaction-restriction fragment length polymorphism and sequencing were performed to genotype taeniid eggs, characterize CE livestock cysts and determine the genetic diversity of E. granulosus sensu stricto (s. s.).

Results

Out of 1002 people screened for CE; 67 (6.7%) participants had abnormal findings and, of these, 7 (1.1%) had simple liver cysts classified as CL by WHO. In livestock, E. granulosus s. s. was identified in 135/153 cysts. Eleven haplotypes for Nad1 and 19 for Cox1 gene were identified in E. granulosus s. s. Helminths detected in dogs included hookworms (n=92; 59.4%), ascarids (n=15; 9.7%), and taeniid (n=1; 0.6%). The sequences of nine (9) taeniid eggs recovered from the single taeniid positive sample identified as E. canadensis (1), T. multiceps (1) and T. serialis (7). Copro-ELISA was positive in 12/77 (15.6%) faecal samples.

Discussion and Recommendations

This study report for the first time E. granulosus s. s. haplotypes in livestock in east Africa and the establishment of E. granulosus s. l. and taeniids life cycle in a non-endemic region.

Isolation and antibiotic sensitivity of Campylobacter species from fecal samples of broiler chickens in North-West Province, South Africa

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Background

Infections with Campylobacter species have gained recognition as the most frequent cause of foodborne gastroenteritis globally. Their significance in South Africa is still an area of study interest. This study was, therefore, carried out to determine the occurrence of Campylobacter species in chickens from North West Province of South Africa as well as their antibiotic sensitivity status

Objectives

The Objective of the study was to determine the occurrence of Campylobacter species in chickens from North West Province of South Africa as well as their antibiotic sensitivity status.

Methods and Analysis

A total of 2400 chicken fecal samples were collected and pooled to a total of 480 samples from five registered active poultry abattoirs in the Ngaka Modiri Molema District of North West Province, South Africa. Polymerase chain reaction (PCR) was used for the detection of Campylobacter spp. targeting the 16S rRNA gene while antibiotic sensitivity was determined using disk diffusion inhibition test.

Results

After isolation, a total of 26 samples were confirmed to be harboring Campylobacter jejuni by PCR and sequencing. C. jejuni was found to be the only isolate detected in all the fecal samples tested. The study further demonstrated that C. jejuni infections were highest in the summer season (3%) followed by autumn and winter at 1%, while there were none detected in the spring. The isolated C. jejuni-positive samples on disk diffusion inhibition test displayed resistance to nalidixic acid, tetracycline, erythromycin, and ciprofloxacin at 98%, 80%, 83%, and 21%, respectively.

Discussion and Recommendations

Although C. jejuni was the only Campylobacter species found in this study, it is significant, as exposure of humans to this pathogen is well known to cause the risk of contracting campylobacteriosis, which is normally characterized by abdominal pain, fever and diarrhea. Immunosuppressed individuals, infected with C. jejuni may have additional complications such as Guillain-Barrè syndrome and Reactive Arthritis with grave consequences. This study further reports a high prevalence of the pathogen in summer compared to other seasons, which may indicate that humans are at a higher risk of exposure to the pathogen during this season. This finding has also been reported in other studies done from other countries. The isolated C. jejuni indicated a very high resistance to Nalidixic Acid, Tetracycline and Erythromycin.The resistance patterns observed are a great concern because these antibiotics are very commonly used in the treatment of this pathogen and their limited use in situations of campylobacteriosis will cause serious public health constraints. It may also indicate that there are still high levels of antibiotics used in the South African poultry industry for either feed efficiency, growth promotion or disease control. This could pose an even higher risk to humans who acquire Campylobacter infection in cases where multi-drug resistance will have occurred.

Improved safety profile of Inactivated Neethling strain of the Lumpy Skin Disease Vaccine

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The Lumpy Skin Disease Virus (LSDV) Neethling vaccine strains have been used for decades for prophylactic immunization of domestic ruminants against the disease. Commercial products against Lumpy skin disease are supplied as live attenuated vaccines and often are associated with adverse reactions warranting studies towards development of safe and efficacious vaccine alternatives. The present study was designed to investigate the ability of Montanide™ Gel 01 PR adjuvanted inactivated **Neethling** vaccine **strain of the lumpy skin disease** to induce immune response in rabbits. Complete virus inactivation was achieved following treatment of live vaccine strain with binary ethyleneimine (BEI) at 2 mM final concentration. Inactivated virus antigen, formulated with Montanide™ Gel 01 was injected at 1,00E+05 and 1,00E+06 $TCID_{50}$ per dose in rabbits. The second injection with same vaccine dosages was administered 21 days after the primary vaccination. Rabbits that received a 1,00E+05 $TCID_{50}$/dose of inactivated LSDV vaccine formulation induced maximum neutralizing antibody titres on day 13 post second vaccinations. Rabbits vaccinated and prime boosted with the 1,00E+06 $TCID_{50}$/dose of inactivated LSDV vaccine formulation, induced neutralizing antibody titres on day 14 after first vaccination. The maximum antibody titres for the 1,00E+06 $TCID_{50}$/dose of the inactivated LSDV vaccine formulation was obtained on day 35 post vaccination. The 1,00E+06 $TCID_{50}$ dose of the inactivated LSDV vaccine Montanide™ Gel-01 PR formulation induced higher neutralizing antibodies. The Montanide™ Gel-01 PR offers safer profile to oil adjuvants and can be developed further to protect target animals against LSDV in non-endemic areas.

Prevalence and characterization of Shiga toxin-producing Escherichia coli in dairy cattle in South Africa

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Background

Shiga toxin-producing Escherichia coli (STEC) is a foodborne pathogen that has been associated with human disease characterized by watery diarrhea, bloody diarrhea and complications including hemorrhagic colitis and the hemolytic uremic syndrome (HUS). STEC are defined by possession of two main Shiga toxin genes. Furthermore, some STEC strains may carry intimin and hemolysin which are responsible for attachment of STEC on the intestinal epithelium and causing bloody diarrhea

Objectives

To determine the occurrence of STEC in dairy cattle, in South Africa 2. To characterized the recovered isolates by serotype and major virulence genes

Methods and Analysis

Microbiological culture 2. Polymerase chain reaction (PCR).

Results

A total of 771 fecal samples from dairy cattle were screened for STEC using microbiological culture and polymerase chain reaction (PCR). Furthermore, 355 STEC isolates were characterized by serotype and major virulence genes (stx1, stx2, eaeA and hlyA). STEC was found in 42.2% (325/771) of dairy cattle fecal samples. The distribution of major virulence genes among the 355 STEC isolates was as follows: 14.6% (52) isolates carried stx1 only, 28.2% (100) isolates carried stx2 only while both stx1 and stx2 were found in 57.2% (203) of isolates.

Discussion and Recommendations

Top seven STEC O157, O26 and O103 STEC serogroups which are commonly associated with human disease were found in 5.4% (19), 3.4% (12) and 0.6% (2) of the isolates, respectively. The findings showed dairy cattle in South Africa are important reservoir and may be a source of virulent strains of STEC that are pathogenic to humans. These data underscore the need for further molecular investigation of STEC isolates from dairy cattle to assess their full virulence potential and capacity to cause disease in humans.

Immunological Evidence of Variation in Exposure and Immune Response to Bacillus anthracis in Herbivores of Kruger and Etosha National Parks

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Background

Exposure and immunity to generalist pathogens differ among host species and vary across spatial scales. Anthrax, caused by a multi-host bacterial pathogen, Bacillus anthracis, is enzootic in Kruger National Park (KNP), South Africa and Etosha National Park (ENP), Namibia. These parks share many of the same potential host species, yet the main anthrax host in one (greater kudu (Tragelaphus strepsiceros) in KNP and plains zebra (Equus quagga) in ENP) is only a minor host in the other.

Objectives

We investigated species and spatial patterns in anthrax mortalities, B. anthracis exposure, and the ability to neutralize the anthrax lethal toxin to determine if observed host mortality differences between locations could be attributed to population-level variation in pathogen exposure and/or immune response.

Methods and Analysis

Using serum collected from zebra and kudu in high and low incidence areas of each park (18- 20 samples/species/area), we estimated pathogen exposure from anti-protective antigen (PA) antibody response using enzyme-linked immunosorbent assay (ELISA) and lethal toxin neutralization with a toxin neutralization assay (TNA).

Results

Serological evidence of pathogen exposure followed mortality patterns within each system (kudus: 95% positive in KNP versus 40% in ENP; zebras: 83% positive in ENP versus 63% in KNP). Animals in the high-incidence area of KNP had higher anti-PA responses than those in the low-incidence area, but there were no significant differences in exposure by area within ENP. Toxin neutralizing ability was higher for host populations with lower exposure prevalence, i.e., higher in ENP kudus and KNP zebras than their conspecifics in the other park.

Discussion and Recommendations

These results indicate that host species differ in their exposure to and adaptive immunity against B. anthracis in the two parks. These patterns may be due to environmental differences such as vegetation, rainfall patterns, landscape or forage availability between these systems and their interplay with host behavior (foraging or other risky behaviors), resulting in differences in exposure frequency and dose, and hence immune response.

ILRI One Health Initiatives in Africa: Concepts and Applications

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The frequency and severity of zoonotic diseases, such as the current COVID pandemic, is increasing as humans encroach on wildlife habitats, and as food production systems intensify. The One Health approach (OH) offers the best chance for solving these challenges by overcoming institutional barriers by cross-sectoral collaboration and providing stronger evidence on effective, economical, and acceptable risk management. The International Livestock Research Institute (ILRI) has various ongoing OH initiatives in collaboration with national and international partners focusing on foodborne diseases, zoonoses, emerging infectious diseases and antimicrobial resistance. The CGIAR One Health initiative (Protecting Human Health Through a One Health Approach), aims to demonstrate how One Health principles and tools integrated into food systems can help reduce and contain zoonotic disease outbreaks, improve food, and water safety, and reduce antimicrobial resistance, benefitting human, animal, and environmental health. The One Health Research, Education and Outreach Centre in Africa (OHRECA) aims to improve the health of humans, animals, and ecosystems through capacity building, strengthening of local, regional and global networks and provision of evidence-based policy advice on One Health in sub-Saharan Africa. One of the capacity-building activities is the partnership with Lilongwe University of Agriculture and Natural Resources (LUANAR) and includes co-supervision and research funding support to final year veterinary students. The CGIAR Antimicrobial Resistance Hub uses a OH approach to support efforts in low- and middle-income countries to mitigate risks of agriculture-associated antimicrobial resistance. The Hub supports the development of cost-effective interventions that are locally relevant and applicable. The CGIAR COVID 19 Hub provides a coordinated research response to the global pandemic threatening health systems worldwide, along with posing serious risks to food security; local businesses and national economies; and hard-fought progress by stakeholders at all levels towards the Sustainable Development Goals. The BUILD Uganda project supports existing livestock health initiatives by helping to scale solutions through a collaborative effort in research, extension and partnerships in Uganda. The Capacitating One Health in Eastern and Southern Africa (COHESA) initiative was set up to Increase the relevance of One Health research and policies in eastern and southern Africa, by enhancing national and sub-regional cross-sectoral collaboration, equipping educational and research institutes to train the next generation One Health workforce, and increasing the capacity to identify and deliver One Health solutions to key problems. While ILRI OH initiatives are promising and posed for success, challenges have been observed in mainstreaming ecosystem health and operationalizing OH. These are being addressed through strengthening existing research collaborations, engaging with stakeholders in food systems at all levels, and building new partnerships with ecosystem actors such as the United Nations Environment Program.

Serotyping and resistance profiling of non-typhoidal Salmonella isolates from poultry in South Africa

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Background

Nontyphoidal Salmonella serovars account for 93.8 million cases of human gastroenteritis of which 80.3 million cases are foodborne and 155000 deaths globally. Poultry birds are considered an important source of foodborne Salmonellosis for humans.

Objectives

To characterise a total of 705 salmonella isolates collected from organs and farm environments of diseased birds on 30 poultry farms throughout South Africa for diversity and antibiotic resistance.

Methods and Analysis

In this study total of 705 salmonella isolates which were collected from organs and farm environments of diseased birds on 30 poultry farms throughout South Africa were characterised by serotype using traditional serotyping and PCR. Furthermore, 200 Salmonella isolates were tested for antimicrobial resistance against a panel 16 antimicrobials by the Kirby Bauer-disc diffusion method.

Results

Serotyping revealed that the top 5 Salmonella serotypes were S. serovar Muenchen 24.1% (170/705), S. serovar Senfenberg 19.0% (134/705), S. serovar Isangi 4.4% (31/705), S. serovar Schwarzengrund 4.1% (29/705) and S. serovar Heidelberg 2.6% (18/705). Antimicrobial resistance profiling of 200 isolates showed that 51% (102/200) of isolates were resistant to tetracycline, 13% (26/200) ampicillin,12,5% (25/200) amoxicillin, 8.5% (17/200) kanamycin, 4.5% (9/200) chloramphenicol, 2% (4/200) sulfamethazine/trimethoprim, 1.5% (3/200) gentamycin and 0.5% (1/200) nalidixic acid. All S. serovar Muenchen were resistant at least at least one antimicrobial. Multiresistance was observed in 13% (26/200) of isolates. Multiresistance was observed among serotypes Muenchen 6.5% (13/200), Heidelberg 6% (12/200), and Schwarzengrund 0.5% (1/200). Of particular interest, was one S. serovar Heidelberg strain367 which was resistant to six antimicrobials including tetracyclines, ampicillin, amoxicillin, chloramphenicol, kanamycin, and sulfamethazine.

Discussion and Recommendations

his study shows that poultry birds in South Africa carry antimicrobial resistant Salmonella serotypes that have been associated with Salmonellosis in poultry and humans, worldwide. The presence of antimicrobial resistant Salmonella serotypes in poultry is a public health concern. Further surveillance of Salmonella on poultry farms and along the food chain and detailed characterisation of Salmonella isolates for antimicrobial resistance and virulence genes will be needed to understand the epidemiology of this important zoonotic foodborne pathogen in South Africa.

Porcine mycobacteriosis in slaughter pigs from South Africa: Mycobacterial species diversity, MAH genotypes and Potential public health implications

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Background

Mycobacterium avium complex (MAC) are the most prominent etiological agents of lymphadenitis in pigs. Mycobacterium avium subspecies hominisuis (MAH) is a member of MAC and has been reported in many parts of the world to be the most prevalent non tuberculous mycobacteria (NTM) to cause mycobacteriosis in humans, mainly in children. Thus the economic and zoonotic impact of MAC species are increasingly being recognized. In South Africa, little is known about the distribution of Mycobacteria and the molecular epidemiology of Mycobacterium avium subspecies hominisuis in slaughter pigs.

Objectives

Determine Mycobacterial spp diversity, genotypes of Mycobacterium avium subsp hominisuis (MAH) in slaughter pigs of South Africa.

Methods and Analysis

In this study, lymph nodes including mandibular, mesenteric and head were collected during meat inspection of slaughter pigs (n=131) with tuberculosis like lesions, during the years 1991-2001. These pigs originated from 44 slaughter houses distributed across seven of the nine provinces of South Africa. Mycobacterial culture, PCR, and sequencing of the 577 bp 16S rRNA Mycobacterium specific gene fragment were employed for species and subspecies identification. Multi-Locus Variable number of tandem repeat Analysis (MLVA) was used to genotype MAH.

Results

The majority of the isolates; 112 (85. 4%) were identified as Mycobacterium avium subspecies hominisuis, 8 (6%) as Mycobacterium avium subsp avium/ sylvaticum, 4 (3.8%) were Mycobacterium tuberculosis, 3 (2.3%) as Mycobacterium intracellulare, and 1 (0.7%) as Mycobacterium bovis. The other isolates were identified each as Mycobacterium lentiflavum (0.7%), Mycobacterium elephantis (0.7%), and Micrococcus spp (0.7%). Coinfection with Mycobacterium bovis and MAH was observed in one sample. Using an eight marker MLVA typing tool, we deciphered at least seven MIRU VNTR INMV types of Mycobacterium avium subspecies hominisuis.

Discussion and Recommendations

Identification of zoonotic Mycobacteria including Mycobacterium avium subsp. hominisuis, Mycobacterium avium subsp. avium , Mycobacterium intracellulare, Mycobacterium bovis and Mycobacterium tuberculosis from slaughter pigs has a potential public health impact and also strengthens recognition of the potential economic impact of MAC. This study has also for the first time in South Africa, revealed M. avium subspecies hominisuis MIRU VNTR INMV genotypes which will aid in the future epidemiological investigation of MAH in South Africa.

Species richness and the encroachment of the invasive cattle tick, Rhipicephalus microplus (Acari: Ixodidae) on camps grazed by sheep in the Eastern Cape Province, South Africa

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Background

The invasive cattle tick, Rhipicephalus microplus, was introduced into South Africa towards the end of the nineteenth century

Objectives

The objective of this study was to establish the seasonal abundance of questing tick larvae on Amathole Montane Grassland camp grazed by sheep.

Methods and Analysis

Ticks questing for hosts were collected monthly for a period of 3 years by dragging flannel strips attached to a wooden spar over the vegetation. At each occasion six replicate drag-samples were made in camps grazed by sheep. Data was checked for normality using the PROC UNIVARIATE of Statistical Analysis System (SAS) 2016 version 9.4. To normalise and stabilize variances, tick count data were transformed using log10 (x + 1) before applying ANOVA. Data were analysed using the generalized linear models for repeated measures to determine the effect of questing ticks on seasonal on tick counts.

Results

Of the questing ticks (n=14,891) collected from the vegetation, the most abundant larvae were those of Rhipicephalus microplus (93.61%) followed by R. appendiculatus (4.71%), R. decoloratus (0.99%), R. evertsi evertsi (0.56%), R. simus (0.09) and Amblyomma hebraeum (0.04%). The R. microplus larvae were significantly higher ($P < 0.05$) in 2015 (2.11±0.108), 2016 (2.02±0.076) and 2017 (1.94±0.075) during spring than any season. No significant differences ($P > 0.05$) from R. appendiculatus questing ticks collected in autumn (0.27±0.007; 0.30±0.052) and spring (0.33±0.007; 0.20±0.052) for 2015 and 2016 respectively.

Discussion and Recommendations

Rhipicephalus microplus is highly adaptable species and is rapidly expanding its range in areas where it was not dominating which poses great epidemiological concerns in terms of diseases transmission in particular bovine babesios. The study showed that the cattle tick, R. microplus is adapting very well on other host species, in this case sheep and encroaching to areas that were too cold for its adaptation. Subsequently, R. microplus is displacing the native tick, R. decoloratus from the vegetation and this is the first record reported in South Africa. This will have wider implications in terms of tick control strategies where vaccination and dipping program need to be followed properly. There is a need to include Asiatic redwater and gallsickness vaccinations for control strategies in such conditions to prevent any disease outbreak.

Genomic Sequencing of Bacillus cereus Sensu Lato Strains Isolated from Meat and Poultry Products in South Africa Enables Inter- and Intranational Surveillance and Source Tracking

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Background

Bacillus cereus sensu lato (s.l.), is a complex of closely related, Gram-positive, spore-forming species that are capable of causing illnesses or death in humans and animals. Illnesses caused by this species include anthrax, anthrax-like illnesses, and foodborne emetic and diarrheal intoxications. However, food safety surveillance efforts that employ whole-genome sequencing (WGS) often neglect these potential pathogens.

Objectives

The purpose of this study was to use WGS to characterize B. cereus s.l. strains isolated during routine surveillance of animal and meat products across South Africa and (ii) compare genomes sequenced in this study (n = 45) to all publicly available, high quality B. cereus s.l. genomes (n = 2,887 total genome).

Methods and Analysis

B. cereus group genomes were characterized using (i) a standardized B. cereus group genomospecies/subspecies/biovar taxonomy ; (ii) the Genome Taxonomy Database Release taxonomy via GTDB-Tk v1.3.0; (iii) the phylogenetic marker gene-based mOTU/specI taxonomy via the mOTU taxonomy database v2.5; (iv) an eight-group panC typing framework (v) seven-gene multi-locus sequence typing (MLST) via PubMLST and BTyper3.

Results

Strains were assigned to panC Groups IV, III, II, and V (n = 28, 8, 2, and 2, respectively). All strains possessed diarrheal toxin-encoding genes, while one strain possessed cereulide synthetase-encoding genes. No strains harbored anthrax toxin- or capsuleencoding genes, including two strains assigned to the Genome Taxonomy Database's B. anthracis genomospecies. The 45 strains were partitioned into 15 lineages via in silico multi-locus sequence typing (MLST), six of which contained multiple strains sequenced in this study, which were identical or nearly identical at the whole-genome scale. Five MLST lineages contained (nearly) identical genomes collected from two or three South African provinces; one MLST lineage contained identical genomes from two countries (South Africa and the Netherlands).

Discussion and Recommendations

This study, provides strong evidence that B. cereus s.l. can be disseminated intra- and internationally via the agro-food supply chain. Our results showcase that WGS has the potential to be used for source tracking of B. cereus s.l. in animals and foods..

Preliminary validation of a single-spot solid-phase competition ELISA for the diagnosis of southern African territories 1 foot-and-mouth disease serotype exposure in goats

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Background

Foot-and-mouth disease (FMD) is a highly contagious and widely distributed disease affecting cloven-hoofed animals that is caused by infection with FMD virus (FMDV), which belongs to the Aphthovirus genus within the Picornaviridae family. Goats are susceptible to FMDV infection, but limited data are available concerning the epidemiology within this species.

Objectives

Perform a preliminary validation of a solid-phase competition ELISA (SPCE) in goats either vaccinated or infected with foot-and-mouth disease virus (FMDV) southern African territories 1 (SAT1) serotype.

Methods and Analysis

Forty goats were vaccinated with a pentavalent FMDV vaccine and subsequently challenged with a SAT1 serotype virus. Blood was collected every seven days until termination at 14 days post-challenge. Single-spot and a half-titration SAT1 serotype SPCE were performed in duplicate at two different time points. Coefficient of variation (COV) and kappa were used as estimate measures of repeatability and agreement, respectively. Accuracy of the single-spot SPCE was estimated relative to a SPCE log10 titer of 1.6 using mixed-effect logistic regression and receiver-operating characteristic curves (ROC). Additionally, sensitivity and specificity were estimated based on serological results 14-days post-challenge and at study enrolment, respectively.

Results

Three hundred and forty-two serum samples were tested in duplicate on two non-consecutive days. The median (interquartile range (IQR)) COV for the single-spot SPCE was 2.1% (0.5, 14.3%) and 2.5% (0.6, 12.8%) for the two testing days. Median (IQR) inter-assay COV was 10.6% (2.5, 42.5%). Kappa (95% CI) was 0.592 (0.516, 0.668) when evaluating agreement at the standard cutoff values. The single-spot SAT1 SPCE had an area under the ROC curve of 0.98 (0.97, 0.99) and a 70% proportion inhibition (PI) value was the optimal cutoff. Specificity and sensitivity of the single-spot SPCE at the 70% PI positive threshold were 83.4 (77.7, 87.9) and 95.8 (90.7, 98.2), respectively. Specificity was estimated as 100 (92.6, 100) and sensitivity as 97.3 (87.4, 99.9) when only considering serum tested at the beginning and end of the study, respectively.

Discussion and Recommendations

The single-spot SAT1 SPCE is accurate for determining FMDV serological status in goats but a higher serum dilution is required because the standard PI cutoff is too low

Animal welfare knowledge, attitudes and practices of stock people in Zimbabwe's large-scale dairy farms

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Stockpeople involved in day-to -day handling of animals in Zimbabwe are rarely assessed for their animal welfare knowledge, attitudes and practices (KAP). However, given the growing demand for milk and dairy products in Zimbabwe and the increasing global demand for animal products that are produced in an animal welfare friendly environment there is potential benefit of studying the KAP of stockpeople towards the welfare of dairy animals. This cross sectional study was carried out among 75 stockpeople from 31large-scale dairy farms in Midlands Province. The KAP questionnaire developed for dairy animals by Higham et al. 2018 was modified to develop the KAP questionnaire used for this study. Consent to conduct the study was sort for first in all the studied farms. After consent to conduct the interview was given, the KAP questionnaire was administered to any three most senior stockpeople. The questionnaire contained four sections. The first section had questions on the socio-demographic characteristics of the stockpeople. The second part of the questionnaire had questions to test the general animal welfare knowledge by stockpeople from Zimbabwe large-scale dairy farms. The third section of the questionnaire had questions to do with the stockpeople's attitudes towards animal welfare while the fourth section had questions to assess the animal welfare practices by stockpeople. Collected data was entered and cleaned in excel where descriptive statistical analysis was done and then later exported to SPSS version 23 for testing associations between stockpeople's KAPs and various other parameters such as level of education.

Results of this study revealed that, animal welfare KAP among stockpeople from Zimbabwe largescale dairy farms are low. These findings were attributed to the low levels of education among stockpeople and limited training received by stockpeople on animal welfare from agriculture extension service providers in Zimbabwe. The low levels of KAP on animal welfare could be compromising productivity and welfare of dairy animals from Zimbabwe large-scale dairy farms.

Socioeconomics and traction animals in a peri-urban area of the Vaal Triangle, Gauteng

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Background

Animal traction is an affordable means of transport in low income areas such as OrangeFarm; Drieziek; Finetown and Walkerville. However, few studies have investigated the socio-economic importance of working equines in such areas.

Objectives

This study investigated the socioeconomic and animal welfare aspects of animal traction in the study area.

Methods and Analysis

Purposively selected owners of traction animals (n=20) participated in this study. Data was collected using structured interviews.

Results

All Participants were males and aged >50 years. They originated mainly from Orange Farm (n=10; 50%) and Finetown Town (n=6; 30%). Nearly half of the respondents had no formal education (n=9; 45%), while 25% could read and write (n=5). 25% (n=5) had completed primary school. One respondent (n=1; 5%) indicated that he had a tertiary education. The average number of people living with respondents was 3.4 people (SD: 1.35). Working equines were their main source of income for most respondents (n=18; 90%). Each respondent on average owned 2.85 (SD: 1.95) working equines. Only one respondent (n=1; 5%) earned >R600 per day; while the majority (n=14; 70%) earned up to R300 per day from working equines. 75% (n=15) of the respondents indicate that they used manure from working equines. The same number (75%; n=15) used bi-products such as milk, hides and meat.

Almost all respondents (n=19; 95%) did not rent out their working equines. Selling of working equines was not popular; being reported by only one respondent. Most respondents used their working equines daily (n=18;90%), mainly in winter (n=17;85%).

Discussion and Recommendations

Working equines are owned predominantly by vulnerable members of society such as people with low formal education, and the unemployed. Moreover, working equines are the main source of income for these people. In addition to acting as a source of income, working equines are a source of manure, milk, hides and meat. Given the important social economic importance of equines among vulnerable members of society, interventions to enhance their health and working life are needed.

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Identification of animal welfare hazards during and around stunning and bleeding of ostriches (Struthio camelus) at a high-throughput abattoir in South Africa: A retrospective study

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Background

Animal welfare hazards are environmental factors that have a potential to compromise the health, physiological status and/ or behaviour of an animal or a group of animals. Animals are sentient beings and it is the ethical responsibility of all human beings to ensure their well-being. A science based humane treatment of ostriches (Struthio camelus) during and around stunning and bleeding at a high-throughput abattoir is also an integral part of the ostrich production value chain and a legislative requirement to ensure meat safety and quality, and to facilitate international trade in ostritch meat and other ostrich products.

Objectives

To identify and highlight some of the major and potential animal welfare hazards during and around stunning and bleeding at a high-throughput ostrich abattoir.

Methods and Analysis

Animal welfare hazards were identified at antemortem and Postmortem inspections, and hygiene assessments undertaken by the official veterinarian and meat inspector stationed at the Cape Karoo International De Aar ostrich and game abattoir. A retrospective study of the hazards identified during and around stunning and bleeding at the CKI De Aar ostrich and game abattoir during the period from August 2021 to the end of May 2022 was undertaken.

Results

Ths slippery floors, mechanical breakdown of the stunning equipment, poor or rough pre-slaughter handling of live ostriches, poor or Inadequate restraint of live ostriches in the pre-stunning race and stunning area, pain associated with underlying injuries (wing injuries, internal organ rupture and hemorrhage, neck skin lacerations and bruises) or disease were identified as the ommon anomal welfare hazards. The absence of a dedicated offi ial veterinarian before the period of study was identifiex as hazard too.

Discussion and Recommendations

Identification of hazards and potential hazards to animal welfare is an important exercise in animal welfare programs. It requires the establishment of a functional HACCP system. Monitoring and evaluating data on animal welfare hazards is important in the review and continual improvement of animal welfare programs including the anticipated review of the Head-only dry Electrical Stunning method commonly used in high-throughput ostrich abattoirs.

POSTER PRESENTATIONS

Theme: Integrating social dynamics in disease control & outbreaks

A serological assessment of rabies-neutralising antibodies in wildlife species to facilitate international movement

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Background

Vaccination of wildlife species against rabies underpins conservation strategies for endangered species, but is also a prerequisite for the international movement of animals from rabies-endemic countries such as South Africa to rabies-free areas.

Objectives

We performed an assessment of circulating antibodies to determine the overall percentage of wildlife carnivores that responded adequately to rabies vaccination.

Methods and Analysis

Between 2017 and 2021, the ARC-OVR received 245 serum samples drawn from previously vaccinated wildlife carnivores. The sera were from jackals involved in the baited-vaccine uptake study and from carnivores destined for export. The samples were heat-inactivated at 56oC for 30 min and then subjected to the rabies-neutralisation antibody test according to the World Organisation for Animal Health. Three-fold serial dilutions of the sera were performed in parallel with an OIE serum of dog origin calibrated to 0.5 IU/ML, and thereafter mixed with a constant dose of previously titrated Challenge Virus Standard adapted to cell culture. After neutralization, baby hamster kidney cells were added to detect residual virus and end-point titres were calculated using the Spear-man Karber formula.

Results

Serum samples from carnivore species (the African wild dog, black-backed jackal, spotted hyaena, lion, African wild cat, cheetah Cape fox, bat-eared fox, meerkat, Bengal tiger, ferret, jaguar, honey badger, serval). Overall, 82.4% (n=202) of the wildlife carnivores responded adequately to vaccination (had antibody titres of ≥0.5 IU/ML), with some demonstrating very high neutralising titres ≥95.5 IU/ML). The rest (n=43; 17.6%,) had antibodies ≤ 0.5 IU/ML and included baseline sera (n=25; 10.2%) collected from jackals in a bait-uptake study.

Discussion and Recommendations

Rabies cell-culture based vaccines are efficacious and have been validated for use in domestic dogs and cats and failure rates of about 2.5% are common. A higher failure rate (3X) was observed in wildlife species. It may be advisable to vaccinate these carnivores twice prior to testing for circulating antibodies.

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

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Background
Foot-and-mouth disease (FMD) is an economically important disease of livestock and a global threat to national and international trade. Foot-and-mouth disease virus (FMDV) is a positive-sense, single-stranded and non-enveloped virus belonging to the genus Aphthovirus in the family Picornaviridae. The virus naturally infects cloven-hoofed species (domestic species and wildlife) and camelids, and causes an acute illness characterised by fever and lesions in the oral cavity, coronary band, interdigital space and teats.

Objectives
The objective of this study was to describe the trade network of livestock farmers in the FMD Protection Zone of Limpopo Province, which will be useful for the development of a strategic surveillance system within the livestock movement network.

Methods and Analysis
All 55 dip tanks within the FMD Protection Zone with vaccination of Limpopo Province were selected for study. Farmers were interviewed at dip-tanks concerning the management and movement of their livestock. The questionnaire included four sections: owner demographics, livestock marketing, enterprise economics and the impact of FMD.

Results
190 questionnaires have been administered to date, 150 males (79%) and 40 (21%) females havebeen sampled. Sixteen percent (31/190) of participants had no formal education, 38% had an education level between grade 1-7 and 45% between grade 8-12. Of those interviewed,93% (177/190) were more than 40 years of age and only 7% (13/190) less than or equal to 39 years of age.

Discussion and Recommendations
Twenty-one dip-tanks have been sampled to date with current respondents reporting that 87% of livestock movements are within the FMD Protection Zone. Most livestock movement is due to trade and funerals are playing a major role of these movements. The remaining 13% are movements outside the FMD Protection Zone mostly representing trade to obtain better pricing. Livestock movements outside of the FMD Protection Zone put the country at risk of continuing FMD outbreaks. It is therefore recommended that more marketing opportunities with better prices be created within the FMD Protection Zone in effort to limit these movements.

Investigating microbiological quality of broiler chicken carcass slaughtered informally and in registered abattoir from emerging small-scale farms in the Gauteng province, South Africa

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Background
Food-producing animals are the major source of many zoonotic foodborne pathogens such as Campylobacter species, and Listeria monocytogenes. The presence of foodborne pathogens in food poses a public health risk with serious socioeconomic implications. Poultry meat is a predominant reservoir of foodborne pathogens, which can cause illnesses and/or death in humans.

Objectives
The aim of the study was to determine the microbiological quality of raw and processed chicken polonies sourced from Gauteng smallholder broiler farmers, intended for both the formal and informal market.

Methods and Analysis
A total of 604 samples consisting of raw chickens slaughtered from registered abattoirs (n=202); slaughtered from home (n=202) and processed chicken polonies (n=200) were tested for Listeria monocytogenes and Campylobacter species using clinical microbiological techniques and molecular assays.

Results
Campylobacter species and L. monocytogenes were found ($P < 0.05$) in 68.8% (287/404) and 43.3% (175/404) of the analysed samples, respectively. Campylobacter had the majority of positive samples were isolated from Emfuleni (92.5%); West Rand

(76.2%); Ekurhuleni (68.8%); City of Johannesburg (60.0%) and City of Tshwane (46.3%), and the differences were statistically significant (P = 0.004). The sampling point with the highest L. monocytogenes occurrence were City of City of Johannesburg (50.8%) and Ekurhuleni (43.3%). Home slaughtered chicken samples yielded the highest occurrence rate of Campylobacter (74.2%) and L. monocytogenes (41.2%) compare to abattoir slaughtered (63.4% for Campylobacter; 36.0% for L. monocytogenes) chickens. All chicken polony samples were negative for targeted bacteria analysed.

Discussion and Recommendations

The results for raw chickens shows a high level of contamination, which could pose a serious food safety and health problem.

Assessment of risk factors for African swine fever in Gauteng province

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Background

African swine fever (ASF) is a highly infectious viral disease of porcine (pig) species. In sub-Saharan African countries, it is characterised as an endemic haemorrhagic fever with the ability to cause 100% mortality in infected pig. In South Africa, reports of ASF date as far back as 1926 and in 1935 the ASF control zone were defined in KwaZulu-Natal, Limpopo, North West (northern parts) and the Mpumalanga (North-eastern parts) provinces. In 2012, for the first time since 1996, an ASF outbreak was reported by the Gauteng Veterinary services outside the ASF control zone. Subsequent to this outbreak, Gauteng has continued to experience more ASF outbreaks. The 2012 and 2016-2022, African swine fever (ASF) outbreaks in Gauteng are suspected to form part of the domestic cycle, which consists of pig-to-pig transmission

Objectives

The objective of this study was to determine the potential risk of ASF spread within and to Gauteng with reference to specific areas, which are currently known to be ASF-free and areas exposed to ASF outbreaks from 2016-2022.

Methods and Analysis

In 2020 and 2021, pig farmers willing to participate in the study had been identified. Hundred and thirty-seven farmers agreed to participate in the study, which allowed the researchers to conduct telephonically interviews (due to COVID-19 epidemic) and/or face-to-face interviews. The latter were achieved by obtaining data from smallholder farmers using questionnaires, which included questions on the general characteristics of the farm and household, herd size and ownership, pig and animal health management, biosecurity measures, pig trade and movement, awareness of ASF, sanitary measures and possible virus introduction routes. Farmers were divided according to three criteria based on their past experience toward the disease and the ASF status of the area in which they were located.

Results

Data collected indicate knowledge gaps regarding ASF in general. Lack of basic biosecurity knowledge as well as application thereof such as free-roaming pigs were identified as risk factors. Results further show that there is evidence of informal movements or trade in the area.

Discussion and Recommendations

The study indicated that movement of domestic pigs or pigs' related products has the potential risk of spreading ASF to Gauteng. A census of pigs was conducted from farms included in the study in order to quantify the number of pigs farmers in the selected regions of Gauteng. However, due to COVID restrictions and voluntary participation of farmers a full census of the areas were not conducted. It is suggested that a full census should be conducted as some farmers reported recently starting piggeries. In terms of determining the risk of ASF to Gauteng, results obtained from questionnaires highlighted risk factors such as free roaming pigs, illegal movement of pigs which is a risk for current and future spread of ASF in this region, gaps in both knowledge and biosecurity.

The Livestock-foods-Humans-environment interface of *Klebsiella pneumoniae* in South Africa: a review study on virulence, resistance, and diagnosis methods for control strategies

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Background

Klebsiella pneumoniae is a Gram-negative bacterium associated with opportunistic infection in patients with a compromised immune system (Runcharoen et al., 2017). The pathogen is found in various environments, a wide range of domestic and wild mammals, and foods (Wareth and Neubauer. 2021). Klebsiella pneumoniae is a neglected pathogen in veterinary and environmental health, and the risk of human infection concerning animal contact and food consumption is hardly investigated. The pathogen has become severely resistant to most antibiotic agents in humans, placing a significant burden on healthcare systems by causing antibiotic treatment failure (Athans et al., 2019). Klebsiella pneumoniae has been reported as a major threat to public health by the World Health Organization and the US Centers for Disease Control and Prevention organizations (Kidd et al., 2017).

Objectives

This study is a systematic review and meta-analysis of K. pneumoniae infection in the past decades in South Africa, emphasizing the prevalence in animals, food, human, environment, and antibiotics resistance.

Methods and Analysis

Electronic databases such as ScienceDirect, PubMed, Google Scholar, and Scopus were used to search systematically for relevant studies published on K. pneumoniae over the past decades. Data were analyzed using comprehensive meta-analysis techniques.

Results

According to the data obtained in this review, the overall pooled prevalence estimates (PPE) of K. pneumoniae stand at 38%, and the raw milk samples were predominantly contaminated (19/51), followed by fruits (12/51), meat (11/51), and vegetables (9/51) in the study of Junaid et al., 2019. The pathogen was resistant to Aztreonam, Cefuroxime, and Cefotaxime antimicrobials. In a study by Essel et al. (2020), out of 292 positive samples collected in the neonates unit in Gauteng Hospital, Klebsiella pneumoniae comprised the largest proportion (32%; 93/292).

Discussion and Recommendations

This study highlights the current data on Klebsiella pneumoniae on animals and animal products, which might infect humans via direct contact with infected animals or by consuming infected animal products. In addition, klebsiella pneumoniae presents resistance to many drugs. Therefore, there is essential to implement a strategic approach to promoting public hygiene, animal husbandry, screening for Klebsiella pneumoniae, and monitoring drug-resistant. This pathogen in animals and food is of public health concern; therefore, more studies are required.

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Post African swine fever outbreak biosecurity investigation in North-West Province, Dr Kenneth Kaunda District in Potchefstroom

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Background

African swine fever (ASF) outbreak was declared in May 2021 around Potchefstroom area after being detected and confirmed from post mortem tissue samples. The virus spread through auction sales due to poor biosecurity protocols such as lack of movement control restrictions, lack of pre-quarantine facility, and absence of health declaration certification etc. This outbreak affected a total of 17,903 pigs, and left farmers, auction and abattoir managers devastated with economic losses estimated to R35,880,000. With the absence of proven vaccines and treatment against this virus, biosecurity is crucial and is the only effective control tool available.

Objectives

This investigation report aimed at assisting affected farmers, auction and abattoir managers with the implementation of effective biosecurity protocols. The objective of this investigation report was to identify on-farm and national biosecurity program gaps and address them.

Methods and Analysis

Data was collected through systematic literature reviews, animal disease act and animal health act reviews and assessment of national biosecurity programs. The data analysed comprised biosecurity questionnaires and farmers, abattoir and auction managers' interviews records. The results from ASF outbreak investigation were analysed to address biosecurity gaps.

Results

This report identified biosecurity knowledge gaps and conducted individual on-farm biosecurity awareness campaigns about foot baths, and disinfecting of vehicle tyres etc. Although this report assisted these affected farmers and market sales managers to implement basic and effective biosecurity protocols in their premises, government needs to enforce animal disease acts for farmers to abide by the law. The South African government should hold law breakers accountable for their acts by introducing strict monetary fines in order to promote good biosecurity practices.

Discussion and Recommendations

This report recommends new surveillance program like annual serological surveillance for African swine fever which currently does not exist. This will strengthen ASF and CSF detection capabilities and enhance outbreak preparedness. The report recommends Phd study inorder to invent technological tool to address biosecurity issues in the future.

Factors that are correlated with knowledge of African Swine Fever among emerging pig farmers in uThukela District, KwaZulu Natal Province, South Africa

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Background
Educating farmers about the risk factors of ASF is vital for preventing the spread of ASF.

Objectives
We identified factors that are correlated with a high knowledge score for ASF among emerging pig farmers in uThukela District, KwaZulu Natal Province, South Africa.

Methods and Analysis
A prospective Cross-sectional study design was adopted for this study. All emerging pig farmers in the study area were invited to participate in the study. However, only 426 farmers consented to participate. A structured questionnaire was used to collect data on the socio-demographic characteristics and knowledge about ASF (cause of ASF, means of transmission, sign of disease, species affected by ASF). The knowledge score was thereafter converted into a binary variable (<60%=0 & ≥60%=1). A binary logistic regression model was fit to the data to assess factors significantly correlated with a high knowledge score (≥60%) for ASF. Statistical significance was assessed at P<5%.

Results
The odds of obtaining a high knowledgeable score was lower among residents of Alfred Duma (Adjusted Odds Ratio (AOR) = 0.524) and Okhahlamba (AOR = 0.383) as compared to farmers from Inkosi Langalibalele. Male respondents had higher odds (AOR= 1.747) of being knowledgeable compared to their female counterparts. The odds of getting a higher knowledge score was higher among respondents aged 18-25 (AOR 1.434), 36-53 (AOR=1.386) and 54-71 (AOR= 1.797) years, as compared to older respondents ($^{>}$ 71 years). Farmers who reared pigs as a source of income and meat, had higher odds (AOR=4.061) of being more knowledgeable compared to those who reared pigs only as a source of meat for the family.

Discussion and Recommendations
In this present study although majority farmers displayed a good attitude towards ASF, majority displayed a lack of knowledge about ASF. Farmers engage in practices that are known risk factors for the spread of ASF. This information could be used to design farmers' educational programmes. Given the limited nature of this study, larger studies are needed to further investigate the knowledge of the risk factors for ASF among farmers.

Cattle management factors related to the incidences of reproductive disorders in communal farms of Mafikeng

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Background
The incidence of reproductive conditions during parturition is a complex subject influenced by factors associated with management and systemic health. Research has emphasised and produced substantial evidence on the impact of proper management in the reproduction of transitioning cows.

Objectives

This study aimed to identify the cattle production management practices that may predispose the animals to the incidences of reproductive conditions in small scale farming.

Methods and Analysis

Questionnaires were distributed to farmers who reported cow reproductive conditions at the NWU (Dale Beighle) Animal Hospital. Questionnaires were used to collect information from communal farmers about the cows with regard to reproductive conditions (i.e. downer cow syndrome, dystocia, retained placenta, vaginal prolapse and abortion) reported. The data collected also included farmer demographics. 135 questionnaires were used to collect information about farm management. Farmers were interviewed during farm visits and at community outreaches. SPSS (version 25) was used to calculate descriptive statistics.

Results

In this study, factors significantly related ($P < 0.05$) to the incidence of reproductive conditions were cows breed, parity, feeding system, whether the farmer has heard about Brucellosis or not and the frequency of getting animals checked by a veterinarian.

Discussion and Recommendations

Livestock farming in communal areas is still a male dominated agricultural sector, with most of the farmers being elderly, having low levels of education and generating less monthly income. The incidence of reproductive conditions can be influenced by the cattle of breed type used, the parity of the cow, knowledge of other diseases posing a threat to the animals, the farm feeding system and the frequency of using veterinary services on a farm. Implementation of strategies for the improvement of farming methods in communal farming is necessary to change the state of livestock agriculture and improve the economic status of communal farmers.

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The outbreak of Aflatoxicosis: Cases in Africa

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Background

Over the past few years, the have been infrequent outbreaks of Aflatoxicosis have been recorded mostly in developing countries. Aflatoxicosis is regarded as one of the serious diseases of poultry, livestock, and other animals. The cause of this disease in poultry and other food-producing animals has been attributed to the ingestion of various feeds contaminated with A. flavus. This toxigenic fungus is known to produce a group of extremely toxic metabolites, of which aflatoxin B1 (AFB1) is the most potent. Avian species especially chicks, goslings, ducklings, and turkey pouts are most susceptible to AFB1 toxicity. No level of Aflatoxin exposure is considered safe for humans and animals. The toxic effects of AFB1 are mainly localized in the liver as manifested by hepatic necrosis, bile duct proliferation, icterus, and hemorrhage. Chronic toxicity in those birds is characterized by loss of weight, a decline in feed efficiency, a drop in egg production, and increased susceptibility to infections. The incidence of hepatocellular tumors, particularly in ducklings, is considered to be one of the serious consequences of aflatoxicosis. Even though prevention and avoidance are the best way to control aflatoxicosis, natural contamination of crops with A. flavus is sometimes unavoidable. Such aflatoxin-contaminated feeds can be decontaminated using various methods which mainly focus on physical removal or chemical inactivation of the toxins in the feeds.

Objectives

- To determine the prevalence of aflatoxicosis in poultry and its effects on humans and the economy.
- To determine recent development in the strategies to prevent mycotoxins contamination, especially aflatoxins in feedstuff.

Methods and Analysis

The awareness of the prevalence of mycotoxins is to use modern techniques to analyze them, the effects of Aflatoxicosis, and the recent developments in the ways to safely eliminate the mycotoxins, especially aflatoxin from the feed fed to producing animals.

Results

Populations in Africa can be exposed to high concentrations of aflatoxin via food causing acute aflatoxicosis, even to this day (Kamala et al., 2018). Diseases in the developing world often go unreported and it is likely that this problem may even be larger than described (Strosnider et al., 2006).

Discussion and Recommendations

Based on the outcomes, it becomes apparent that aflatoxins are a complex problem, for which a general approach addressing the wide variety of aspects will be needed to prevent, mitigate, or reverse aflatoxin-related negative impacts. This review indicates that more emphasis should be put on studies on evidence-based cost-effective mitigation strategies for aflatoxins, the scale and spread of the problem, and its impacts on public health and economics for use in evidence-based policies.

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The “One Health” concept as a potential key driver of job creation in the Eastern Cape Province, South Africa

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Background

The creation of employment in South Africa is one of the government’s key goals, as outlined in the original National Planning Commission’s National Development Plan (2011) the Department of Trade and Industry’s New Growth Path (2009) the recently crafted National Development Plan 2030 as well as in the SDGs in which the country participates.

The agricultural sector in its wider sense has been known from time immemorial as a global job creator especially in the rural set ups. In South Africa, it has been touted as capable of potentially creating millions of employment opportunities through expanding irrigation schemes/systems in agriculture, bringing underutilised land in the communal areas under production, picking and supporting labour intensive agricultural sectors and regions, and supporting the creation of upstream and downstream industries.

Job creation presupposes a healthy interplay between the human and animal component operating in a conduceive ecological environment. The Eastern Cape Province boasts areas of competitive advantages as compared to other Provinces in South Africa, and these could easily become potential catalysts for job creation in the province. Among these are; having the highest livestock population in the whole country, underutilised arable and grazing lands, a healthy proportion of forests and untapped water resources in certain areas.

The current challenge is the glaring and very high unemployment rate overall mainly being experienced by the youth, school leavers and women as demonstrated by the recent STATS SA 2002 report on the employment status in the country in general and in Eastern Cape in particular.

The “One Health” concept as recently redefined by the (One Health High Level Expert Panel, OHHLEP) is a comprehensive and holistic vision under the stewardship of the FAO, WHO, UNEP and OIE, originating from the animal health sector to embrace human health as well as the environment. This paper discusses “One Health” as a practical intervention which could work as a catalyst to create jobs in Eastern Cape because of its interdisciplinary and cross-sectorial nature and its potential ability to operate across the animal, human and environmental areas.

This is discussed in a wider and pragmatic manner and its possible application especially in the welfare of human beings and its contribution to sustainable development.

Theme: Adaptive Epidemiology for healthy communities

Characterisation and antimicrobial resistance profile of *Staphylococcus* spp. isolated from canine specimens submitted to a diagnostic laboratory in South Africa, 2012 - 2017

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Background

Antimicrobial resistance among Staphylococcus is increasing in both human and veterinary medicine. Moreover, healthy humans and animals are known to harbour multiple drug resistance staphylococci, including Methicillin Resistant (MR) - coagulase positive Staphylococcus (CoPS) and MR- coagulase negative Staphylococcus (CoNS).

Objectives

This study characterises the distribution and antimicrobial resistance profile of Staphylococcus species isolated from canine specimens submitted to a diagnostic laboratory in South Africa between 2012 and 2017.

Methods and Analysis

A retrospective data set of 1 627 Staphylococcus isolates from dog specimens tested at a veterinary diagnostic laboratory over the study period was used in this study. Descriptive statistics were computed and presented in terms of person, time, and space. Logistic regression models were used to investigate predictors of multidrug resistance (MDR) among Staphylococcus species.

Results

A total of 10 different Staphylococcus serotypes were recorded. Of the 1 627 isolates recorded, 91.76% (1493/1627) were CoPS, 5.78% (94/1627) were CoNS and 2.46% (40/1627) were coagulase-variable. Overall, S. pseudintermedius was the most isolated species (85.56%, 1392/1627), followed by S. aureus (5.84%; 95/1627) and S. epidermidis (5.16%; 84/1627). Overall, 9,28% (151/1627) of Staphylococcus species were reported in 2012, 24.4% (397/1627) in 2016 and 27.35% (445/1627) in 2017. The highest number of staphylococci reported were from Kwazulu-Natal (44.93%, 731/1627), followed by the Western Cape (24.95%, 406/1627). Up to 11.92% of isolates were susceptible to all the antimicrobials tested. Meanwhile, 68.8% (1038/1627) isolates were multi-drug resistant. Multi-drug resistance was highest among S. aureus species (73.7%). Multi-drug resistance was not associated with age, gender, season, species type, and clinical diagnosis. However, isolates collected between 2013 and 2017 had higher odds of exhibiting MDR as compared to isolates recorded in 2012.

Discussion and Recommendations

The high levels of AMR and MDR observed in this study are a public health concern. Therefore, continued monitoring of AMR among Staphylococcus spp. and judicious use of antimicrobials in veterinary medicine should be promoted. The increasing trend of S. pseudintermedius infections observed in this study is concerning. Future studies to identify local factors responsible for the observed geographic differences in risk of both AMR and MDR are needed.

A preliminary report: prevalence of ecto- and endo-parasites in the free-roaming pigs in peri-urban areas of Gert Sibande District Municipality of Mpumalanga province, South Africa

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In Mpumalanga province, a sizeable population of pigs roam freely, particularly around the dumping sites in peri-urban areas. However, little information is available on the management, health and performance status of these pigs. Therefore, this study aims to investigate the performance and the occurrence of ecto- and endo-parasites in free-roaming pigs in the peri-urban areas of Gert Sibande District Municipality.

The snowball method was used to identify the participants, however, stratified method was used to sample pigs (n=131) for both the internal parasitic load per gram of faeces (i.e., eggs per gram) and the prevalence worms (the number of positives samples that present with egg/oocytes divided by the total number of the sample tested) were computed. Skin scrapings were analysed qualitatively and quantitatively for lice. The associations between the parasites, age, gender and breed were analysed using Chi-square test and ANOVA. Data was analysed using the Statistical Package for Social Sciences (SPSS). Significance was accessed at P<0.05.

The most common parasites that were observed included: *Asaris suum* (55%), *Haemotopinus suis* (58.8%) and *Sarcoptes scabiei* (68.7%). The other species (i.e., *Siphonaptera, Moniezia expansa and Fasciola hepatica*) constituted only 1.5%. Pigs aged 1 to 12 months had faecal load of 2,800 – 3,100 eggs per gram (EPG) in faeces of pig while for the pigs ≥12 months, the faecal load was 2800 – 5200 EPG. About 61.8% of the pigs examined for body condition scoring (BCS) were rated relatively thin to emaciated, and all of the pigs in this category, tested positive for both ecto- and endo-parasites. With regards to weight, all the free-range pigs weighed less than the standard weight for the age category for commercial farms or smallholder intensive pig farms. Since *Ascaris suum* and *Coccidia Oocysts* can affect human and other animals, risk communication and community engagements is using appropriate and customised information, education and communication materials is recommended. Efforts should be made to ensure behavioural change through communication, not only by increasing knowledge but by focusing on factors that produce paradigm shifts in pig production and health management to reduce the risk of zoonotic infection and food associated risk of infestation for human.

Wirevax' one health approach one health approach to reduce antimicrobial resistance

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Background

Small ruminant production in South Africa and the globe is the most important commodity for food production, however these ruminants are so prone to internal parasite (Emery & Wagland 1991. Depending on the size of the worm burden, infection with this heamonchus helminth can clinically manifest as a rapidly developing anaemia with oedema, inappetence, loss of condition, bottle jaw and death. Unfortunately control still relies to a large extent on the use of anthelmintics. However, since widespread anthelmintic resistance affects almost the entire spectrum of anthelmintic groups, there is an urgent need to develop effective and practical alternative control approaches as this is a one health approach. The wirevax vaccine was the most complementary tool to use and minimise the use of anthelmintic. because the animals will have immunity against wireworm and there will be lack of chemical residue in the animal product, this vaccine boost the immune system of the small ruminant against H. contortus immunity (Knox & Smith 2001).

Objectives

Assessing the effectiveness of the use of wirevax in reducing the use of antimicrobial use in small stock.

Methods and Analysis

A total certain number of animals are selected in the group depending on how large the flock is, they are treated with the anthelmintics to lower the base line counts before the first injection is given and dung samples are taken from each animal and sent to the lab.

Results

Most of the farms that are using wirevax have less mortality compared when they did not use it. FEC of animals on the vaccine were reduced and the number of worm burden on the pastures minimized. Only animals that are anaemic were dosed according to the famacha scoring.

Discussion and Recommendations

After three vaccinations given three weeks apart depending on the region and climate sheep that are challenged immediately after the third vaccination is administered there is improvement in the average counts for the flock.

References

1. OIE Guide 2021, Responsible and prudent use of anthelmintic chemicals to help control anthelmintic resistance in grazing livestock species.
2. Emery & Wagland 1991, Knox & Smith 2001 Vaccine against gastrointestinal nematode parasite of ruminants.

Genomic Characterisation and antimicrobial resistance profiles of *Listeria monocytogenes* isolated from pig farms

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Background

Listeria monocytogenes is a zoonotic foodborne pathogen, transmissible from the natural agricultural environment to animals and humans. In recent years, the pig production industry has experienced a series of monetary losses as a result of the L. monocytogenes outbreak which threatened the economy of South Africa. This outbreak also had a detrimental effect on the health system of the country. In South Africa however, there is limited information regarding the genomic diversity of L. monocytogenes. Therefore, an overview of the genomic diversity of L. monocytogenes strains circulating at different levels of the pork production chain needs to be determined so as to be able to identify routes of contamination of the pathogen and thus improve meat safety.

Objectives

The main aim of this study was to investigate the population structure and antimicrobial resistance profiles of L. monocytogenes strains isolated from commercial pig farms in five selected provinces of South Africa using whole genome sequencing technology.

Methods and Analysis

77 isolates of L. monocytogenes were analysed using whole-genome sequencing to determine their population structure.

Results

Based on whole-genome sequence analysis, 77 isolates of L. monocytogenes were differentiated into four molecular serogroups with IIa (45.5%) being the most prevalent followed by IIc (26.0%), IVb (22.1%) and IIb (6.5%). Overall, 11 clonal complexes (CCs) were identified in this study, with the predominance being observed from; CC204 (23.4%), CC1 (19.5%) and CC2 (16.9%). Genetic elements associated with biocide, antimicrobial and heavy metal resistance were noted in 24.7 %, 48% and 11.7% of the isolates, respectively. Listeria pathogenicity island 1 and 3 that harbored clusters of virulence genes were present in 38.8% of the isolates. Five different plasmids were found in 68.9% of the isolates.

Discussion and Recommendations

This study has given baseline data on the genomic diversity of L. monocytogenes strains that are associated with biocides, heavy metal and antibiotics resistance genes. The data again demonstrated the genotypes of L. monocytogenes that are prone to contaminate the farm environment and possibly cause diseases in animals and humans.

Quantitative risk assessment of the likelihood of importing mechanically recovered poultry meat contaminated with *Salmonella* into South Africa

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Background

Salmonella has been identified as a public health concern as it has been linked with foodborne disease outbreaks globally. There is evidence that trade in animal and animal products contribute significantly to the spread of infectious diseases. Elsewhere, mechanically recovered poultry meat has been reported as a source of pathogenic organism including Salmonella species. However, there are limited published studies on the likelihood of Salmonella contamination in meat products imported into South Africa.

Objectives

This study used a quantitative risk assessment approach to investigate the likelihood of importing mechanically recovered poultry meat contaminated with Salmonella into South Africa.

Methods and Analysis

This study used secondary dataset of mechanically recovered poultry meat imported through a port of entry into South Africa. Furthermore, the study used peer-reviewed published studies from countries exporting mechanically recovered poultry meat to South Africa between 2016 and 2017. A quantitative risk assessment model for the likelihood of importing a mechanically recovered poultry meat consignment contaminated with Salmonella was constructed in Microsoft Excel (Microsoft Redmond. WA). The Monte Carlo simulation was performed using a commercial software @Risk (version 7.6, Palisade, Newfield, NY) at 10,000 iterations.

Results

The overall likelihood of importing mechanically recovered poultry meat contaminated with Salmonella into South Africa was calculated as 0.000588 (5th= 0.00005886--95th=0.00573). The prevalence of Salmonella in the exporting country (ρ=1.00), the sensitivity of the culture (ρ=0.05) and PCR (ρ=0.05) test, the within consignment likelihood (ρ=0.02), state decision (ρ=0.03) were positively correlated with the probability of importing a contaminated mechanically recovered poultry meat consignment. While the number of consignments imported into the country was negatively correlated (ρ=-0.01) with the probability of importing a contaminated consignment.

Discussion and Recommendations

Based on the quantitative risk assessment model, the likelihood of importing mechanically recovered poultry meat contaminated with Salmonella into South Africa was considered to be negligible. The prevalence of Salmonella in the exporting countries, the sensitivities of culture and PCR tests were positively correlated with the overall likelihood of importing Salmonella species contaminated consignments. Meanwhile, the within consignment likelihood and decision of the state veterinarian to release mechanically recovered poultry meat consignments as well as number of consignment imported were weakly associated. In the previous study on the prevalence of Salmonella in mechanically recovered poultry meat, Salmonella serotypes known to cause foodborne illnesses including Salmonella Heidelberg and Salmonella Schwarzengrund were reported. Therefore, consideration must be made to align the SOP with the regulations of Meat Safety Act 40 of 2000 which requires identification, prevention, elimination, or reduction of a disease to an acceptable level. In addition, arbitrary acceptable level of risk must be clearly defined to ensure consensus on the acceptable risk.

Antimicrobial Resistance of foodborne pathogens in South Africa

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Background

Foodborne pathogens are challenging subjects of food microbiology with their antibiotic resistance and their impact on public health. Preventing and controlling antibiotic resistance is a complex issue which involves many different sectors and requires a comprehensive approach to stop the spread of antimicrobial resistance

Objectives

The aim of this study was to classify and characterise foodborne pathogens and their antibiotics resistance profiles in the meat samples.

Methods and Analysis

A total of 100 samples such as chicken meat, chicken gizzard, beef intestines, beef head meat and wors were collected randomly in Johannesburg CBD. Meat samples were analysed for microbial contamination using the conventional biochemical and pathogens were confirmed based on 16S rRNA partial gene sequences (DNA extraction, PCR amplification, and sequencing).

Results

The 16S rRNA reveal the presence of Staphylococcus aureus (22.5%), Bacillus subtilis (3.5%), Bacillus cereus (25%), Bacillus spp (16%), Kurthia spp (7.5%), Enterococcus faecalis (22.5%) and Citrobacter spp (3%). The isolated bacteria were evaluated for their antibiotic resistance profiles against eight common antibiotics (Ampicillin, Tetracycline, Chloramphenicol, Erythromycin, Ciprofloxacin, Streptomycin and Sulphonamides), using the disc diffusion method as described by Kirby-Bauer. The results obtained from the three streets under the study revealed varying degree of resistance. Some isolates bacteria from this study were observed to be multidrug resistant pathogens such as, Kurthia spp was found to be resistant to (ampicillin, tetracycline, chloramphenicol, ciprofloxacin and erythromycin), Staphylococcus aureus was resistant to (ampicillin, tetracycline, sulphonamides, streptomycin, chloramphenicol and ciprofloxacin), Bacillus cereus was resistant to (ampicillin, tetracycline, chloramphenicol, ciprofloxacin and Erythromycin).

Discussion and Recommendations

Food contamination by different microorganisms may be due to the poor hygienic conditions under which street vendors manipulate and prepare meat. The bacterial isolates showed a different level of phenotypic resistance to different antibiotics tested. Most of these bacterial isolates showed resistance to more than two antibiotics tested. S. aureus showed resistance to ampicillin, tetracycline, sulphonamides, streptomycin, chloramphenicol and erythromycin. Bacillus cereus showed resistance to ampicillin, tetracycline and erythromycin.

Surveillance of West Nile Virus in horses and humans in South Africa for 2021

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Background

West Nile virus (WNV) is a mosquito-borne flavivirus that causes arboviral neurological disease. In South Africa, WNV is endemic causing disease in horses, humans, and several other species. Neurological signs in horses can be used as a signal for outbreaks of WNV, with most cases occurring in late summer and autumn. Human cases are under reported and the disease severity underestimated.

Objectives

The aim of this study was to determine the incidence of WNV in horses, as well as in humans in South Africa, using a One Health approach, for the year 2021.

Methods and Analysis

Patients presenting with acute febrile disease of unknown cause with or without neurological signs in three sentinel hospitals sites in Mpumalanga (Matikwana and Mapumaleng) and Gauteng (Kalafong hospital), were actively enrolled and specimens screened using a commercial WNV IgM ELISA kit from Euroimmun as well as a PCR-based macro-array chip that includes a WNV targets. In 2021, 120 equine samples with febrile and neurological signs were submitted through the veterinary network. Flavivirus specific real time RT-PCR was used to screen all samples, but no WNV positives obtained. This can be due to the short viraemic period of flaviviruses. A commercial equine WNV IgM ELISA kit from InBios was used to screen samples and 10 samples tested positive (8.33%).

Results

In 2021, 84 samples were tested from January to June with 13 samples testing positive using the ELISA kit (15.48%). Positive samples were subjected to serum neutralization assays, where 6 samples had WNV neutralizing antibodies (7.14%). Risk factors identified include age, where older people are more susceptible, as well as people residing in rural areas presenting with a higher risk of exposure. A commercial equine WNV IgM ELISA kit from InBios was used to screen samples and 10 samples tested positive (8.33%). Neutralization assays were performed, with 9 samples having neutralizing antibodies against WNV (7.5%). Positive cases presented with neurological symptoms and fever, but no fatalities reported. Only 10% of the horses that tested positive for WNV were vaccinated, with the majority being unvaccinated.

Discussion and Recommendations

The results suggest that WNV is prevalent in South Africa, affecting both humans and horses, but that there may be other flaviviruses circulating as well. This highlights the importance of raising awareness and increasing surveillance in all areas, as well as encourage vaccination.

Preliminary findings of a descriptive epidemiological study of food-borne diseases recorded at a hospital in O.R. Tambo District, Eastern Cape Province, South Africa

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Background

Food-borne diseases (FBDs) and the associated morbidities and mortality are serious public health concern. However, within the rural areas of South Africa there is limited understanding of the burden of FBDs (Bisholo et al., 2018)

Objectives

This study describes the distribution of FBDs reported at a hospital in rural South Africa between January 2016 to December 2020.

Methods and Analysis

Retrospective data of cases of FBDs treated at a rural hospital between 2016 and 2020 were used in this study. Data was analysed using descriptive statistics.

Results

During 2016 to 2020, the hospital recorded 419 cases of food-borne disease. Out of 419 cases, 195 (46.54%) and 224 (53,46% were females and males respectively. The median age of the patients was 18 (Range: 2-96) years. Majority of cases (n=405; 96.66%) were associated with food of animal origin, followed by 09 (2.15%) associated with foods of plant origin and 5 (1.19%) with consumption of contaminated water. 176 (42,0%) cases were associated with eating cows injected with medicine, followed by 110 (26,25%) associated with eating a dead cow, 54 (12,89%) with a cow bitten by a snake and 27(6,44%) with chicken served at school. Some cases were associated with drinking water from a river (n=5; 1,19%), sour milk (n=7; 1,67%) and unpasteurised milk (n=2; 0,477%). Some cases were associated with eating ready-to-eat food (n=5; 1,19%) and dead sheep (n=18; 4,30%). Very few cases were associated with eating wild mushrooms (n=3; 0,72%), spoiled rice (n=4;0,95%), sick chicken (n=3; 0,72%), samp and beans (n=2; 0,48%) and spoiled chicken (n=2; 0,48%).

Discussion and Recommendations

Most cases of FBDS were males, and they were mainly due to consuming food of animal origin. Among cases of FBDs associated with food of animal origin, meat from animals injected with medicine was responsible for the majority of cases. Educating communities about the dangers of consuming meat from treated and dead animals is needed. Based on the number of reported cases from males, educational programs targeting males are recommended. Health facilities need to confirm diagnosis by doing laboratory analysis and not rely only on the patients' symptoms.

Prevalence and risk factors of Coxiella burnetii infection in cattle on farms in Limpopo province, South Africa

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Background

Coxiella burnetii is a worldwide bacterial pathogen and the causative agent of Q fever. The appearance of Q fever in animals has been reported across the world but in South Africa, there are few studies on the prevalence of Q fever and associated risk factors in livestock.

Objectives

A cross-sectional study was conducted to determine the prevalence of C. burnetii in cattle on farms in Limpopo province, South Africa, as well as to assess the risk of transmission to humans and animals.

Methods and Analysis

Data from ELISA and PCR were analysed using both univariate and multivariate logistic regression.

Results

Out of 383 cattle tested for antibodies against C. burnetii, the overall seroprevalence was 24.28%. Molecular detection of C. burnetii in sheath scrapings and vaginal swabs by PCR targeting the IS1111 gene revealed that 15.67% were positive.

Discussion and Recommendations

Multivariable logistic regression revealed local municipality (OR 1.09; 95%CI 1.00 - 1.20; P≤0.043) and herd size (OR 2.24; 95%CI 1.21 -4.15; P≤0.010) as being associated with C. burnetii seropositivity in cattle. Only abortion history (OR 0.31; 95%CI 0.11 – 0.89; P≤0.030) was associated with C. burnetii positivity by PCR. Sequences analysed on NCBI BLAST for sequence identity showed that all had similarities to C. burnetii transposase gene fragment, confirming molecular detection. This study demonstrated that C. burnetii is widespread in the study areas and should be considered a possible source of human Q fever in the province.

Q fever: Seroprevalence, Risk Factors in Slaughter Livestock and Genotypes of *Coxiella burnetii* in South Africa

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Background
Q fever is a neglected zoonosis in South Africa, causing significant losses in livestock Trough reproductive disorders. However, there are limited studies on the extent of Coxiella burnetii infections in livestock in South Africa, and a lack of knowledge about the types of C. burnetii strains that are currently circulating in the country.

Objectives
Therefore, a cross-sectional, abattoir-based study was conducted to determine the seroprevalence of C. burnetii, associated risk factors and to characterize C. burnetii strains from slaughter livestock at red meat abattoirs in Gauteng, South Africa

Methods and Analysis
For detection of IgG antibodies against C. burnetii, the IDEXX Q fever 2/strip antibody test kit was used according to manufacturer's instructions (IDDEX Laboratories, Liebel-fld-Bern, Switzerland).PCR for detection of C. burnetti in tissues of the seropositive animals.Eight PCR positive DNA samples from eight animals were genotyped using the Dutch six-locus MLVA panel

Results
Of the 507 animals tested, 6.9% (95%CI: 4.9–9.5%) were positive for antibodies against C. burnetii. The seroprevalence was 9.4% (31/331) in cattle, 4.3% (3/69) in sheep, and 0.9% (1/107) in pigs. Out of the 63 tissue samples from 35 seropositive animals including material from two sheep aborted foetuses from Mangaung district (Free State province), 12.7% (8/63) tested positive by IS1111 PCR. Genotyping of the eight PCR-positive tissues from eight animals by MLVA revealed two novel genotypes, not available in Coxiella MLVA databases

Discussion and Recommendations
It is concluded that slaughter animals pose a risk of exposing abattoir and farm workers to C. burnetii in South Africa.

Efficacy of plant species from the Celastraceae family on multidrug-resistant *Staphylococcus aureus* isolated from subclinical bovine mastitis cases

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Background
Bovine mastitis is a common infection in dairy herds with considerable economic implications for farmers. Staphylococcus aureus is the predominant organism associated with chronic mastitis and resistant strains are unresponsive to commonly used antimicrobials. However, the role of plants as an alternative or complementary treatment for resistant S. aureus has not been fully investigated.

Objectives

The study aims to determine the antibacterial activity and cytotoxicity of the selected plants extracts from the Celastraceae family against S. aureus.

Methods and Analysis

Six confirmed multidrug-resistant (MDR) S. aureus cultures isolated from subclinical mastitis cases were used. Acetone and ethanol leaf extracts of Elaeodendron croceum, Elaeodendron transvaalense, Maurocenia frangula, Pleurostylia capensis, and Putterlickia pyracantha leaves were tested for antibacterial activities against the S. aureus isolates using a serial microdilution assay. Cytotoxicity of the plant extracts was evaluated using Vero monkey kidney (Vero) and bovine dermis cells using an MTT assay.

Results

Only the acetone extracts of E. croceum, E. transvaalense, M. frangula and P. capensis had good activity against all tested isolates, with minimum inhibitory concentration (MIC) values ranging from 0.05-0.94 mg/ml. Almost all the leaf extracts tested were non-cytotoxic against both the bovine dermis and Vero cells at the highest concentration tested with the exception of the acetone extract of E. croceum that was toxic to both the Vero cells (0.0035±0.0033) and bovine dermis (BD) cells (0.0079±0.0008). All plants extract had a selective index (SI) value below one except for P. capensis and M. frangula against isolate 42.

Discussion and Recommendations

The acetone leaf extracts of the selected plants could be considered for further investigation because of their good antibacterial activity. Although, the crude extracts had low SI values, they should not be discarded in the initial stage. Therefore, further studies are needed to isolate bioactive and safe compounds from the acetone leaf extracts of E. croceum, E. transvaalense, M. frangula, P. capensis and P. pyracantha.

Efficacy of deltamethrin against ticks on goats at Makhuduthamaga rural areas and detection of *Ehrlichia ruminantium* in *Amblyomma hebraeum*

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Background

The aim of this study was to develop an improved strategy for the control of tick infestation on indigenous goats owned by emerging farmers in Limpopo Province. The acaricidal efficacy was determined using a pour-on deltamethrin treatment on goats infested by ticks in Makhuduthamaga rural areas. The study also contributed to the process of isolating current strains of heartwater to further our understanding of disease dynamics and pathogenicity for small ruminants.

Objectives

To determine acaricidal efficacy of deltamethrin (Clout®) on indigenous goats against ticks with particular reference to A. hebraeum and the detection of E. ruminantium.

Methods and Analysis

The study was conducted between February and July 2018. In total, five livestock owners in three villages were involved in the study. Goats were divided into two groups: treated and untreated control groups, each consisting of five goats. Goats in the treatment group were treated with the pour-on acaricide deltamethrin Clout®, whereas the untreated goats from within the same household served as controls. Approximately 50 A. hebraeum ticks were collected from untreated goats not enrolled in the study for detection of Ehrlichia ruminantium and cryopreservation as ground-up-tick-supernatants.

Results

Topical treatment with pour-on deltamethrin (Clout®) reduced tick numbers by 94.5% on indigenous goats in the treatment group compared to the control group. In total, 5,671 ticks were collected from the control group, with average of 9.44 ticks per goat, whereas a total of 296 ticks were collected from the treated group, with an average of 0.52 ticks per goat. Furthermore, it was observed that the number of ticks counted on the control goats slowly declined during the trial, which coincided with the approach of seasonal conditions that are less favourable for ticks. Ehrlichia ruminantium was detected in field collected Amblyomma hebraeum ticks: one of the eight ground-up-tick-supernatants was found to be positive by pCS20 PCR.

Discussion and Recommendations

Reducing the acaricidal application interval to two weeks was recommended, since ticks were already re-infesting the goats toward the end of the application interval of three weeks. Including goats in strategic tick control programmes is recommended in order to reduce lameness due to A. hebraeum infestation and the risk of contracting heartwater disease.

Investigation of orthobunyaviruses in animals with unsolved febrile and neurological disease in South Africa

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Background

Orthobunyaviruses represent a genus of arboviruses transmitted by mosquitoes and Culicoides midges. Schmallenberg and Shuni virus (SHUV) are emerging orthobunyaviruses in the Simbu serogroup in Africa, the Middle East and Europe. Information on the distribution of orthobunyaviruses in South Africa is limited and thus the contribution of this family to disease is unknown.

Objectives

1. To investigate the prevalence of orthobunyaviruses in animals through PCR screening.
2. To conduct a phylogenetic analysis by obtaining the full genome of orthobunyavirus strains other than Shuni virus from positive animal cases through next-generation sequencing in order to determine the molecular epidemiology of orthobunyaviruses.
3. To make use of neutralisation assays to identify seropositive serum in order to establish the seroprevalence of infection in animals.

Methods and Analysis

Specimens from cases of unsolved febrile and neurological disease in animals were submitted through a veterinary surveillance network for zoonotic arboviruses to the ZARV programme. Screening was carried out by real-time reverse transcription polymerase chain reaction (RT-PCR) for the Simbu serogroup as well as a pan-Orthobunyavirus PCR assay followed by DNA sequencing. Positive specimens were inoculated on tissue culture. Horse serum were screened with neutralisation assays in order to identify animals harbouring antibodies against SHUV.

Results

A total of 3/165 (1.8%) animals from 2021 were PCR-positive for the Simbu serogroup. Only 2/3 of these could be confirmed with the pan-Orthobunyavirus PCR. Phylogenetic analysis showed that a horse with neurological signs was likely infected with SHUV while the second positive specimen, an aborted caprine foetus, was infected with a virus closely related to Shamonda or Schmallenberg viruses. This might represent a new orthobunyavirus but requires confirmation. The sample that was not detected with the pan-Orthobunyavirus PCR assay was confirmed to be positive for SHUV, which was also a horse with neurological symptoms. A total of 11/109 (10%) horse samples from 2018 tested positive for SHUV neutralising antibodies. This suggests that exposure to orthobunyaviruses, like SHUV, is more common that the incidence by PCR suggests.

Discussion and Recommendations

SHUV as well as other orthobunyaviruses may be associated with neurological infections in South Africa. This study highlights the necessity for additional serological methods for identifying the incidence and prevalence of these viruses in South Africa.

Contagious Ecthyma (CE) Infection in Eastern Africa: A Constant Threat to Livestock Productivity

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Background

Parapoxviruses (PPVs) a group of distinct viruses belonging to the Parapoxvirus (PPV) genus of the Poxviridae family that are globally distributed and affect many wild and domestic ruminants in particular cattle, sheep, goats, and camels resulting in numerous contagious diseases of a nature that may challenge farming animals industry, especially the pastoralism sector in the east of Africa leading to immense economic losses.

Objectives

One of the main infections arising from many prototypes of the PPVs is Contagious ecthyma (CE), a proliferative exanthematous dermatitis disease caused by Orf virus (ORFV) in sheep and goats and by camel PPV (CPPV) or pseudocowpoxvirus (PCPV) in camels.

Methods and Analysis

This disease is characterized by pustule and scab lesions and was neglected for a while as most herders believe in its self-limitation nature; however, in recent years, its morbidity and case fatality for different outbreaks from many countries of the region reached high rates than before with frequent seasonality and estimated to be around 43 % and 6.5 % respectively.

Results

Thus, led to a devastating negative impact on the livelihoods of livestock owners in the region due to a reduction in milk and meat productivity and young animals' mortality, which may demand the implementation of more effective control measures and applying comprehensive field investigations alongside vaccination campaigns to minimize the risk of this infectious disease.

Discussion and Recommendations

We aimed by this presentation to shed some light on this disease that is considered endemic in the region by reviewing and analyzing published work related to the epidemiology, genetic diversity, phylogenetic relationship, transmission criteria, species barrier, and the zoonotic possibility of this important animal infection.

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Health screening of tilapia (*Oreochromis* species) populations held at a tropical aquarium with particular focus on two specific pathogens: *Mycobacteria* spp. and Tilapia Lake Virus

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Background

Fish mycobacteriosis is a significant cause of morbidity in finfish especially in intensive aquaculture systems though mortality can be quite low. Tilapia lake virus disease (TiLVD), also referred to as syncytial hepatitis of tilapia (SHT) is an economically important disease of tilapia.

Objectives

The study aimed to determine the presence of Mycobacterium species and tilapia lake virus (TiLV) in tilapia cohorts of a tropical aquarium at an Institute of Aquaculture.

Methods and Analysis

This was done through gross examination, histopathological analysis of Haematoxylin and Eosin (H&E) and Ziehl -Neelsen stained (ZN stain) tissue sections as well as nested polymerase chain reaction (nPCR) and sanger genetic sequencing on sump swabs and fish tissue extracted DNA for Mycobacterium spp. For TiLV, in addition to gross and histopathological examination, real time quantitative PCR (RT-qPCR) was used to detect the presence of TiLV RNA in tilapia fish tissue extracted RNA.

Results

The results indicated that Mycobacterium spp. were present in the water systems and fish in the tropical aquarium while TiLV was not detected in the tilapia fish tested.

Discussion and Recommendations

Mycobacteria species were present in the water systems of the tropical aquarium (TA) as well as in the fish species held in the TA as shown by the results of this study. It was evident that nPCR and ZN stain have limitations in the diagnosis of mycobacteria species. More robust screening techniques are needed to effectively detect mycobacteria. Detection to species level was not possible in all sequenced samples so the existence of zoonotic species could not be ruled out. Therefore, it is important for the aquarium personnel and visitors to wear appropriate protective clothing when working in the aquarium to prevent exposure to mycobacteria through water and/or infected fish. RT-qPCR did not detect TiLV in RNA extracted from tilapia fish sampled from TA and histopathological analysis did not indicated lesion typical of TiLVD on all the tilapia tissue section observed. These results show that TiLV appears to be absent in the tilapia population held at the TA. To affirm this a bigger sample size should be considered to test for TiLV in the TA. A non-lethal method which uses mucus samples from the skin of the fish can be used to test a large number of fish for TiLV by RT-qPCR and cell culture (Liamnimitr et al. 2018). This method is non-destructive and may therefore not attract substantial animal welfare and ethical review when testing a large number of fish.

Molecular and serological investigation of Shuni virus in South Africa

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Orthobunyaviruses are a group of emerging zoonotic viruses that occur worldwide but may have more impact in Africa. There are several neglected re-emerging zoonotic Orthobunyaviruses associated in Africa such as Shuni Virus (SHUV), Ngari virus (NRIV) and Bunyamwera virus (BUNV) while Schmallenberg virus remerged in Europe but may have an African origin. SHUV belongs to the genus Orthobunyavirus within the order Bunyavirales, family Peribunyaviridae and SHUV is classified in the Simbu serogroup and it was first isolated in 1966 in Nigeria from a slaughtered cow. Over the years SHUV has also been isolated from other animals such as horses, livestock such as goats, sheep, and wildlife in Africa. The first identified case of SHUV in humans was in 1966 which was described in a febrile child during surveillance. Orthobunyaviruses are a group of emerging zoonotic viruses that occur worldwide but may have more impact in Africa. There are several neglected re-emerging zoonotic Orthobunyaviruses associated in Africa such as Shuni Virus (SHUV), Ngari virus (NRIV) and Bunyamwera virus (BUNV) while Schmallenberg virus remerged in Europe but may have an African origin. SHUV belongs to the genus Orthobunyavirus within the order Bunyavirales, family Peribunyaviridae and SHUV is classified in the Simbu serogroup and it was first isolated in 1966 in Nigeria from a slaughtered cow. Over the years SHUV has also been isolated from other animals such as horses, livestock such as goats, sheep, and wildlife in Africa. The first identified case of SHUV in humans was in 1966 which was described in a febrile child during surveillance. Shunivirus was described in horses with neurological signs in South Africa and Zimbabwe in the 1970's. A study of neurological infections in horses and other animals identified SHUV in 21/24 (87.5%) of neurological cases in horses with a fatality rate of 40%? A pilot study in humans also identified it in 5% CSF samples from patients submitted for viral diagnoses to the NHLS Virology laboratory in 2018. It was subsequently also identified in 11/221 (5%) mosquitoes and biting midges (Cullicoides) in South Africa. The goal of this study was to investigate the incidence of Shuni Virus in fevers of unknown cause with or without neurological signs in sentinel hospitals in Gauteng and Mpumalanga province (2019-2021) using active surveillance as well as animals submitted with neurological signs from across the country. Genome sequencing of any new cases as well as retrospective isolates will be used to characterize the molecular epidemiology of the virus. In addition IgM ELISA will be developed to determine if cases are being missed due to a short viremia in humans and animals.

Effects of dietary protein supplementation on body weight gain and reproduction in female boer goats

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Background

Fluctuations in quality and quantity of forage on small farms in the North West Province are major constraint for goat production. Reproductive efficiency is directly related to viability of off spring, kidding, kidding interval and length of reproductive cycle. Goat reproduction could be improved with better management practices and knowledge of normal physiology of reproduction performance of boar goats . Sheep and goats are very important species due to their biological identity such as short generation, interval, twinning, short growth periods and medium space requirements.

Methods and Analysis

The study on boer goats was approved by the Ethics Committee of the North-West University (Mafikeng Campus). Twenty-four female boar goats with similar body weight and age (3 months old and 10.56±1.28 kg body weight) were randomly allocated into three treatment groups: Treatment 1, 2 and 3 (8 goats per treatment) in a completely randomised design. The goats were supplemented with 23.51 g protein and 8.55 g energy per kg incremental. Live body weight was recorded every 14 days. All animals were dewormed with an anthelmintic drug (Prodose from Virbac) two weeks before the start of the trial. They were also vaccinated against pulpy kidney, anthrax and heart water diseases. The does were penned individually in a well-ventilated pen, supplemented with the level of crude protein 23.51 g and energy 8.55 g per kg. Goats were also fed basal diet of hay ad libitum and had free access to fresh water. Feeding allocations and refusal to eat were recorded daily for each goat. Animals were weighed monthly prior to the morning feeding. The goats were bred when they reached sexual maturity and monitored throughout the day. All animals were kept in pens throughout the study (365 days). Animals were supplemented with concentrate mixtures consisting of maize, grass and soybean meal, based on their weight and nutritional requirements as follows: Treatment 1: maintenance X 1; Treatment 2: maintenance X 2; and Treatment 3: maintenance X 3 8. The increment of supplemental diets was based on live weight gain and daily feed consumption. In addition, all animals had free access to drinking water. Blood collection was done by a qualified animal health technician through the jugular vein. About 10 ml of blood was collected immediately after restraint to minimise the effect of excitement on the mineral levels of blood, especially phosphorus. Blood was collected on the first day of the experiment and every second week post-feeding into one set of sterilised bottles, containing ethylene-diamine tetra acetic acid (EDTA) as the anti-coagulant. Blood samples were then stored for 24 hours at 4°C to allow adequate separation of the serum from the clot. Clotted blood (collected in red stoppered tubes) was centrifuged in a macro centrifuge at 10,000 rpm (revolution per minute) for ten minutes. Data were analysed using repeated measures on the procedures of SAS 21 on the General Linear Model (GLM) according to the following linear model: ij i ij $Y = \mu + D + E$, where: Yij=observation of the dependent variable ij; μ = fixed effect of population mean for the variable; Di = effect of dietary treatment (i = 4); and Eij = random error associated with observation ij, assumed to be normally and independently distributed. Statistical significance was declared at $P<0.05$.When the analysis of variance revealed the existence of significant difference among treatment means, the probability of difference (PDIFF) option in the LSMEANs statement of the GLM procedure of SAS 21 was used to separate the means. The level of significance was set at P<0.05.

Results

The results show gain of body weights with significant difference (P<0.05) between the three treatments. Treatment group 3 showed high body weight gain (9.46±0.5 kg), followed by Treatment 2 (8.36±0.6 kg) and Treatment 1 (7.79±0.5 kg), respectively. Feeding of goats with high protein treatment significantly (P<0.01) increased protein intake (3X maintenance vs 1X maintenance) compared to low protein treatment. These results indicate that, increasing levels of supplemental protein improved live weight gain and reproductive performance of female goats. Therefore, supplementation of higher level of dietary protein (11.98 MJ ME/kg dry matter) may be suggested for optimizing growth and reproductive performance of female goats under grazing conditions, good health and good reproduction.

Discussion and Recommendations

A significant difference (P<0.05) was observed between different groups of goats fed at three different levels. Treatment group 3 had higher body weight gain than Treatment group 2, while the maintenance group (Treatment 1) had the highest body weight increase impared to the experimental groups (Treatment groups 2 and 3). The results obtained in this study are in line with other studies (Madibela et al., 2002 and Sahu et al., 2013) where a correlation was found between body weight gain of goats and protein supplementation. The body weight gain observed after supplementation is also confirmed by Andesogan et al. (Sahu et al., 2013,) who found that feeds of high nutritive value promote high levels of production and that the performance of ruminants is greatly influenced by the amount of nutrients consumed. The study still needs to be extended to educate farmers that cost benefit analysis needed even where farmers have crop residues in their farms. To optimise the productive potential of Tswana goats, it is important that the reproductive management programme be implemented for the improvement of reproductive aspects of goats. It is, therefore, concluded that improved feeding with better management could ensure the improvement of reproductive performances of Tswana goats. Thus, the adoption of improved supplementary feeding practices by communal farmers could be improved by creating awareness among farmers with regard to the rearing of goats through on-farm trials and participatory approaches. Future studies on supplementation feeding by goat farmers in the study areas could be conducted to assess the effects of dietary protein supplementation on body weight gain in female boar goats.

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Epidemiology research at ILRI to support the control of zoonotic diseases

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Livestock have been called the engine of development in low- and middle-income countries (LMICs). They support the livelihoods of the poorest and offer a pathway out of poverty; livestock is a sunrise sector, rapidly growing in response to demand and hence offering an opportunity for economic growth along with nutritional improvement.

2021 saw the launch of a book on the impacts of 45 years of research conducted by the International Livestock Research Institute (ILRI) and its partners. The book represents four years of effort from more than 70 authors. Among the main findings were that the international community invested nearly US$2 billion in global livestock research from 1975 to 2018: most was financed in ILRI, most was spent in sub-Saharan Africa and most had substantial and objectively verifiable impacts.

While the research detailed in this book covers all aspects of livestock, fully 9 of the 18 chapters are relevant to One Health. Among the main findings are:

- Veterinary epidemiological and economic impact sciences increased understanding of infection dynamics and generated a wealth of methodologies and approaches that have since been applied in every corner of the world.
- One Health approaches estimated the burden and risk factors for neglected as well as emerging zoonoses, identified their drivers and developed strategies for reducing those risks.
- Field research on trypanosomiasis determined that rational use of curative and preventive trypanocidal drugs is the most sustainable and scalable control method.
- Research on food safety elevated the importance of informal markets where most of the poor buy and sell food, introduced risk assessment to low- and middle-income countries, conducted dozens of disease burden studies and developed new approaches to managing food safety in informal markets.

The book captures ILRI benefits to research, capacity development and end users. It marshals substantial evidence to show that livestock research improved food and nutrition security, prosperity, and natural resource management in lower-income countries.

Capacitating One Health in Eastern and Southern Africa (COHESA)

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The world is facing unprecedented, inter-connected threats to the health of people, animals and the environment. Threats to health security originating from animals and ecosystems can best prevented and managed by One Health (OH) which recognizes the interconnection of people, animals, plants, and their shared environment. But attaining the OH dividend requires greater operationalization of OH science and harnessing the power of youth to solve the problems of the present and future. In line with this approach, this project aims to enhance national and sub-regional cross-sectoral collaboration between government entities with OH mandates and OH stakeholders across society, to equip educational and research institutes to train the next generation One Health workforce, and to increase the capacity of government and non-governmental stakeholders to identify and deliver OH solutions to key problems. To conceptualize the above objectives, we conducted an expert integrative review to identify OH capacity potential and gaps in eastern and southern Africa, to develop a four-year, eleven-country project to translate OH science to development impact. We identified neglected zoonoses, emerging zoonoses, food safety and livestock associated antimicrobial resistance as key OH domains, with soil health subsidiary. Multi-criteria processes identified 11 priority countries (Botswana, Ethiopia, Kenya, Malawi, Mozambique, Namibia, Rwanda, Tanzania, Uganda, Zambia, and Zimbabwe, of which four are deep dive) and four support areas (observatory, platforms, future workforce and field solutions). A consortium was developed of research and research translation institutes (three Africa-based) linked to multipliers in priority countries. Future OH capacity will be enhanced through strengthening educational institutions to deliver recognised OH courses. Delivery of solutions for a specific OH issue is planned for Ethiopia, Kenya, Mozambique and Zimbabwe, with the approach then used as a model for OH delivery. This initiative will ensure government entities capacitated in the development of evidence based One Health strategies and policies, education institutes strengthened in building OH capacity of the present and future workforce, and research institutes capacitated in identification, development, adoption and delivery of One Health solutions.