

Field Epidemiology in action

August 19-23, 2019

Coastlands Hotel, Umhlanga



17[™] ANNUAL SASVEPM CONGRESS

















Abstracts

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Programme

MONDAY, 19 AUGUST 2019

Time	Title	Speaker
07h30	Registration opens - arrival coffee and tea / Industry Networking	
08h00	Welcome and Opening	Krpasha Govindasamy
08h30	Introduction and workshop logistics	Vashnee Govender
08h45	Pre-Workshop MCQ real-time	Hetani Mdose
09h00	Introduction to Surveillance	Lazarus Kuonza
10h15	Case Study, Part 1 (Question 1-5)	Group Work
11h00	Mid-morning refreshments/Posters/Industry networking	
11h30	Case Definitions and Line Listing	Khuliso Ravhuhali
12h15	Case Study, Part 1 (Question 6-10) Group Work	
12h45	Lunch	
13h30	Descriptive data analysis & Interpretation	Lazarus Kuonza
14h30	Case Study, Part 2 (Question 11-13)	Group Work
15h30	Mid-afternoon refreshments/Posters/Industry networking	
16h00	Case Study, Part 2 (Question 14-16)	Group Work
17h00	Wrap-up	Hetani Mdose
17h30	Welcome Reception	

TUESDAY, 20 AUGUST 2019

Time	Title	Speaker	
07h30	Registration opens - arrival coffee and tea / Industry Networking		
08h00	Recap of Day 1		
08h30	Introduction to Day 2 outbreak investigation	Geoff Fosgate	
08h45	Outbreak investigation Step I	Geoff Fosgate / Group work	
09h15	Outbreak investigation Step II	Geoff Fosgate / Group work	
10h00	Mid-morning refreshments/Posters/Industry networking		
10h30	Outbreak investigation Step III	Geoff Fosgate / Group work	
11h15	Outbreak investigation Step V	Geoff Fosgate / Group work	
12h10	Outbreak investigation Step VI Geoff Fosgate /Group wo		
12h45	Lunch		
13h30	Outbreak investigation Step V continued	Geoff Fosgate / Group work	
14h00	Outbreak investigation Step VI & Workshop Evaluations for Day 1 and Day 2	Geoff Fosgate / Group work	
15h00	Mid-afternoon refreshments/Posters/Industry networking		
15h30	Group presentations	Group Work	
16h30	Post-Workshop MCQ real-time	Geoff Fosgate	
17h00	Wrap-up	Vashnee Govender	

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WEDNESDAY, 21 AUGUST 2019

Opening Session Opening Session Opening Session Opening Session Opening Session Opening Session Opening KeyNOTE: Human brucellosis – a challenge for vets and meds One Health: Brucellosis One Health: Brucellosis Opening O	Time	Theme	Title	Speaker
Session KEYNOTE: Human brucellosis – a challenge for vets and meds Development and analytical validation of a genus-specific Brucellosis Development and analytical validation of a genus-specific Brucellosis Brucellosis Secoprevalence of brucellosis among abattoir workers and associated risk factors in abattoirs in Gauteng province, South Africa: A One Health Approach Discussion Time	07h30	Registration of	pens - arrival coffee and tea / Industry Networking	
Development and analytical validation of a genus-specific Prucellosis Prucellosis Prucellosis Fucellar real-time PCR assay targeting the 16S-23S rDNA internal transcribed spacer (ITS)	08h00		Welcome and Opening	Krpasha Govindasamy
One Health: Brucellosis Brucella real-time PCR assay targeting the 16S-23S rDNA Rejoice Nyarku	08h15		_	Sascha Al Dahouk
Seroprevalence of brucellosis among abattori workers and associated risk factors in abattoris in Gauteng province, South Africa: A One Health Approach	09h15		Brucella real-time PCR assay targeting the 16S-23S rDNA	Rejoice Nyarku
10h15	09h35	Bruceilosis	associated risk factors in abattoirs in Gauteng province,	Francis B. Kolo
Seroprevalence of brucellosis, knowledge, perception and health seeking behaviour of farm workers and paraveterinarians at the human-cattle farm interface, Gauteng, South Africa, 2014 - 2016	09h55		Discussion Time	
health seeking behaviour of farm workers and paraveterinarians at the human-cattle farm interface, Gauteng, South Africa, 2014 - 2016 One Health: Brucellosis	10h15	Mid-morning r	efreshments/Posters/Industry networking	
Brucellosis Gauteng Abattoirs Bovine Brucellosis Policy Review Descriptive analysis of human population at high risk of zoonotic brucellosis at the human-cattle-farm interface, Gauteng, 2016 Poster Session Lunch A case of simultaneous brucellosis and tetanus in Limpopo Province, South Africa, February 2019 Socio-economic impact of bovine brucellosis in the Mabeskraal village and surrounding communities in the Moses Kotane local municipality in the North West Province of South Africa. Human diagnostics for Brucellosis – Open Discussion with Prof. Al Dahouk SASVEPM SASVEPM SASVEPM Stakeholder Engagement Shoo Brucellosis A case of simultaneous brucellosis and tetanus in Limpopo Province, South Africa, February 2019 Socio-economic impact of bovine brucellosis in the Moses Kotane local municipality in the North West Province of South Africa. Human diagnostics for Brucellosis – Open Discussion with Prof. Al Dahouk Sascha Al Dahouk Community of practice on sanitary and phytosanitary risk assessment assessment: A step towards a national risk assessment agency? African Swine Fever National Animal Health Forum (NAHF) Discussion Time Micrane Polydorou Discussion Time	10h40		health seeking behaviour of farm workers and paraveterinarians at the human-cattle farm interface, Gauteng,	Krpasha Govindasamy
Descriptive analysis of human population at high risk of zoonotic brucellosis at the human-cattle-farm interface, Gauteng, 2016 Poster Session Lunch A case of simultaneous brucellosis and tetanus in Limpopo Province, South Africa, February 2019 Socio-economic impact of bovine brucellosis in the Mabeskraal village and surrounding communities in the Moses Kotane local municipality in the North West Province of South Africa. Human diagnostics for Brucellosis – Open Discussion with Prof. Al Dahouk SASVEPM Stakeholder Engagement Stakeholder Eng	11h00			Cheryl McCrindle
12h00 Poster Session 12h20 Lunch 13h20 One Health: Brucellosis One Health: Brucellosis Alprovince of South Africa. 14h00 Mid-afternoon refreshments/Posters/Industry networking 15h30 SASVEPM Stakeholder Engagement 16h10 Fig. 12h20 Session 12h20 Lunch A case of simultaneous brucellosis and tetanus in Limpopo Province, South Africa, February 2019 Socio-economic impact of bovine brucellosis in the Mabeskraal village and surrounding communities in the Moses Kotane local municipality in the North West Province of South Africa. Human diagnostics for Brucellosis – Open Discussion with Prof. Al Dahouk Sascha Al Dahouk Community of practice on sanitary and phytosanitary risk assessment agency? African Swine Fever National Animal Health Forum (NAHF) Discussion Time Krpasha Govindasamy Unarine Makungo Unarine Makungo Mulunda Mwanza Mulunda Mwanza Ficic Etter Assecha Al Dahouk Sascha Al Dahouk Marzanne Polydorou Discussion Time	11h20			Alicia Cloete
12h20Lunch13h20A case of simultaneous brucellosis and tetanus in Limpopo Province, South Africa, February 2019Unarine Makungo13h40One Health: BrucellosisSocio-economic impact of bovine brucellosis in the Mabeskraal village and surrounding communities in the Moses Kotane local municipality in the North West Province of South Africa.Mulunda Mwanza14h00Human diagnostics for Brucellosis – Open Discussion with Prof. Al DahoukSascha Al Dahouk15h00Mid-afternoon refreshments/Posters/Industry networking15h30SASVEPM Stakeholder EngagementCommunity of practice on sanitary and phytosanitary risk assessment: A step towards a national risk assessment agency?Eric Etter agency?African Swine FeverMpho MajaNational Animal Health Forum (NAHF)Marzanne PolydorouDiscussion Time	11h40		zoonotic brucellosis at the human-cattle-farm interface,	Krpasha Govindasamy
13h20 13h20 One Health: Brucellosis 14h00 One Health: Brucellosis 14h00 Socio-economic impact of bovine brucellosis in the Mabeskraal village and surrounding communities in the Moses Kotane local municipality in the North West Province of South Africa. Human diagnostics for Brucellosis – Open Discussion with Prof. Al Dahouk Sascha Al Dahouk SASVEPM Stakeholder Engagement 16h10 16h30 A case of simultaneous brucellosis and tetanus in Limpopo Province Makungo Unarine Makungo Mulunda Mwanza Mulunda Mwanza Mulunda Mwanza Sascha Al Dahouk Frovince of South Africa. Community of practice on sanitary networking African Swine Fever African Swine Fever National Animal Health Forum (NAHF) Discussion Time A case of simultaneous brucellosis and tetanus in Limpopo Unarine Makungo Mulunda Mwanza Mulunda Mwanza Mulunda Mwanza Mulunda Mwanza Fric Etter Sascha Al Dahouk Sascha Al Dahouk Sascha Al Dahouk Marzanne Polydorou Discussion Time	12h00	Poster Session		
13h40 One Health: Brucellosis	12h20	Lunch		
13h40 One Health: Brucellosis	13h20			Unarine Makungo
15h00 Mid-afternoon refreshments/Posters/Industry networking 15h30 SASVEPM Stakeholder Engagement 16h10 Tengagement 16h30 Tengagement Prof. Al Dahouk Community of practice on sanitary and phytosanitary risk assessment agency? African Swine Fever National Animal Health Forum (NAHF) Discussion Time Sascha Al Dahouk Sascha Al Dahouk Sascha Al Dahouk Fric Etter Mpho Maja Marzanne Polydorou Discussion Time	13h40		Mabeskraal village and surrounding communities in the Moses Kotane local municipality in the North West	Mulunda Mwanza
15h30 SASVEPM Stakeholder Engagement 16h10 16h30 Community of practice on sanitary and phytosanitary risk assessment: A step towards a national risk assessment agency? African Swine Fever National Animal Health Forum (NAHF) Discussion Time Community of practice on sanitary and phytosanitary risk assessment agency? Mpho Maja Marzanne Polydorou Discussion Time	14h00			Sascha Al Dahouk
15h30 SASVEPM Stakeholder Engagement 16h10 16h30 End of Day 1 assessment: A step towards a national risk assessment agency?	15h00			
15h50 16h10 16h30 16h55 End of Day 1 Stakeholder Engagement African Swine Fever Mpho Maja National Animal Health Forum (NAHF) Marzanne Polydorou Discussion Time	15h30	SASVEPM	assessment: A step towards a national risk assessment	
16h10 National Animal Health Forum (NAHF) Marzanne Polydorou 16h30 Discussion Time Discussion Time	15h50			Mpho Maja
16h30 Discussion Time 16h55 End of Day 1		∟ngagement		
	16h30			
18h30 Welcome Reception	16h55	End of Day 1		
	18h30	Welcome Rece	ption	

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THURSDAY, 22 AUGUST 2019

Time	Theme	Title	Speaker
08h00		Cross species transmission of Mycobacterium bovis	Petronillah Sichewo
081100		infection at the wildlife/livestock interface in South Africa	Petronilian Sichewo
08h20		Serological prevalence of Q-fever in slaughter animals in	Maruping Mangena
001120		red meat abattoirs in Gauteng province, South Africa	ivial uping ivialigena
		Identification and characterisation of the common	
08h40		aetiologies of cattle respiratory diseases in Mahikeng local	Felicia Tshinavhe
		municipality, South Africa	
		Bioaccumulation of heavy metals, exposure assessment	
09h00		and risk characterization of common carp fish (Cyripnus	Mpho Tawana
	Postgraduate	carpio) consumers in the Hexriver catchment in	
	student	Rustenburg	
09h20	presentations	Lumbosacral Disease in Police, Military and Correctional Services Working Dogs: A descriptive review of 77 cases	Shira Amar
091120		diagnosed in the Western Cape, South Africa (2012-2016)	Silia Ailiai
		Molecular characterization of highly pathogenic avian	
09h40		influenza clade 2.3.4.4 H5N8 viruses causing outbreaks in	Belinda Peyrot
031110		terns and other coastal birds in South Africa in 2018	Jeimaa r eyroc
		Epidemiology of trichinellosis in Greater Kruger National	
10h00		Park, South Africa	Louis J. La Grange
401-20		Molecular characterisation of Lumpy skin diseases in	Datings Mark such
10h20		Mafikeng municipality	Patience Mashamba
10h40	Mid-morning r	efreshments/Posters/Industry networking	
		Establishing whether the population structure of zebra in	
11h10		the Western Cape African horse sickness control zones is	John Grewar
		competent to act as a reservoir host for AHSV	
		Cystic echinococcosis as a neglected and emerging	
11h30	Field	zoonotic threat in Africa: the Nigerian and South African	Eric Etter
	Epidemiology	picture Rehavioural charges in costs infected with feet and	
11h50	in Action	Behavioural changes in goats infected with foot-and- mouth disease virus	Tanja Wolf
		Acaricide Resistance patterns in one-host <i>Rhipicephalus</i>	
12h10		spp at rural dip tanks and commercial farms in Kwa- Zulu	Caryn Shacklock
121110		Natal	Caryin Shacklock
12h30	Voting for stud	ent presentation prize (Chaired by Dr Grietjie de Klerk)	
12h45	Lunch		
		Outbreak Investigation of Avian Influenza in a South	Kroson Diller
13h45		African Zoological Institution	Kresen Pillay
1/1505		Longitudinal sero-surveillance of foot and mouth disease	Lin-Marie de Klerk-Lorist
14h05		in an isolated buffalo herd in the Kruger National Park	LIT-Marie de Kierk-Lorist
14h25	Field	Seroconversion of livestock during an active foot-and-	Geoff Fosgate
1-11/25	epidemiology	mouth disease outbreak	Jesii i osgate
	in Action	Investigating the epidemiology of potentially zoonotic	
14h45		Hepatitis E virus in commercial pigs, Cape Town, South	Le <mark>sley van He</mark> lden
		Africa	
15h05		Limitations in control and distribution of single-host ticks	Nku <mark>luleko Nyan</mark> giwe
		(Acari: Ixodidae) in South Africa: Current Status A Preliminary Study of Bovine Genital Campylobacteriosis	
15h25	AHT	and Trichomoniasis of Cattle in Mafikeng, North West,	Odirile T.L. Ramafoko
131123	presentation	South Africa	Cullic I.L. Namaruku
15h45	Mid-afternoon	refreshments/Posters/Industry networking	
16h00	SASVEPM AGM		
17h00	Free Time		
19h00		the African Sky venue at Coastlands Umhlanga	

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FRIDAY, 23 AUGUST 2019

Time	Theme	Title	Speaker
08h00		Limitations of diagnostic tests using rabies as an example	Claude Sabeta
08h20		The use of novel single-chain antibody fragments against sat serotype foot-and-mouth disease viruses in diagnostics	Melanie Chitray
08h40		Development of rapid, multiplex xMAP® assays for the detection of haemoparasites, and causes of abortion in cattle	Melvyn Quan
09h00	Laboratory & Diagnostics	Construction of a recombinant antibody phage display library derived from the immune repertoire of FMD–SAT infected buffalo. Potential new diagnostic reagents?	Pamela Opperman
09h20		Biorisk Analysis in Veterinary Laboratories	Songelwayo Chisi
09h40		The efficacy of a plant-produced virus-like particle vaccine against H6 avian influenza in specific pathogen free chickens	Tanja Smith
10h00		Discussion Time	
10h20	Mid-morning re	freshments/Posters/Industry networking	
10h50		A chameleon called Sattoo broke the heart of Bushwillow Creek	Lin-Mari de Klerk-Lorist
11h10	Field Epidemiology in Action	AHS Control in of South Africa and the Veterinary Procedural Notice	John Grewar
11h30		One Health- Doing what we can as students	Nabeelah I. Rajah
11h50		Modelling the risk of foot-and-mouth disease virus (FMDV) outbreaks in South Africa	Mohamed M Sirdar
12h10		Close of Congress	Krpasha Govindasamy
12h30	Lunch		

SESSION CHAIRS

	Session 1 - One Health: Brucellosis	Dr Krpasha Govindasamy
Day 1	Session 2 - One Health: Brucellosis	Dr Francis B. Kolo
21 August 2019	Session 3 - One Health: Brucellosis	Dr Alicia Cloete
	Session 4 - SASVEPM Stakeholder Engagement	Dr Japh <mark>t</mark> a Mokoele
	Session 1 - Postgraduate student presentations	Dr Charles Katsande
Day 2 22 August 2019	Session 2 - Field Epidemiology in Action	Dr Wonderful Shumba
	Session 3 - Field epidemiology in Action & AHT Presentation	Dr Vashnee Govender
Day 3	Session 1 - Laboratory & Diagnostics	<mark>Dr Mohame</mark> d Sirdar
23 August 2019	Session 2 - Field Epidemiology in Action	D <mark>r Krpasha G</mark> ovindasamy

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Theme	Title	Speaker
	Prevalence of leptospirosis in donkeys and associated risk factors in South Africa	Kibambe Daddy
	Investigating Campylobacter species diversity in slaughter age broiler chickens of the Ngaka Modiri Molema district, North West South Africa	Kealeboga Mileng
Field Epidemiology in	3. Seroprevalence of Toxoplasma gondii in communal livestock at Ratlou Local Municipality in the North West Province, South Africa	Katleho Nthabiseng Mosikidi
Action	4. Identification and characterisation of viral bloody diarrhoea aetiology in puppies, presented to the Animal Health hospital, North-West University	Kayamba Ntumba
	5. Influence of human factors in the transmission of taenia solium cysticercosis in villages of Alfred Nzo and or Tambo districts of the eastern cape province, South Africa	Msawenkosi Sithole
	6. The geographical distribution of R (B) decoloratus and R (B) microplus in cattle herds in KwaZulu Natal	Selinah Maphalala
	7. Prevalence of pathogens causing subclinical mastitis and drugs resistance in small ruminants in Mafikeng	Koos Mmutle
	8. Assessment of bacteriological quality and handling of bovine raw milk collected from communal areas in Mahikeng, SA	Gaboipofe Florah Mokgaotsi
	9. Serum biochemical parameters and possible correlations between different cow reproductive conditions	Keitiretse Molefe
Laborata m. Q	10. Pre and post ovariohysterectomy study of haemopoetic cell profile of bitches presented at Dale Beighle Veterinary Hospital (NWU, Mafikeng Campus)	Lorato Portia Pule
Laboratory & Diagnostics	11. The impact of storage facilities on animal feed quality with reference to mycotoxin contamination around Ngaka Modiri Molema District, North West Province of South Africa	Galian Setsetse
	12. A case control study of risk factors for bovine brucellosis in KwaZulu-Natal, South Africa	Thami Nogwebela
	13. The use of bulk tank milk testing as an adjunct to other udder health evaluation methods	Tracy Schmidt
	14. Detection and Quantification of Antibiotic Residues in Communal Goats Milk In Mahikeng Local Municipality, South Africa	Katlego Lucricia Ndlovu
	15. Assessment of microbial quality of dried fish sold in the informal market around Johannesburg and, its public health implications in South Africa	Siphiwe Rendy Nkosi
	16. Molecular Characterization and Antibiotic Resistance of Foodborne Pathogens in Street Vended Ready -to -eat Meat in South Africa	Tshipamba Mpinda Edoaurd
One Health	17. Effect of protein supplements on reproductive performance	Mpho Sylvia Tsheole
	18. The study of poisonous plants of veterinary significance in the Rooigrond area, North West Province	Fiki <mark>le Mbali Ma</mark> seko
	19. Development of indicator cells for virus detection	Tham <mark>i Nogwebel</mark> a
	20. Food safety knowledge, perceptions and practices among students at the North-West University (Mafikeng Campus)	Lebog <mark>ang O Ramaf</mark> oko

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ORAL PRESENTATIONS

One Health: Brucellosis

Human brucellosis – a challenge for vets and meds

Speaker / Author: Al Dahouk, S.

German Federal Institute for Risk Assessment, Berlin, Germany (Sascha.Al-Dahouk@gmx.de)

Despite various surveillance and control programs in livestock around the world, brucellosis is still one of the most relevant bacterial zoonoses with about 500,000 human cases annually reported and a high number of unrecorded cases. Since human infection is directly linked to the prevalence of animal brucellosis, eradication in livestock and food hygiene control measures are indispensable to reduce the global burden of disease. In low and middle income countries, however, anticipated economic losses clearly prevent farmers from removing and culling infected animals from their herd. Traditional food consumption habits comprising unpasteurized dairy products and raw meat significantly contribute to disease transmission. In non-endemic countries, most cases are travel-associated or due to illegal import of contaminated food products of animal origin.

Acute human brucellosis is a feverish flu-like disease and hepatosplenomegaly is common. Because of unspecific signs and symptoms at the initial stage of infection, brucellosis is often misdiagnosed leading to chronic courses with protean clinical manifestations and focal complications e.g. sacroiliitis, spondylitis, endocarditis, and meningoencephalitis. Since clinical presentation of human brucellosis is variable, the presumptive diagnosis by physicians must be laboratory confirmed. Laboratory diagnosis of human brucellosis can be made by culture, serological tests, and molecular assays. A positive blood culture is a frequent incidental finding in acute brucellosis whereas blood cultures are rarely positive in chronic cases. Especially in protracted disease prolonged incubation periods up to six weeks and numerous subcultures are necessary to detect a *Brucella* infection. The identification of *Brucella* spp. using classical microbiological methods is laborious, time-consuming, and hazardous which is why polymerase chain reaction (PCR) assays, whole-genome sequencing (WGS) and mass spectrometry (MALDI-TOF MS) are more and more applied to identify members of the genus *Brucella* and to sub-differentiate its species in routine microbiology laboratories.

If clinical awareness is high, serological tests may play a decisive role in the indirect diagnosis of human brucellosis. Serological tests are mainly based on the agglutination of serum antibodies with a whole cell antigen. Anti-Brucella antibodies are directed to a smooth lipopolysaccharide (sLPS) which is very similar to surface antigens found in other gram-negative bacteria, such as Escherichia coli O:157, Francisella tularensis, Yersinia enterocolitica O:9 and various Salmonella species, leading to a lack of specificity and subsequently false-positive results. Furthermore, cut-off values are difficult to determine in endemic regions where individuals are repeatedly exposed to Brucella spp. Nevertheless, serological methods like Rose Bengal test are still widely used as a cheap option in the diagnosis of human brucellosis. Although PCR assays are known to be highly sensitive and specific and can be used for direct detection of Brucella DNA in the serum of brucellosis patients, positive test results are inconclusive and clinical interpretation is often difficult. After all, DNA detection does not prove an ongoing infection and PCR results often remain positive for years in patients who have obviously recovered after successful antibiotic therapy.

Briefly summarized, blood culture and serological methods are the gold standard in the diagnosis of human brucellosis because validated alternative methods are missing. Of course, novel diagnostics in human brucellosis should be rapid and safe but they must also provide evidence of the live agent to facilitate therapeutic decision-making.

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Development and analytical validation of a genus-specific Brucella real-time PCR assay targeting the 16S-23S rDNA internal transcribed spacer (ITS)

Speaker / Author: Nyarku, R. E¹
Co-authors: Hassim, A^{1,2} & Quan, M^{1,2}

Background

In South Africa, bovine brucellosis is considered a priority, state controlled zoonotic disease, due to the economic impact of the disease. Based on provincial crude data, a gradual increase in the occurrence of brucellosis has been observed over the years with an increasing prevalence of above 25%. Diagnostics for Brucella, which are based on bacteriology and serology are subject to many inhibiting factors and varied interpretations. Current published diagnostic assays have inconsistent results. The detection of brucella carriers in bovine mainly depends on regular detection by screening tests such as the milk ring test and Rose Bengal Plate Test (RBT), but there is a high percentage of false positive and false negative results. In addition, these diagnostics are not completely effective and only about 84%–98% of infected herds can be detected. Objectives

In this study, we developed and analytically validated a genus specific Brucella 16S-23S rDNA internal transcribed spacer region (ITS) real-time PCR assay capable of detecting any Brucella species for a high-throughput, non-invasive approach.

Method and Materials

The analytical performance of the developed assay was determined based on its sensitivity and specificity in blood and milk matrices.

The stage one validation pathway of the OIE standards on validation of diagnostic assays for infectious diseases was used for the study design. The assay was developed using Primer Express software (Thermo Fisher Scientific) and data were analysed using Microsoft Excel.

Results

The assay was specific to only brucella species. An efficiency of 99.1% and 93.6% was recorded in blood and milk respectively.

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Seroprevalence of brucellosis among abattoir workers and associated risk factors in abattoirs in Gauteng province, South Africa: a One Health Approach.

Speaker / Author: Kolo, F.B.¹

Co-author(s): Adesiyun, A², Fasina, F¹, Katsande, C.³, Dogonyaro, B¹, Harris, B⁴, Rossouw, J⁵, Geyer, H⁵, Van Heerden, H¹

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Background

Brucellosis known as undulant fever or Malta fever in humans is an infectious disease that is transmitted from infected animals to susceptible humans. Brucellosis in humans is most often an occupational disease affecting animal owners or workers, veterinarians, animal technicians and abattoir workers. In a recent study, *Brucella* species were isolated from slaughtered animals at abattoirs in Gauteng province. There are no reports or recent studies on the prevalence of brucellosis among abattoir workers in South Africa.

Objective(s)

This study determined the occurrence of brucellosis and associated risk factors among abattoir workers in Gauteng province.

Method and Materials

A total of 103 abattoir workers and managers were interviewed and tested with serological assays using the Rose Bengal test (RBT), BruceCap ELISA and IgG-ELISA from six abattoirs where brucellosis-positive slaughtered cattle and sheep were identified. A pre-tested questionnaire was administered to each of the consenting workers at the selected abattoirs to obtain demographic data and information on risk factors for brucellosis

Results

Of the 103 respondents tested, the frequency and distribution of female and male workers was 16 (15.5%, 95%CI=9.15-24.0) and 87 (84.5%, 95%CI=76.0-90.8) respectively. The distribution and seroprevalence for exposure to brucellosis was 21 (20.4%, 95%CI=13.1-29.5) using combination of either RBT, Brucecap ELISA or IgG-ELISA. From each of the tests conducted, seroprevalence using RBT, BruceCap ELISA and IgG-ELISA was 13 (12.6%, 95%CI=6.89-20.6), 9 (8.74%, 95%CI=4.07-15.9) and 18 (17.5%, 95%CI=10.7-26.2) respectively.

Discussion and Recommendations

This study determined for the first time in South Africa, the occurrence of antibodies against *Brucella* spp. among abattoir workers, which could be due to abattoir exposure or previous exposure to *Brucella*. This underscores the fact that the abattoir facilities can be used for active and passive surveillance of diseases of public health importance. The evidence-based data provided by this study will be invaluable to policy makers. We recommend implementation of brucellosis testing of current and new abattoir workers country wide to establish base-line data and this will provide appropriate preventive practices to reduce the infection rate among these high risk workers. and evaluate the magnitude of infections by *Brucella* spp. among the workers.

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Seroprevalence of brucellosis, knowledge, perception and health seeking behavior of farm workers and para-veterinarians at the human-cattle farm interface, Gauteng, South Africa, 2014 - 2016

Speaker / Author: Govindasamy, K.1

Co-authors(s): Russouw, J², Abernethy, D.A.³, Harris, B.N⁴

Objective(s)

Brucellosis is a zoonotic disease of global health importance that disproportionately affects low and middle income countries. Alleviation of the burden of brucellosis in Africa, has been considered to a route of poverty alleviation and a means of establishing food security on the continent. Despite this, it is considered a 'forgotten neglected disease' by the World Health Organization, with human cases being reported to be underdiagnosed or reported and disease in animals poorly controlled. In South Africa, bovine brucellosis is endemic and controlled by governmental Veterinary Services through quarantine, test and slaughter and vaccination since the 1970s. Despite this, there has been an increasing trend of cattle herd prevalence over the last five years but no increase of reported human cases. The objective of this study was to determine the level of exposure to brucellosis in farm workers and veterinary field officials on farms with Brucella positive cattle herds as well as assess the knowledge, perceptions and health seeking behavior of these occupational groups.

Materials and methods

A multidisciplinary field team investigated the extent and distribution ofexposure to brucellosis amongst farm workers and veterinary field officials, on cattle farms with Brucella positive cattle herds, identified through routine veterinary surveillance between 2014 and 2016. A cross sectional seroprevalence survey was conducted on all farm workers on these farms using the RBT, Elisa IgG and Brucella Capt serological tests. Structured questionnaires were used to capture human, social and herd management risk factors. A descriptive analysis was done using R.

Results

Thirty nine case farms were observed with 7 429 head of cattle altogether. A total of 203 farm personel were tested on the case farms, 9 persons were tested on a control farm. 22 paraveterinary officials (animal health technicians), were tested, 14 of which service the 39 case farms. 4 veterinarians were tested, comprised of a state vet (1/3) and 3 community service veterinarians. 208 farm workers from 41 farms were tested. 48.8% farms had at least 1 seropositive farm worker with 14.4% (n=30) of farm workers were positive to at least one test. 14.1% (28/199) of farm personnel and 73% (19/26) of veterinary officials on these case farms were seropositive for Brucella infection on the Elisa IgG test. 25% (7/28) of the farm workers and 42% (8/19) of the veterinary officials testing positive on the ElisalgG test, tested seropositive on the BrucellaCapt test (7/28). 3.5% of farm personnel on case farms tested positive on the BrucellaCapt test, ranging from titres of 1:320 to 1:640. 24% of all farm personnel tested (50/208), practised poor health seeking behaviour defined as a choice to ignore the listed symptoms of brucellosis, pray, see a pastor/traditional healer or self-medicate rather than seek out medical attention at a local clinic, general practitioner or hospital. 22% of these (11/50), were positive on the ElisalgG test, with 2 of the 11 being positive on the BrucellaCapt test as well. The health seeking behaviour amongst veterinary officials was far worse, with 77% (20/26) practising poor health seeking behaviour. 68% (13/19) of Elisa IgG seropositive veterinary officials will NOT seek out medical attention when they experience the listed symptoms and 75% (6/8) of BrucellaCapt seropositive staff will not seek out medical attention when they experience the listed symptoms

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Conclusions

The high brucellosis seroprevalence (14.4%) in farm workers and veterinary officials (73%) and poor health seeking practices of these occupationally exposed persons is a critical gap in the detection and response to brucellosis in people. We discuss the implications of this to the agricultural economy, food security in of Africa as well as the effect on global health. A transdisciplinary One Health approach to the detection and management of endemic and epidemic zoonotic diseases will be proposed as a solution to the gap identified in this study. Such an approach is in alignment with the African Union vision 2030 and the Sustainable Development Goals.

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Occupational risk of brucellosis at critical control points in Gauteng abattoirs

Speaker / Author: McCrindle, C.M.E.¹

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Background

Bovine brucellosis is an important occupational zoonosis, causing acute and chronic fever, joint pains, urogenital symptoms and disability. It is hard to control, especially in Africa; and presents challenges in regard to the occupational health of agricultural and abattoir workers [1]. Current policies in South Africa do not require that cattle are tested for brucellosis prior to slaughter.

Objective(s)

This cross-sectional study [2] investigated the occupational risk of brucellosis transmission to abattoir workers in 21 of the 22 registered beef abattoirs in Gauteng.

Method and Materials

The prevalence of bovine brucellosis in Gauteng was estimated using secondary surveillance data from 62 471 cattle. Each abattoir was visited and audited and key informants were interviewed in depth. The hazard assessment critical control point method [3] was used to identify the most likely points for transmission of brucellosis and mitigation procedures currently in place. Risk was assessed as likelihood of exposure multiplied by the severity of consequences.

Results

Sero-prevalence in beef cattle in Gauteng was estimated at 1%. Consequently, likelihood of exposure was high, as workers were exposed to one positive animal for every 100 they slaughtered. Of the 21 abattoirs investigated, only four provided gloves, five provided goggles and seven trained their employees on preventing brucellosis. None of the abattoirs (n=6) that slaughtered known positive cattle, had a standard operating procedure in place. The highest likelihood for transmission of brucellosis to workers was in the lairages, at the time of exsanguination; or during removal and disposal of offal and condemned material. There was also a possible environmental risk from contaminated effluent, as *Brucella abortus* is known to survive in water.

Discussion and Recommendations

It is recommended that slaughter cattle are tested for brucellosis to reduce the likelihood of occupational exposure and that test results are included in the signed health attestation, when they are consigned. Abattoirs should also mitigate the risk of occupational transmission of brucellosis at identified critical control points using appropriate protective clothing. Brucella-specific standard operating procedures should be developed for occupational health as well as waste-water management.

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Bovine Brucellosis Policy Review

Speaker / Author: Cloete, A.

In South Africa, a control and eradication programme for brucellosis in cattle was first established in 1969 and on 9 December 1988 the National Bovine Brucellosis Scheme (R. 2483) was promulgated under the Animal Diseases Act, 1984 (Act No. 35 of 1984). Up until the late 1980's, bovine brucellosis was well controlled whilst the programme was government driven and funded. Brucellosis has spread throughout the country over the last decade and is currently a high risk disease due to its widespread distribution and a lack of adequate knowledge of the disease by livestock owners. Due to reluctance of testing and inadequate reporting to the relevant authorities, the current prevalence of bovine brucellosis in cattle in South Africa is unknown.

Brucellosis control efforts are currently disjointed, inconsistent and not adequately funded. A revision of the Bovine Brucellosis Scheme (R.2483 of 9 Dec 1988) is required to enhance its effectiveness and scientific validity. The purpose of the Bovine Brucellosis Policy Review is to set out and clarify the broad framework of the disease control strategy to be followed for bovine brucellosis in cattle. The policy objectives need to be agreed upon in principle to allow for further development of more detailed implementation plans on each objective. The "Draft Document - Bovine Brucellosis Control Policy, South Africa" is in the submission process for printing in the Government Gazette for public comment.

The policy objectives identified include focussing on (i) vaccination, (ii) education, (iii) testing, (iv) movement control, (v) slaughter, (vi) reporting, (vii) effective implementation of control measures. The same central policy is to be applied across all 9 Provinces. Implementation plans for the policy objectives will be broken down into short, medium, long term and continuous goals which will be fully described and consulted on before they are implemented. This will include budget determinations and socio-economic impact assessments. The achievement of these goals will be partially dependent on the availability of human and financial resources. The policy needs to be implemented as a multipronged approach with regular reevaluation of the goals achieved on a yearly basis. As certain goals are achieved the focus can be shifted to achieving subsequent goals. In terms of the Veterinary Strategy, as adopted in 2016, an effective, implementable and sustainable brucellosis control policy will also be used as a model for other diseases in future as this policy will lay the foundations required for effective disease control efforts.

An update will also be provided on progress made over the last few years to address brucellosis control in cattle.

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Descriptive analysis of human population at high risk of zoonotic brucellosis at the human-cattle-farm interface, Gauteng, 2016

Speaker / Author: Govindasamy, K.¹ Co-author: Kalake, A¹, Harris, B.N²

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Background

Bovine brucellosis is a zoonotic state regulated controlled animal disease according to the Animal Disease Act of 1984, in South Africa. It is transmitted to humans through the consumption of infected dairy products, through the slaughter of infected animals, and through handling of aborted fetuses or afterbirths of infected cows. In South Africa, human brucellosis is a notifiable medical condition that is considered to be underdetected, under-diagnosed and under-reported whilst globally, human brucellosis is regarded as a forgotten neglected zoonotic bacterial disease of global health importance. The neglect of brucellosis has been partly attributed to a lack of awareness amongst medical professionals as to the zoonotic risk of brucellosis to their patients. Despite an ongoing government veterinary service bovine brucellosis eradication program since 1989 in South Africa aimed to prevent human brucellosis and economic loss to farmers, there have been no published reports on the provincial distribution and extent of Brucella infected cattle herds within local health municipalities or the human population at risk of brucellosis on these cattle farms. This has been attributed to the scarcity and poor quality of routinely reported epidemiologic data from provincial veterinary services. This paucity of evidence supports the ongoing neglect of zoonotic brucellosis and contributes to the persistence of bovine brucellosis.

Objectives

Determine the historic spatial distribution of Brucella infected cattle herds in Gauteng and describe the human population at high risk of brucellosis on cattle farms in 2016, by local health municipality, district and metropolitan city in Gauteng province.

Method

Integration of routinely reported bovine brucellosis data from different branches of the Gauteng Provincial Veterinary Services. Annual Animal Health Reports from 1989 – 2018, were mined for epidemiologic data related to bovine brucellosis. Each infected and newly infected herd was located within an existing spatial farm parcel boundary map. This data was then integrated into the of the Gauteng Veterinary Services Animal Census 2016 data, by associating every cattle herd surveyed in 2016 to a spatial farm parcel. The 2016 GVS Animal Census collected data on the number of people on cattle farms, whether or not people on the farm drank raw milk from the cattle and when the period of the last brucellosis herd test. Farm parcels reported to have had a history of Brucella infected cattle herds and the date of the last brucellosis herd test, were used to define cattle herds surveyed in 2016 into high, medium and low risk categories. The human population at high risk of brucellosis, where considered to be those on cattle farms where it was reported that people drank unpasteurized milk.

Results

A total of 3564 cattle herds were surveyed in 2016. The human population at risk on cattle farms represented 52.9% (1881/3554) of cattle herds visited during the 2016 animal census of GVS and accounted for 8564 persons. 79.9% (6824/8564) of the people on these farms were male. 18.5% of the women (322/1740) and 17.1% (1165/6824) of men on these farms drink raw milk from the cattle. 50.3% (1795/3564) of the cattle herds surveyed in 2016 were located within a farm parcel that had a Brucella infected cattle herd history reported between 1999 and 2018. The total human population at risk on these farms was 5210, with the majority of 78.9% (4119/5210) being male. 10.25% of people on high risk cattle farms drink raw milk compared to 17.6% and 26.8% on medium and low risk cattle farms.

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A case of simultaneous brucellosis and tetanus in Limpopo Province, South Africa, February 2019

Speaker / Author: Makungo, u.

Introduction

Brucellosis in humans across South Africa occurs mainly from ingestion of unpasteurised dairy products or from occupational-related exposures to infected animals or laboratory specimens. Majority of human brucellosis are caused by *Brucella abortus and* cases go frequently unreported owing to flu-like clinical manifestation, which includes a wide differential diagnosis. Only complicated cases of either brucellosis or other conditions are often recognised. Here, we describe a brucellosis infection detected in a fatal tetanus case from Limpopo Province.

Methods

A confirmed case of brucellosis in a 54-year old male was notified from a private health facility. Brucella sp. was isolated by blood culture at a private laboratory and the isolate was submitted for whole-genome sequencing at National Institute for Communicable Disease (Centre for Emerging Zoonotic and Parasitic Diseases). Following the laboratory notification, Limpopo Department of Health and NICD carried out an outbreak investigation to ascertain existence of an outbreak, identify the source of infection, and implement control measures. Demographic information, data on occupational activities and risk factors for brucellosis infection were collected through interviews with the case family and identified contacts. Giyani Veterinary services collected serum sample from some of the identified sick and milking cows.

Results

The patient was admitted on 10 January 2019 as clinical tetanus case with a 1-day history of fever, fatigue, myalgia, muscle spasm and stiffness of the neck and demised 7 days from the date of onset of symptoms. During the investigation, the family reported that the deceased started consuming unpasteurised milk from his cattle after early March 2018. The herdsman reported some of the cattle started aborting between September and October 2018. Unpasteurised milk was sold to some of the villagers and seven villagers reported consuming unpasteurised milk bought from the herdsman after March 2018. There was no report of direct contact with any animal products other than the unpasteurised milk. No person reported signs and symptoms suggestive of brucellosis at the time. No clinical samples were collected from any of the nine contacts. Multi-locus sequence typing (MLST) showed that the isolate was ST72 and was similar to a B. abortus isolated from bovine in Mozambique (www.pubMLST.org). Ribosomal MLST also identified the isolate as B. abortus. Giyani Veterinary Services reported collection of five serum samples from two aborting and three milking cows out of 51 cattle. Brucella abortus antibodies were detected in 2 out of 5 serum samples collected from the aborting and milking cows.

Conclusion

The consumption of unpasteurised milk was therefore the most likely source of the infection. The herdsman stopped milking the cows and selling the milk. Health promotion information was given regarding prevention of brucellosis (e.g. heating of fresh milk before consumption). No further cases were reported.

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Socio-economic impact of bovine brucellosis in the Mabeskraal village and surrounding communities in the Moses Kotane local municipality in the North West Province of South Africa.

<u>Speaker / Author: B.M. Modisane, B.M.</u> Co-authors: Mwanza, M; Chisi, S.; Midzi, E.

Introduction

The study determined the socio-economic impact of bovine brucellosis in the Mabeskraal village and surrounding communities in the Moses Kotane Local Municipality in the North West Province of South Africa and assessed the knowledge, of the farmers on the disease and ways to avoid the disease.

Methodology

Two Animal Health Technicians collected, distributed and helped to fill in a questionnaire with randomly selected cattle farmers in their respective wards. A total of 126 responses were received. Data generated from serological testing was obtained from the state veterinarian of the area and used to compute prevalence of brucellosis.

Results

The median number of household members was five. Slightly more than 50% (n = 181) of the household members were over 50 years of age. Just below 50% (n= 187) of household members had matriculated. The farmers owned from as little as five to as many as 213 cattle.

The inter-village prevalence of brucellosis was (76%). The within herd prevalence was 0% -31%.

The risky practices included lack of vaccination of heifers, non-detection and non-removal of aborted tissues, keeping of cattle that have aborted and indiscriminate buying or selling of cattle and inability to isolate buyins.

The number of calves at foot in the study area was 12% (n=316).

Recommendations

The study recommended that awareness campaign, test, slaughter and vaccination campaigns be intensified.

Key words: Brucellosis; Prevalence; Socio-economic factors; Risk factors; Practices

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Stakeholder Engagement

Community of practice on sanitary and phytosanitary risk assessment: a step towards a national risk assessment agency?

<u>Speaker / Author: Etter^{1,2,3}, E. M. C</u> Co-authors: Korsten L.⁴, Abolnik C.¹

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With 106.057 ZAR Billion in 2018 (current prices) agriculture represented 2.44% of the GDP of South Africa. Despite this relatively small contribution to the national wealth agriculture remains one of the main employment provider of the country particularly in rural areas as well as a major earner of foreign exchange through international trade. This activity is regulated by sanitary and phytosanitary (SPS) measures that require an effectively regulated framework and technical expertise in risk assessments. To provide a supportive and seamless trade framework for the country a Community of Practice (CoP) model has been funded by the National Research Foundation (NRF) supported by the Department of Agriculture, Forestry and Fisheries (DAFF) to support government in high level strategic negotiations and positioning and support industry to prevent the introduction and spread of major pests and pathogens in plant, animal and public health. This CoP aligns with the Veterinary Strategy Plan which stipulated the needs for a national agency to define, coordinate and develop risk analysis (RA) in the field of sanitary, phytosanitary, environmental and occupational risk assessment. The primary research objective of the CoP SPS RA framework will be to assess the risks associated with, and to develop and test surveillance, diagnostic and control models to detect the emergence of, selected plant diseases, insect pests, animal diseases and animal health-related conditions, including zoonoses, food borne diseases, chemical residues, mycotoxins and antimicrobial resistance. The second objective of the CoP is to train postgraduate students and government regulators in RA and advanced epidemiology and diagnostics, thus building human capacity. The third objective will be to provide government and other stakeholders with relevant information and scientific advice on the risk of emergence, entry and spread of diseases in SA in order to facilitate inter-sectorial coordination mechanisms at national and regional level to respond to SPS issues. This CoP, with the development of collaborations and relationships, will build some strategic partnerships with the local and international scientific community in the areas of SPS Risk Assessments. It will provide scientific coordination of expert committees set up by DAFF and provide technical support for the establishment of the sanitary agency proposed in the Veterinary Strategy. In the longer term and with the establishment of this national SPS Agency/Authority, South Africa will meet it international commitments to the WTO in terms of Codex, IPCC, OIE rules and regulations, as risk assessment is one of these commitments.

Acknowledgement:

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Postgraduate Student Presentations

Cross species transmission of *Mycobacterium bovis* infection at the wildlife/livestock interface in South Africa

Speaker/Author: Sichewo, P.R 1,3,

Co-authors: Etter, E., 2, 5, 6 & Michel, A. 1, 4

Bovine tuberculosis affects cattle in South Africa and is known to be endemic in wildlife with the African buffalo (*Syncerus caffer*) being recognized as the maintenance host. Spoligotyping and mycobacteria interspersed repetitive unit-variable number of tandem repeat (MIRU-VNTR) genotyping methods were performed to investigate the molecular characteristics of *Mycobacterium bovis* (*M. bovis*) isolates from cattle and wildlife, their distribution and transmission at the wildlife/livestock interface in northern kwa-Zulu Natal (KZN), South Africa. DNA was extracted from microbiological cultures of milk, nasal and tissue samples from bTB positive cattle and tissue samples from bTB infected wildlife. Spoligotyping and Mycobacterial Interspersed Repetitive Units-Variable Tandem Repeats (MIRU-VNTR) on 13 loci was used for molecular characterisation of the *M. bovis* isolates. SB0130 was identified as the dominant spoligotype pattern at the wildlife/livestock interface, while VNTR typing revealed a total of 29 VNTR profiles in the KZN province signifying genetic variability. The detection of 5 identical VNTR profiles in cattle and buffalo suggests *M. bovis* transmission between species. MIRU-VNTR confirmed co-infection in one cow with three strains of *M. bovis* implying introduction of infection from unrelated sources. Our findings highlight inter and intra species transmission of bovine tuberculosis at the wildlife/livestock interface and the need for the implementation of adequate bTB control measures to mitigate the spread of the pathogen.

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Serological prevalence of Q-fever in slaughter animals in red meat abattoirs in Gauteng province, South Africa

Speaker/Author: Mangena, M.L1

Co-authors: Gcebe, N²., Thompson P.², Adesiyun, A.A^{1,3}

Q-fever is one of the most underestimated and ignored zoonoses in South Africa (SA). The disease is caused by infection with the intracellular bacterium, Coxiella burnetii (C. burnetii). The last published report on Qfever prevalence in animals in SA was in 1987 and there is a need for recent data on Q-fever as well as strains currently circulating in the country. The objective of the study was to determine the seroprevalence of Qfever in slaughter livestock in abattoirs in Gauteng province, South Africa. In this cross-sectional study, a total of 507 serum samples were collected from 19 red meat abattoirs in different districts of Gauteng province during slaughter. Blood was collected using BD-Vacutainer® SST™ II Advance 10 ml serum collection tubes and serum harvested by centrifuging the clotted blood at 1000 x g for 10 minutes. For detection of C. burnetii IgG antibodies, IDEXX Q-FEVER 2/strip test kit was used according to manufacturer's instructions; data coded and analyzed using Microsoft Excel software. Out of the 507 animals tested, 6.7 % (34/507) tested positive for Q-fever. The seroprevalence by animal species was 9.1 % (30/331 of cattle tested), 4.3 % (3/69 of sheep tested) and 0. 9 % (1/107of pigs tested) for cattle, sheep and pigs respectively. For the three animal species tested, the seroprevalence of Q-fever was statistically significantly (P=0.0083) higher in females, 11.2% (17/152) than in males. 4.8 % (17/355). The seroprevalence of Q-fever by district is 11.7% (22/188), 10.0% (2/20), 4.3% (7/162), 3.4% (3/87) and 0.0% (0/50) for City of Tshwane, Metsweding, Sedibeng, Ekurhuleni and West Rand respectively. The results show that Q-fever is more prevalent in bovine; and in females than males. Thus, more follow-up studies are required to characterize the types of *C. burnetii* strains currently circulating in South Africa.

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Identification and characterisation of the common aetiologies of cattle respiratory diseases in Mahikeng local municipality, South Africa

Speaker / Author: Tshinavhe TF¹

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Bovine Respiratory disease (BRD) is one of the most significant health problems in the livestock sector worldwide, resulting in significant economic losses for the livestock industry. Several studies have addressed BRD prevalence in cattle worldwide, including South Africa. Nevertheless, the common pathogens cause of BRD in Mahikeng Local Municipality cattle, in the North West Province is unknown. The aim of this study was to determine the common pathogens involved in BRD in Mahikeng Local Municipality. Following identification, the bacterial pathogens were evaluated to suggest suitable antibiotic treatment. Two Hundred (blood and nasal discharges) samples were collected from cattle showing signs of respiratory distress in different communal areas. Serum samples were tested for antibodies to Infectious Bovine Rhinotracheitis (IBR), Bovine Viral Diarrhoea Virus(BVDV), and Bovine Parainfluenza Virus type 3(PI3V) using ELISA. Conventional Polymerase Chain Reaction (PCR) was used to identify the bacteria and the endpoint of PCR assay was sent to sequence analysis. Following identification, 6-disc diffusion containing different antimicrobials were used to evaluate the isolates for their antimicrobial susceptibility. According to ELISA results (71.8%) of samples were positive to Bovine Parainfluenza Virus type 3 followed by Infectious Bovine Rhinotracheitis (68.2%) and Bovine Viral Diarrhoea Virus (60%) respectively. Sequence analysis of the isolates in this study were close related to NCBI-Blast isolates; Escherichia Coli, Shigella dysenteriae, Escherichia Coli O145, Listeria welshimeri, Neisseria, Enterococcus casseliflavus, Enterobacter cancerogenus, Corynebacterium callunae, Clostridium pasteurianum and Kosakonia cowanii. There were high levels of resistance against Gentamicin (96.8%), Chloramphenicol (93.7%), and Penicillin G (88.2%) respectively whereas 87.3% of isolates showed resistance to Norfloxacin. In addition, E. coli were at least susceptible to all the antimicrobials tested. Chi-Square test results showed that there was statistically significant (p-value < 0.05) association between the antimicrobials and antimicrobial resistance. The findings of this study demonstrate that BVDV, IBR, and PI3V are common pathogens of BRD in Mahikeng Local Municipality and control measures to prevent economic losses to cattle industry is important.

Keywords: Bovine Respiratory Disease; cattle; bacteria; virus, Mahikeng Local Municipality

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Bio-accumulation of heavy metals, exposure assessment and risk characterization of common carp fish (*Cyripnus carpio*) consumers in the Hexriver catchment in Rustenburg

Speaker / Author: Tawana, M. 1

Co-author(s): Marume, U.². & Nyirenda, M.¹

Background

Fish are the basic supplier of organic proteins and have become a recently popular component of daily dietary intake to the globally rapidly growing population.

Objective(s)

This study investigated the Bio-accumulation of heavy metals, exposure assessment and risk characterization of common carp fish (*cyripnus carpio*) consumers in the Hexriver catchment in Rustenburg.

Method and Materials

Freshwater common carp fish samples were collected from Hex River (Bospoort dam) and analysed for arsenic and mercury by inductive coupled plasma mass spectrometry (ICPMS).

Results

Raw samples were also heat treated and digested to determine the bio accessible fraction. The mean concentration levels of the heavy metals in muscle tissue of common carp from the referenced site of collection for Arsenic were 0.10 ppm in raw fish, 0.98 ppm from boiled fish, and 0.13 for fried fish while for Mercury there was 0.01 ppm from raw fish, 0.13 ppm in boiled fish and 741.89 from fried fish. For the static *in vitro* digestion the findings for As were 0.93 ppm (raw fish), 4.24 ppm (boiled fish) and 1.39 ppm (fried fish) while for Mercury were 0.01 ppm (raw fish), 0.27 ppm for (boiled fish) and 0.22 ppm (fried fish) and the range for consumer health risk parameters were estimated daily intake of As (0.037 to 0.119 for adults and 0.021 to 0.067 for children) and Hg (0.002 to 0.007 for adults and 0.003 to 0.010 for children) with regard to THQ of As (0.125 to 0.389 for adults and 0.070 to 0.224 for children) and Hg (0.002 to 0.008 for adults and 0.003 to 0.011 for children), while for CR of As (0.056 to 0.179 for adults and 0.032 to 0.101 for children) were compared with the acceptable values recommended by South African department of health (SA-DOH) and the United States Environmental Protection Agency (USEPA).

Discussion and Recommendations

These results indicate that cooking processes and the digestive enzyme can elevate the level of As and Hg concentration in fish and also suggests that Rustenburg community might be susceptible to As and Hg toxicity if they frequently consume the common carp fish from the Hex river.

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Lumbosacral Disease in Police, Military and Correctional Services Working Dogs: A descriptive review of 73 cases diagnosed in the Western Cape, South Africa (2012-2016)

<u>Speaker / Author: Amar, S.¹</u> Co-author: Van Helden, L²

Background

Canine lumbosacral disease is commonly diagnosed in working dogs. Affected dogs become debilitated, resulting in a shortened working career. A study of German Shepherds in the Swiss Police force determined that 27% of the study population were excluded from duty or on restricted duty due to degenerative lumbosacral stenosis. The United States Military Dog Programme reported that spinal disease was the third most common reason for removal of dogs from training.

Objective

The aim of this study was to evaluate cases of lumbosacral disease in military, police and correctional services working dogs in the Western Cape, in terms of examining the time span between diagnosis and removal from working duties and identifying factors that significantly affect the survival time.

Method and Materials

Veterinary records of 73 working dogs with lumbosacral disease were reviewed. Inclusion in the study was based on a diagnosis of lumbosacral disease from radiographic evidence obtained at Wingfield Animal Health Centre between 2012 and 2016. Recorded data included sex, breed, unit, utilization, location of spinal pathology, age at diagnosis and age at termination of duties. Survival analysis including Cox proportional hazards regression modelling was conducted using R version 3.3.5, package "survival".

Results

Eight of the 73 dogs were right-censored from the study. The median survival time was 230 days (95% CI 174 - 448 days). The probabilities of surviving to six months and one year post diagnosis were 55.8%. and 40.4% respectively. In the multivariate Cox analysis, sex and age at diagnosis were significant predictors (P < 0.05) of survival time. Female dogs had a shorter median survival time compared to males (181 versus 335 days; P = 0.0078). The effect of unit, utilisation, breed and location of spinal pathology on the survival time were not significant.

Discussion and Recommendations

Government units with working dogs must be aware of the expected working life of their canines. Time for training of replacement dogs must be considered to avoid a shortfall. Further research to identify reasons for delayed diagnosis and the effect of varying treatment measures on survival time is warranted.

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Molecular characterization of highly pathogenic avian influenza clade 2.3.4.4 H5N8 viruses causing outbreaks in terns and other coastal birds in South Africa in 2018.

Author: Peyrot, B.M.¹

Co-author(s): Roberts, L.3, Anthony, T.1 & Abolnik, C.2

Background

The Gs/GD (goose/Guangdong) highly pathogenic H5 influenza virus detected in China in 1996 has since evolved into genetically distinct clades and subclades. In June 2017 clade 2.3.4.4 H5N8 HPAI caused the first notifiable avian influenza outbreaks in gallinaceous poultry in South Africa. It spread rapidly and has caused outbreaks in most provinces of the country. Farmed ostriches, commercial and backyard poultry, zoological collections and wild birds were infected. The first coastal birds that became infected were reported in December 2017, when major die-offs of terns and other coastal bird species started to occur in the southern regions of the Western and Eastern Cape provinces. Outbreaks in the area continued until June 2018. This was the first report of major mortalities from HPAI in coastal birds in South Africa since an outbreak of HPAI H5N3 was reported from common terns (*Sterna hirundo*) by Rowan *et al.* in 1961.

Objective(s)

To investigate the molecular epidemiology of H5N8 highly pathogenic avian influenza (HPAI) viruses by full genome sequencing and phylogenetic analysis, and comparison with the five variants of H5N8 HPAI responsible for outbreaks in avian species in South Africa in 2017.

Method and Materials

Clade 2.3.4.4 H5N8 HPAI viruses were isolated from carcasses of terns, cormorants, penguins, gulls and an oystercatcher as part of continuing monitoring and surveillance of the 2017-18 avian influenza outbreak. The full genomes of twenty-three coastal bird isolates were sequenced using Ion Torrent sequencing. Molecular analyses were carried out to compare these isolates with strains that circulated in South Africa in 2017 and in other parts of Africa prior to that.

Results and Discussion

Multiple alignments of the eight gene segments of each isolate were prepared and compared with those of H5N8 viruses isolated in South Africa in 2017. The coastal bird strains that were isolated from the southern regions of the Western and Eastern Cape provinces clustered together with the same H5N8 HPAI variant that had been circulating among terrestrial birds in these two provinces since August 2017.

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Epidemiology of trichinellosis in Greater Kruger National Park, South Africa

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Background

Knowledge on the development of changes influencing the infectivity, epidemiology and survival of *Trichinella* spp. in different climatological environments is important. This knowledge allows for the elucidation of epidemiology of *Trichinella* infections and the prediction of probable host-parasite cycles within specific ecological niches. The recent identification of new host species infected with three *Trichinella* taxa within the Greater Kruger National Park (GKNP) prompted a revision of previously published hypothetical life cycles for these species. Unravelling the enigmatic epidemiology of these potentially zoonotic species from the genus *Trichinella* is important from a public health perspective as it may aid in establishing not only the potential risk for human infection but ultimately proper control and prevention measures.

Objective(s)

To illustrate and describe the hypothetical life cycles of *Trichinella* spp. endemic in the GKNP using data gathered from surveillance studies spanning the period 1964-2016.

Method and Materials

The hypothesized life cycles were established based on the epidemiological factors and prevalence data gathered from both the GKNP and similar wildlife protected areas in Africa where the same host- and parasite species are known to occur.

Results

A recent study showed *T. zimbabwensis* to be the most prevalent, but also to infect the widest host range of all the *Trichinella* species isolated thus far from the GKNP. This would certainly suggest the general knowledge and perceptions of interspecies predation and scavenging among terrestrial- and aquatic predators to be marginal. Successful incursion from the sylvatic cycle and the subsequent maintenance of the flow of parasites between sylvatic, synanthropic and domestic environments relies on parasite and ecological characteristics, human behaviour and availability of synanthropes. This would ultimately result in unique life cycles for each taxon within a specific ecological niche.

Discussion and Recommendations

The anecdotal nature of some of the presented data confirms the need for more intense epidemiological surveillance in the rest of South Africa and continued efforts to unravel the epidemiology of *Trichinella* in this unique and diverse protected landscape.

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Molecular characterisation of Lumpy skin diseases in Mafikeng municipality

Speaker / Author: Mashamba, P.1

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Background

Livestock plays a very important role in the economy of the most nations in the world. The disease sometimes results in the outbreaks that negatively impact the productive capacity thus resulting in subsequent reduction in supply of meat and meat products.

Objective(s)

Was to molecular detect the LSD virus from clinically suspected specimens using real -time PCR assay, as a basic step for rapid and accurate diagnosis.

Method and Materials

A total of 200 samples (100 blood samples and 100 nodular skin lesions) were collected from clinically infected cattle of LSD. ELISA method was used to detect antibodies of LSDV in clinical samples. In addition, Real-Time PCR high-resolution melt assay and conventional PCR were performed to genotype LSDV strain.

Results

Bar chats, pie charts, and histograms were used to summarize the percentage frequencies of Cochran's Q test, and Pearson Chi-Square test was used to determine the association between variable.

LSD-Serum neutralisation test results showed that out of 100 serum samples analysed, 67% samples were positive to LSDV antibodies while 33% were negative, with the highest incidence occurred in Masutlhe (95%) followed by Tswaing (74%) and Six Hundred (71%) respectively. Whereas, (58%) of positive samples were recorded in Meetmekaar and (50%) was reported in Lokaleng.

Pearson Chi-Square revealed that, there was a significance difference between the villages of Mahikeng Local Municipality whereby P value was found to be less than 0.05 (P<0.05).

The Real-Time PCR assay showed that all the samples (15/15) (100%) tested positive for LSDV. Furthermore, conventional PCR assay, utilizing a LSDV P32 based primer set, did identify LSDV in all assayed specimens (15/15) at 752bp.

Discussion and Recommendations

The findings of this study were found to be link with different studies whereby, the used of PCR for the detection of LSDV was found to be useful. Therefore, the study concluded that, strains of LSDV isolated in this study prove that, Livestock hold by small farmers in Mafikeng within the North-West province, is under the risk of experiencing episode of Lumpy skin diseases with serious consequences on the economy of the stake holders.

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Field Epidemiology in Action

Establishing whether the population structure of zebra in the Western Cape African horse sickness control zones is competent to act as a reservoir host for AHSV

<u>Speaker / Author: Grewar, JD¹</u> Co-author(s): Porphyre, T²

Introduction

The purpose of this work is to characterize the spread of African horse sickness (AHS) in populations of plains Zebra (*Equus burchelli*) in the Western Cape Province (WCP) in order to feedback information to the South African horse industry on the potential of these populations to act as a wildlife reservoir of virus in the control and surveillance areas. This work addresses three main objectives relevant to the WCP and the understanding of AHS spread in plains Zebra: assess the high-risk period in which AHS will circulate persistently in the WCP Zebra population evaluate the risk of each holding in WCP to generate widespread and persistent circulation of AHS in Zebra assess the required size of a Zebra population to allow persistent circulation of AHS in the WCP

Materials and Methods

A hybrid-deterministic-stochastic vector-host compartmental model of AHS transmission was developed and paid particular attention to the impact of the seasonal variations with regards to the dynamics of the zebra population and vector activity. Factors influencing the model included environmental, host, vector and disease factors relating to annual carrying capacity, seasonal foaling, vector mortality and biting rates as well as latent and infectious periods of the AHS virus.

Results and Conclusion

The results of our analyses on the transmission and circulation of AHS in plain zebra in South Africa provided an improved understanding of how AHS virus spread in this wildlife population, particularly it clarified conditions in which incursions would persist and become endemic in zebra. Particularly, our results showed that the population of plain zebras currently present in the WCP are not sufficiently large for AHS incursion events to become endemic. Other results relating to the required population for persistence both inland and on the coast of the WCP will be expanded on. Overall, our results provide evidence that the risk of AHS persistence from a single introduction event in a given plains zebra population in WCP is extremely low. However, given the lack of knowledge in the ecology of both the vector and host populations as well as the lack of epidemiological data in zebra, a moderate level of uncertainty should be considered.

Acknowledgments

The authors gratefully acknowledge CapeNature for providing data and intellectual inputs on the zebra populations in the Western Cape Province. We also gratefully acknowledge Dr Natascha Meunier (Roslin Institute) for providing intellectual input in the conduct of the research project and Dr Stella Mazeri (Roslin Institute) for the compilation of the climate data.

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Cystic echinococcosis as a neglected and emerging zoonotic threat in Africa: the Nigerian and South African picture

Speaker / Author: Adebayo M.D¹. (Presented by Etter, E.)

Co-authors: Porphyre V²., & Etter E.^{1,2,3}

Cystic Echinococcosis (CE), caused by cestodes, is one of the most important parasitic zoonoses worldwide especially where there is a close relationship between humans, livestock and wildlife. Nigeria and South Africa asides being the top two economies in Africa share close demographic similarities, therefore necessitating an assessment of historical and epidemiological situations in both countries. A total of 49 and 31 available articles on CE were reviewed respectively for Nigeria and South Africa. The earliest recorded case was in 1961 in human, in Kano Northern Nigeria whereas as early as 1926, in present day KwaZulu-Natal Province of South Africa, the first report of the parasite was made in sheep. Also, the first documented account of wild carnivores as definitive host of E. granulosus in Africa was in South Africa. Most reports from both countries were abattoir studies based on post-mortem findings. A few human case series were described, and these were done in a more systematic approach in South Africa (unlike in Nigeria), with genotyping of circulating strains of Echinococcus reported to be E. granulosus (G1), E. canadensis (G6/7) and E. ortleppi (G5). Similarly, a conservative estimate of 137 human cases is expected yearly in South Africa. There is higher intermediate host infection (hydatid cysts) prevalence in Nigeria, highest being camels (70.9%). ELISA techniques revealed a prevalence of 12.5% in dogs in a study conducted 5 years ago and covering 3 states of Nigeria. In South Africa, the prevalence of CE infection in dogs was between 0.9-20%. Reports of sylvatic transmission of CE in South Africa was also documented. Most studies done in both countries were of small sample size and retrospective in nature, thus, lacking diagnostic measures that are sensitive enough. Recently, epidemiological data of CE in human, livestock and wildlife has not been adequately reported in both countries. The two countries as a matter of urgency need to put up individual national strategies and bilateral co-operations to evaluate, bridge the gaps in the epidemiology of the zoonosis and control its endemicity. Likewise, risk maps should be created for better surveillance, control and intervention priorities among susceptible populations.

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Behavioural changes in goats infected with foot-and-mouth disease virus

Speaker / Author: Wolf, TE1

Co-author(s): Lazarus, DD²; Opperman, P^{2, 3}; Heath, L³; Ganswindt, A¹ & Fosgate, GT²

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Background

Animals encountering an infectious disease react not only with a physiological response, such as the activation of the immune system, but also alter their behaviour in effort to battle the illness and promote recovery. The individual sets new behavioural priorities including a general decrease in behavioural activity (e.g. reduced mobility and social interactions). There is currently a paucity of information concerning the behavioural changes of goats when infected with foot-and-mouth disease (FMD) virus.

Objectives

The overall aim of this study was to evaluate behavioural changes in goats experimentally infected with FMD virus. Specifically, to compare 'sickness behaviour' in goats infected with FMD virus to the same animals when healthy or afflicted with respiratory or eye infections.

Methods

Thirty-seven goats were observed before and after controlled infection with a Southern African Territories 1 (SAT1) serotype FMD virus. Animals were housed in five groups of 5-10 individuals per group. Behavioural data were collected using scan sampling for daily activities and continuous sampling for social behaviours. Each group was observed for at least 2 hrs per week over an 8-week study period. Animals were categorised as healthy, FMD lesions present and sick with another condition for statistical analysis.

Results

Overall, the feeding and walking behaviour observed in the goats was not affected by sickness (p > 0.05). However, sickness did affect social behaviours. Dominance behaviour, for example, changed significantly (p = 0.013) when individuals showed clinical signs of sickness. Although, these behavioural changes only occurred when animals had respiratory or eye-related disease, not when FMD lesions were present.

Discussion and recommendation

Sickness behaviour in goats is characterised by changes in social behaviour, but these changes are not significant when animals are infected with FMD virus. FMD lesions in goats do not appear to cause a severe interruption of normal physiology and therefore no behavioural alterations are necessary to support the recovery process. This has implications for farmers and veterinarians, as individual goats might be FMD virus infected without showing obvious clinical signs and therefore can transmit the virus within and potentially across herds.

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Acaricide Resistance patterns in one-host *Rhipicephalus spp* at rural dip tanks and commercial farms in Kwa- Zulu Natal

Speaker / Author: Shacklock, C.¹ Co-author/Supervisor: Stoltsz, H.

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This project ascertains the presence or absence of acaricide resistance in ticks in an area of Kwa Zulu Natal where tick-borne diseases pose a real and dire threat to communal and commercial livestock. The results of this study will assist farmers and state veterinarians in their tick control strategies and aid in the battle against stock losses due to ticks and tick-borne diseases.

The aim of the project was to collect one-host *Rhipicelphalus* spp. (Blue ticks) from cattle presented at communal dip tanks and from cattle on commercial dairy and/or beef farms to test for the presence of acaricide resistance. The ticks were identified as either R (B). microplus or R(B). decoloratus, the engorged female ticks incubated and the hatched larvae subjected to the Shaw Larval Immersion test (SLIT). The Shaw Larval Immersion test was developed in 1966 by RD Shaw (Shaw, 1966) to determine the spectrum of acaricide resistance in tick populations. The 3 acaricides of choice for the study are from the classes of acaracides most frequently used in KZN, namely amidines, organophosphates and pyrethroids.

The spectrum of resistance was established in the tick populations of the respective communal and commercial cattle herds, and it is clear that the alarming rate at which resistance is developing to many acaricides is cause for concern. Strategic interventions need to be prioritized to slow down this detrimental process.

SHAW, R. 1966. Culture of an organophosphorus-resistant strain of Boophilus microplus (Can.) and an assessment of its resistance spectrum. *Bulletin of Entomological Research*, 56, 389-405.

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Outbreak Investigation of Avian Influenza in a South African Zoological Institution

Speaker / Author: Pillay, K.

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Avian influenza affects mainly wild birds and occasionally domestic or commercial poultry. In 2017, an outbreak of a highly pathogenic strain of avian influenza A (H5N8) occurred in South Africa. A female blue crane died acutely at Johannesburg Zoo on the 26th August 2017 and tested positive for H5N8. The institution was placed under quarantine until the incidence of the disease could be determined.

A surveillance programme was initiated n conjunction with state veterinary authorities. A risk-based sampling protocol was implemented by risk categorization of enclosures. Samples collected included combined oro-pharyngeal and cloacal swabs, fecal swabs from enclosures and medical over-shoes after walking through enclosures. All captive and free-ranging avian mortalities were tested for highly pathogenic avian influenza (HPAI) using real-time PCR.

Over a year, 46 wild bird mortalities and 20 captive bird mortalities (including five culls) were recorded. Of these mortalities, eight (17.4%) wild birds (95% CI 7.82-31.42%) and three (15%) captive birds (95% CI 3.21-37.89%) tested positive for HPAI. The samples from 14 live birds tested negative. Shed environmental pathogens were not detected in nine avian enclosures.

The importance of ongoing surveillance and dynamic quarantine and containment protocols has been highlighted from the first documented HPAI outbreak in a Zoological insitution in South Africa. A unique setting of a large multiple species captive environment with public access presents challenges that require special attention to maintain biosecurity. A pro-active approach will improve management practices to safeguard key collection birds which include critically endangered species. The results of this study show how quick intervention can mitigate disease spread through a captive environment.

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Longitudinal sero-surveillance of foot and mouth disease in an isolated buffalo herd in the Kruger National Park

Speaker / Author: Maree, F.1 (Presented by de Klerk-Lorist, L)

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Background

The greatest challenges in the control of foot-and-mouth disease (FMD) in southern Africa are the maintenance and transmission of the virus among the primary wildlife reservoir, African buffalo (*Syncerus caffer*), and the occasional spread from buffaloes to cattle. Once cattle are infected they may maintain SAT infections without the further involvement of buffaloes.

Objective(s)

To examine the dynamics of FMDV susceptibility and antibody dynamics in an isolated buffalo herd within an enclosure in the KNP.

Method and Materials

In a longitudinal sero-surveillance study, 49-69 buffaloes from a breeding herd in an 800 hectare enclosure in the Kruger National Park were sampled every 2-4 months for a period of three years and the antibody levels to all three SAT serotypes assessed.

Results

The SAT serotypes' antibody dynamics differ significantly, with buffaloes mounting a very robust antibody response to SAT1. The proportion of buffaloes with antibody titres to SAT1 was the highest, whilst the seroprevalence of SAT2 decreased over time and antibody titres to SAT3 were weak and short-lived. The loss of sero-positivity was not affected by gender or reproductive status, but younger animals and those in poor body condition were likely to loose SAT2 antibody titres, whereas anti-SAT1 and anti-SAT3 titres decreased in conjunction with low total immunoglobulins. Buffaloes frequently changed sero-status, but only a fraction of titre increases are explained by (re-)exposure to the viruses. We also found that maternal antibodies to all three SAT serotypes waned in calves between 2-6 months of age, implying calves would become susceptible during this time.

Discussion and Recommendations

We propose that SATs have evolved different strategies to co-exist in buffaloes, with SAT1 being highly transmissible and adapted to buffaloes. Our results suggest that in a buffalo herd, individuals susceptible to FMDV infection may become available in two ways; (i) due to loss of maternal antibodies in calves, and (ii) sub-adult and adult animals losing their protective antibodies to SAT viruses throughout the year. Identifying key periods of high FMD transmission risk is crucial to focusing sparse resources for prevention of spill-over infection from wildlife-livestock interface.

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Seroconversion of livestock during an active foot-and-mouth disease outbreak

Speaker / Author: Fosgate, GT1

Co-author(s): Sirdar, MM^{1,2}; Opperman, P^{1,2}; Lazarus, DD¹; Mulumba, M²; Mampane, RL³; Mashau, V³; Mburu, MG³; Mohlabe, K³; Neluvhalani, L³; Gobiye, M⁴; Heath, L²

Background

Foot-and-mouth disease (FMD) is a highly contagious transboundary animal disease that affects many domestic and wildlife species. Infection with FMD virus (FMDV) causes fever, lameness, loss of appetite, and the development of vesicular and subsequent ulcerative lesions on areas of the body susceptible to friction including the epithelium of the mouth, tongue, gums, nose, and feet. Goats and sheep are susceptible to FMDV infection but do not consistently develop clinical signs.

Objective

The objective was to estimate FMDV exposure in small ruminants and cattle within dip tanks where cattle had active infection.

Method and Materials

Fifty high-risk goats (and sheep) were targeted from a minimum of four FMD-affected dip tanks for a total sample size of 200 goats. The same number of unvaccinated cattle was targeted. Village leaders identified high-risk goat flocks. All goats on selected farms were sampled until the desired number was obtained. Cattle were sampled at dip tanks by animal health technicians on the day of FMD vaccination. Whole blood was collected from the jugular (small ruminants) or coccygeal veins (cattle) in plain evacuated tubes. Serum was tested for antibodies against FMDV structural proteins at Transboundary Animal Diseases using solid-phase competition ELISA.

Results

Two hundred and forty-five goats, 15 sheep, and 120 unvaccinated cattle were sampled from five FMDV infected villages. Two goats (0.8%; 95% confidence interval 0.1-2.7%), two sheep (13.3%; 2.3-37.5%), and 3 unvaccinated cattle (2.5%; 0.6-6.7%) were serologically positive. The FMD seroprevalence was not different between small ruminants compared to cattle (P = 0.683). One sampled goat had a suspect FMD mucosal lesion but was serologically negative at initial and follow-up testing six weeks later.

Discussion and Recommendations

Small ruminants are not prophylactically vaccinated for FMD and their role in the epidemiology is unknown. FMDV exposure was not different between small ruminants and livestock and this suggests a homogenously mixing population in relationship to FMDV transmission. A descriptively lower seroprevalence in small ruminants compared to cattle would be evidence that small ruminants are simply spill-over hosts. However, the movement among communities of subclinically infected small ruminants might be a source of FMDV transmission.

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Investigating the epidemiology of potentially zoonotic hepatitis e virus in commercial pigs, Cape Town, South Africa

Speaker / Author: van Helden, L.S.1

Co-author(s): Korsman, S.², Grewar J.D.³, Thompson, P.⁴, Isaacs, S.², Picozzi, K.⁵, Andersson, M.⁶ & Preiser, W.⁶

Abstract

Hepatitis E virus (HEV) causes an emerging disease worldwide. Genotype 3, a zoonotic form of the virus transmitted between pigs and humans, has been shown to cause sporadic cases of hepatitis in people and was recently isolated from three patients with hepatitis in Cape Town, South Africa.

The seroprevalence of HEV was therefore investigated in a cross-sectional study of 16 commercial pig herds supplying pork to Cape Town. A high overall seroprevalence was found, with all 16 farms included in the study having seropositive pigs in their herds, and a median within-herd prevalence of 0.93. In addition, a strain of HEV genotype 3e related to strains found in human patients from Cape Town was identified in a sampled pig.

Risk factors on farms from which sampled pigs had originated were investigated using a questionnaire during personal interviews with farmers. Preliminary univariate analysis of on-farm factors, using a multi-level logistic regression model to take clustering into account, identified several factors associated with HEV seropositivity in pigs at slaughter. These included age-group mixing, increased contact between pigs and manure, inadequate pen resting times, and lack of general biosecurity measures.

These findings indicate that strategies to monitor and control HEV must be approached from a one-health perspective to include prevention of transmission between pigs, prevention of zoonotic spread to animal workers and pork consumers, and control of farm and abattoir waste to prevent contamination of the environment.

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Limitations in control and distribution of single-host ticks (Acari: Ixodidae) in South Africa: Current Status

Speaker / Author : Nyangiwe, N¹,

Co-author(s): Ntondini, Z², Kadzere, C.T¹. & Marufu, M.C³

Background

Ticks are widely distributed throughout the world, especially in tropical and subtropical areas. Tick-borne diseases affect around 80% of the world's cattle population. Globally, costs associated with ticks and tick-transmitted pathogens in cattle range between US\$ 22-30 billion. In Africa, tick-borne diseases (TBDs) impede cattle production and TBDs are estimated at US\$ 160 million. Ticks of the *Rhipicephalus* (*Boophilus*) spp are single-host, and take around three weeks to complete their life cycle on hosts. In South Africa, two *R*. (*Boophilus*) species and are prevalent. They include the endemic *R*. (*B*.) decoloratus and the Asiatic intruder, *R*. (*B*.) microplus. These ticks are mostly associated with the build-p of resistance to acaricides; the *R*. (*B*.) microplus whose preferred host is cattle is mostly affected.

Objective(s)

This paper examines the current state of knowledge on spread of *R*. (*Boophilus*) ticks, their impact on animal health and production as well as the limitations on achieving effective control.

Method and Materials

Literature on tick control strategies, tick distribution, and resistance to chemical control measures and on the effect of climate change on tick distribution was extensively studied in order to explore the relationship between tick ecology and animal production systems.

Results

Climate change appears to be a pivotal factor in the spread of *R. (B.) microplus* to new territories in several regions in Africa. It is also apparent that where this has occurred, there has been supersession of *R. (B.) decoloratus* by *R. (B.) microplus*. Distribution of *R. (B.) microplus* is associated with outbreaks of Asiatic Redwater in regions where only African Redwater had been previously recorded. The uncontrolled movement of domestic animals and the build-up of acaricide resistance to one-host ticks complicates control measures.

Discussion and Recommendations

Along with climatic factors, uncontrolled movements of domestic animals remain the primary reason for the large numbers of ticks into new regions. Therefore, there is urgent need for alternative and efficient measure to control ticks, especially for the *R. (B.) microplus* which is currently invading new territories.

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A chameleon called Sattoo broke the heart of Bushwillow Creek

Speaker / Author: De Klerk-Lorist, L1

Co-author(s): Maree, F.F.², Scott, K.K², Lorist, R.¹, Van Dyk, D.S.¹ & Steinman,

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Background

Regulation 20 (8) states that "No buffalo may be moved onto the same land where cattle are being kept, and no cattle may be moved onto the same land where buffalo are being kept".

But what if Ferdinand or Miss Daisy would have been allowed visiting rights to the buffalo bulls in the hunting camp... Could it have prevented the broken heart of Bushwillow Creek? Can a Judas be the saver instead of a consumer of silver? Can a Judas catch a chameleon?

Objective(s)

To question the persistence of SAT2 in buffalo especially in the absence of SAT 1 & 3 and to demonstrate the integral role of fencing in biosecurity.

Method and Materials

Random sampling for FMD testing of buffalo bulls and cows from two neighbouring buffalo camps on a single property

Results

Positive serological results were obtained from the hunting bulls while animals originating from the breeding camp tested negative.

Discussion and Recommendations

The presentation will address the perceived benefits of annual testing of buffalo herds, especially to monitor and to improve general herd health. Equally important it will illustrate how simple fence and feed considerations can enhance biosecurity, proving once again that fences play a vital role in FMD control.

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AHS Control in of South Africa and the Veterinary Procedural Notice

Speaker/ Author: Weyer, C.T.¹ (Presented by Grewar, J.)

Co-authors Dr Camilla T Weyer*

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Given the significance of African horse sickness (AHS) to the international trade and movement of horses South Africa has maintained an AHS Controlled Area since 1997 in a historically AHS-low risk area of the Western Cape Province, which is described within the country's legislation in order to promote the export of equines. AHS is a controlled and notifiable disease in South Africa and South African legislation defines the AHS free, surveillance and protection zones constituting the AHS Controlled Area in the Animal Diseases Act (Act 35 of 1984). The rest of the Western Cape Province and South Africa is considered an AHS infected area (endemic). Recently a Veterinary Procedural Notice for AHS control was released for public comment. This document is an amalgamation of all the protocols and control documents for AHS control combined into one. The period of comment is now completed, and the VPN will be published.

Maintenance of the AHS controlled area involves a four-pronged approach: Movement control of equids into and within the AHS controlled area, AHS vaccination control, Equid population census and holding registrations and lastly AHS surveillance both within and outside the AHS controlled area. Equid movement control and census or registration of equids within the AHS controlled area, forms the bulk of the regulatory aspects involved in the maintenance of the AHS controlled area increasing traceability and the ability to respond quickly to detected or suspected disease incursions. In the AHS controlled area, the AHS surveillance strategy is based on guidelines as set out in the OIE Terrestrial Animal Health Code and consists of a four-level strategy namely: Passive Surveillance, Sentinel Surveillance, Wildlife Surveillance and Vector Surveillance. In the rest of RSA, outside of the AHS controlled area, surveillance is limited to testing of AHS suspected cases. It is vitally important that the correct test is performed to confirm infection, and agent identification in the form of a PCR is currently the suggested test. In an endemic area where vaccination occurs (as is the case in most of RSA) serology is inappropriate as a diagnostic method and therefore serum samples are not the specimen of choice. AHS is a controlled disease the diagnostics must be done at a DAFF approved laboratory.

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One Health- Doing what we can as students

Speaker/ Author: Rajah, N.I.

The University of Pretoria's Faculty of Veterinary Science exposes students to One Health as part of their academic program. The Onderstepoort Para-veterinary and Veterinary Students Committee (the student faculty house), Veterinary Students Community Outreach, International Veterinary Students Association and the country's OIE junior ambassador position provide additional opportunities to expose students to handson education awareness in primary animal healthcare, animal welfare, zoonoses and One Health. There are also chances for international collaborations through other IVSA member organisations at veterinary faculties worldwide and the OIE.

The Medical and Veterinary Rural Integrated Community (MAVERIC) outreach is a collaborative initiative by the University of Pretoria's veterinary and medical students, which is hosted annually since 2015. Supervised, veterinary students provide primary animal healthcare- including basic physical examination, vaccinations, deworming, dipping, basic wound treatment, food dispensing and animal welfare services, while medical students provide basic human healthcare services, which includes basic physical examinations, blood pressure testing and sugar testing.

MAVERIC broadens academic, cultural and social knowledge, and instils a sense of social responsibility amongst students and professionals. More work needs to be done- in terms of plotting community dynamics in order to highlight other areas of improvement, working on educational approaches and resources, as well as increasing awareness and participation from other disciplines- where both students and professionals, state and private, are involved. These experiences serve to empower communities and provide holistic training to undergraduate students.

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Modelling the risk of foot-and-mouth disease virus (FMDV) outbreaks in South Africa

Speaker/Author: Mohamed M. Sirdar, M.M^{1,2}

Co-authors: Fosgate, GT¹; Gummow, B^{1,3}; Mampane, RL⁴; Rikhotso, O5; Du Plessis, B⁵; Blignaut, B^{1,2}

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FMD control in South Africa includes cloven hooved animal movement restrictions, prophylactic vaccination of cattle, clinical surveillance, and disease control fencing. This study aimed to inform South Africa's FMD control policy by modelling the risks of FMD outbreaks in the protection zone of the country.

Data were collected from provincial veterinary services databases of Mpumalanga and Limpopo Provinces concerning April 2007 to March 2016. Information included georeferenced locations for all registered diptanks, monthly dipping and inspection reports and state veterinarian monthly disease and vaccination reports.

Descriptive analysis was conducted and generalised mixed-effect logistic regression models were developed to estimate the association between available risk factor information and FMD outbreak occurrence. Investigated predictor variables included a) cattle and goat populations per dip-tank per month, b) cattle and goat inspections per dip-tank per month, c), cattle vaccination (proportions and intervals) and d) cattle and goat movements in-and-out of each dip-tank. Dip-tanks were added to models as random effects while FMD outbreaks' reported serotypes were analyzed as a stratifying variable.

Additional predictor variables included rivers, roads, railways, distance to the nearest game reserve fence, spatially predicted vaccine match and human density. Ordinary kriging and spatial aggregation were used for interpolation of these variables and fishnets were used to join these data to the dip-tank level information. Spatial autocorrelation was evaluated by performing a Moran's I test on the model residuals from the final multivariable mixed-effects logistic regression model. Goodness-of-fit of the model was assessed based on Schwartz's Bayesian Criterion and the Akaike's Information Criterion. Odds ratios and 95% confidence intervals were used to estimate the association between FMD outbreaks and the examined risk factors. All statistical procedures were performed using SPSS (v.25) and results were interpreted at the 5% level of significance. ArcGIS 10.5 was used to process the spatial data, conduct spatial analysis and create thematic maps of disease risk.

The results of this study could be used to strengthen the current FMD control measures via focused surveillance. Improved FMD control would lead to a more robust rural economy and contribute to poverty alleviation.

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AHT Presentation

A Preliminary Study of Bovine Genital Campylobacteriosis and Trichomoniasis of Cattle in Mafikeng, North West, South Africa

Speaker / Author: Ramafoko, O.T.L.1

Co-author(s): Mwanza, M1

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Background and Objective

Bovine Trichomoniasis and Bovine genital campylobacter are venereal diseases of cattle. These diseases remain a cause of reproductive failure and infertility that's present in many regions of the world in which natural service is the major means of mating cattle. The significance relates to the reality that in communal areas there is no control of animals and animals roam freely which can result in easy contamination. Materials and Methods: Samples were collected in five farming villages in Mafikeng, North West Province, Republic of South Africa. In this study, 30 males and 156 females were sampled which were in the breeding age of ≥ 18 months. Preputial sheath washes (in PBS and OBP Glucose Trichomonas transport media) for the wet mount slide preparation analysis. Blood was collected using the red stopper Vacutainer tubes and centrifuged at 1500 rpm for 10 minutes. Serum samples were subjected to the Abnova Campylobacter antigen ELISA kit Assay screening test. Results: All the sheath wash samples came out to be negative. For ELISA of the 30 males, 26 reacted positive and 4 reacted negatively to the serologic screening test. The total number of females of 156 females, 139 females reacted positive and 17 females reacted negatively to the test. Conclusion: A general farmer awareness of the impact that the carrier animals can have on their beef operations is the first step to developing a progressive cattle operation.

Keywords: Venereal, Infertility, Abortion, Trichomonas, Campylobacter

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Laboratory & Diagnostics

Limitations of diagnostic tests using rabies as an example.

Speaker / Author: Sabeta, C.1

Co-author(s): Mohale, D.; Ngoepe, E.; Phahladira, B.

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Rabies, is an acute, progressive and fatal encephalomyelitis, primarily transmitted via the bite contact of domestic dogs Canis lupus familiaris. The true burden and public health impact of this fatal but preventable disease is greatly underestimated. However, an estimated 61,000 human deaths occur annually globally [1]. The rabies virus (RABV), is a non-segmented, negative sense RNA virus and prototype species of the Lyssavirus genus (Rhabdoviridae family, order Mononegavirales). In South Africa and the region, the RABV is maintained in dogs and wildlife, including the yellow mongoose Cynictis penicillata and other wildlife carnivores such as the black-backed jackal (C. mesomelas) and the bat-eared fox (Otocyon megalotis) [2, 3]. The World Organisation of Animal Health has recommended specific test methods for agent identification and detection of immune responses to lyssaviruses. In this presentation, the principles of the test methods for rabies diagnosis will be discussed briefly but more importantly the factors that generally lead to the underreporting of positive rabies cases on the African continent will be further discussed. The test methods for rabies diagnosis for both agent identification and detection of immune responses include the direct fluorescent antibody test (DFA) [4], the direct rapid immunohistochemical test (dRIT), enzyme linked immunosorbent assay (ELISA), virus isolation (both cell culture and mouse inoculation tests), immunohistochemical tests and conventional reverse-transcription PCR. Virus neutralisation and ELISA based assays and their limitations will be discussed in relation to detection of immune responses. This presentation will highlight that of antigen detection for rabies diagnosis, laboratories should not rely only a single primary method, but should consider other recommended in order to minimise underreporting of the disease.

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The use of novel single-chain antibody fragments against sat serotype foot-and-mouth disease viruses in diagnostics

Speaker / Author: Chitray, M.

Co-authors: Opperman, P,², Van Wyngaardt, W., Fehrsen, J., Frischmuth, J. and Maree, F.⁴

Background

Fundamental for the effective control of FMD in endemic regions, is reliable diagnosis and good quality vaccines. Monoclonal antibodies are an essential requirement for the production of sensitive and specific reagents in an ELISA. Here, we report on the use of single chain variable fragments (scFvs) selected from a naïve semi-synthetic chicken IgY phage display library, known as the Nkuku® library in the detection of SAT1, SAT2 and SAT3 viruses. Serotype-specific, soluble scFv's react with different binding profiles to intra-serotype viruses, aiding in the selection of antigenically appropriate vaccines for an outbreak situation. Alternatively, the knowledge concerning the antigenic composition of SAT viruses may be used in the production of engineered vaccines with broad cross-reactivity.

Material and methods

Biopanning of the Nkuku[®] library with SAT1, SAT2 and SAT3 FMD viruses resul<mark>ted in th</mark>e selection of six novel serotype-specific scFvs. These scFvs were tested as FMDV diagnostic reagents and utilised to identify scFv binding footprints on the capsid.

Results

One SAT1, three SAT2 and two SAT3 FMDV serotype-specific scFvs were obtained, which were tested in an indirect and a sandwich ELISA to determine their sensitivities and specificities in these two specific ELISAs. Additionally, scFv binding footprints were mapped and one confirmed to include residue 159 of the VP1 capsid protein.

Discussion

ELISA and structural data were utilised to predict potential SAT1 and SAT3 epitopes and using a synthetic peptide, a SAT2 antigenic site was confirmed. Epitopes predicted corresponded to previously identified antigenic sites. Such knowledge can be used in the design of chimeric FMDV vaccines to afford better immunological protection. The use of the scFvs as diagnostic reagents in an ELISA format has proven beneficial for potential use in improved diagnostic assays.

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Development of rapid, multiplex xMAP® assays for the detection of haemoparasites, and causes of abortion in cattle

Speaker / Author: Quan, M.1

Co-author(s): Nkosi, F.1. & Troskie, M.1

The need to develop technologies that allow rapid, cost effective, high throughput detection of pathogens of livestock may be met, in part, by xMAP® technology (Luminex Corporation, Austin, TX, USA). The power of the xMAP® technology lies in the massive multiplexing capabilities of the system, as up to 500 different analytes be detected simultaneously in a single reaction tube, reducing time, labour and costs over traditional methods. This technology makes use of 5.6 µm polystyrene beads, known as microspheres, which can be dyed with up to 500 spectrally distinct colours. Each microsphere set are labelled with either DNA probes or proteins on its surface, which are used to capture pathogen nucleic acid/protein, or antibodies in animal samples. A third fluorochrome coupled to a reporter molecule quantifies hybridisation at the microsphere surface. The Luminex analyzer identifies each microsphere particle and any fluorescent reporter molecules captured during the assay.

We report on the development of two separate assays. The first assay was developed from the Reverse Line Blot assay [1,2] for the genus-specific detection of *Theileria* spp., *Babesia* spp., *Ehrlichia* spp. and *Anaplasma* spp. The second assay was developed for the multiplex detection of common causes of bovine abortions, viz. *Brucella* spp., bovine alphaherpesvirus, bovine viral diarrhea virus, *Neospora caninum* and *Listeria moncytogenes*.

Individual assays were optimised as real-time qPCR assays before conversion to the Luminex xMAP® bead-based system.

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Construction of a recombinant antibody phage display library derived from the immune repertoire of FMD-SAT infected buffalo. Potential new diagnostic reagents?

Speaker/ Author: Opperman, P.,1,2

Co-author(s): Chitray, M¹., Nefefe, T¹., Fehrsen, J¹. and Maree, F. ^{1,3}

Introduction

Foot-and-mouth disease (FMD) is one of the most economically important and socially devastating livestock diseases. To ensure proper control of the disease, vaccination programs and rapid and precise laboratory diagnosis is critical. The current recommended OIE diagnostic assay for diagnosis and screening of FMDV samples is the liquid phase blocking ELISA (LPBE). Although LPBEs for detecting the SAT serotypes are well established, there is still a need to improve the sensitivity and specificity. Antibodies have been harnessed as diagnostic and research reagents but are plagued with limitations. We aim to select SAT serotype-specific single chain variable fragments (scFvs) from an immune phage display library with the intentions to achieve improved FMD diagnostic tests.

Material and Methods

The immune library was prepared from spleen samples from buffalo infected with SAT1/KNP/196/91, SAT2/KNP/19/89 and SAT3/KNP/1/08. Construction of the buffalo library was initiated by extracting RNA from the spleen samples and amplifying the coding sequences for the immunoglobulin variable light and heavy chains by PCR. The constructed buffalo library was bio-panned with representative viruses for each of the SAT serotypes displaying broad neutralising characteristics.

Results

This is the first time a recombinant antibody phage display library derived from the immune repertoire of FMD–SAT immune buffalo has been constructed. The total library size was 3.84 x10⁷ cfu. A total of 270 SAT1, 540 SAT2 and 270 SAT3 virus-specific binders were obtained and selected clones sequenced. One unique SAT1 and one SAT3 binder was obtained and each were specific to the virus to which they were bio-panned and did not cross react to the other SAT serotypes. Their use in the development of improved diagnostic assays is currently being investigated.

Discussion

The current LPBE used at ARC-OVR for FMDV diagnosis uses polyclonal sera as both capture and detecting reagents. Polyclonal sera containing a heterogeneous complex mixture of antibodies of different affinities can result in background signals of serological assays. The selected FMDV-specific scFvs will be used to improve the sensitivity and specificity of the current diagnostic ELISA for FMDV.

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Biorisk Analysis in Veterinary Laboratories,

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Biorisk analysis (BRA) is a process of identifying acceptable and unacceptable risks (risks of accidental infection) and laboratory biosecurity risks (risks of unauthorized access, loss, theft, misuse, diversion or intentional release) and their potential consequences. It can also be used to identify the specific biosafety and biosecurity measures needed to contain and work safely with specific biological agents/and or their products and toxins in a veterinary laboratory.

BRA consists of four components i.e. biohazard identification, biorisk assessment, biorisk management and communication. Use of these terms should be followed to ensure adherence to OIE nomenclature and also with standardized BRA methodology already in use by OIE Member states. Biohazard identification is the first step in BRA which identifies possible biohazards. Examples of biohazards are organisms and their products, transformed cell lines and certain types of nucleic acids. Risk is defined as "the likelihood of the occurrence and the likely magnitude of consequences of an adverse event or effect to animal/human health or to the environment". Risk consists of defined elements e.g. likelihood, uncertainty, consequences which must be addressed during BRA. Biorisk assessment is the second step in BRA and involves Identifying the likelihood and the potential consequences (severity of harm) associated with exposure to or release of the biologic agent or any of its components. Two approaches can be utilized to conduct biorisk analysis i.e. qualitative and quantitative approaches, either approach has got its own advantages and disadvantages. The third component known as biorisk management is a process of identifying, selecting and implementing measures that can reduce the level of risk. Lastly risk communication should be done throughout the BRA and findings should be communicated to all stake holders.

The outcomes of BRA should inform the policy/policies on risk management and policy formulation. BRA should deliver outcomes in terms of country's obligations to WHO and OIE in the control of zoonosis and trans-boundary diseases (TBD).

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The efficacy of a plant-produced virus-like particle vaccine against H6 avian influenza in specific pathogen free chickens

Speaker / Author: T. Smith^{1,2}

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Background

In South Africa an inactivated avian influenza vaccine based on a 2002 H6N2 isolate was produced and commercialised following the first outbreak in chickens in the early 2000's and is still employed today to protect flocks, despite substantial antigenic drift. Plant-produced virus-like particles (VLPs) have been shown to be advantageous with regard to efficacy, safety, production speed, scalability and cost. To evaluate its potential for poultry vaccines, a plant-produced hemagglutinin-based H6 VLP vaccine was tested for efficacy in chickens in a prime-boost vaccination regime, in comparison to the commercial vaccine.

Objective(s)

Determine the immunogenicity and ability of the H6 VLP vaccine to reduce viral shedding in specific pathogen free chickens against challenge with a heterologous H6N2(2016) virus, in comparison to the commercial vaccine, using qRT-PCR.

Method and Materials

The study consisted of three groups: A (H6 VLP vaccine, n=12), B (commercial vaccine, n=12), and C (non-vaccinated control, n=12). Blood was collected after primary vaccination, booster vaccination, and viral challenge to evaluate the immunogenicity via hemagglutination inhibition (HI). Oropharyngeal and cloacal swabs were collected 2, 3, 4, 7, 14 and 21 days post challenge to determine the shedding profile using qRT-PCR.

Results

A single dose of the H6 VLP vaccine elicited a higher immune response to two doses of the commercial vaccine, with mean HI titers of 9.3 log₂ and 8.8 log₂, respectively. Following challenge, the H6 VLP vaccine significantly reduced viral excretion from the respiratory and gastrointestinal tracts by more than 100-fold and 6-fold, respectively, in comparison to the non-vaccinated control and shortened the duration of shedding by at least a week. In contrast, despite high antibody titers prior to viral challenge, the commercial vaccine not only failed to reduce shedding in comparison to the non-vaccinated control group but exacerbated oropharyngeal viral shedding until 21 days post challenge, demonstrating the cost of antigenic mismatch between the vaccine and challenge strains.

Discussion and Recommendations

The plant-produced H6 VLP vaccine, which facilitates differentiation between infected and vaccination animals (DIVA), presents a new generation of poultry vaccines that is highly efficacious and can be updated rapidly to match the latest field virus, and this technology will greatly benefit the poultry industry.

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POSTER PRESENTATIONS

One Health

Detection and Quantification of Antibiotic Residues In Communal Goats Milk In Mahikeng Local Municipality, South Africa.

Speaker / Author: Ndlovu K.L, A¹ Katlindlovu1@gmail.com

Co-author(s): Ngoma, L.^{1,2}, & Mwanza, M.^{1,2}

Background

The easy accessibility over counter and use of antibiotics by farmers and Animal health practitioner remain a concern in South Africa because of antibiotic resistance observing recently.

Objective

The objective of this study was mainly to evaluate the risk exposure of consumers to antibiotics through goat's milk among populations in the Mafikeng rural communities.

Method and Materials

In this study, 13 villages were randomly selected and 266 raw milk samples were collected from milking goats and the 5 following antibiotics: Tetracycline, Sulfamethazine, Amoxicillin, Erythromycin and Streptomycin were analysed using the Eliza screening method and confirmed through the HPLC technique.

Result

Preliminary results showed the presence of of Amoxicillin residues to be 35.3%. Amoxicillin residues in Tsetse village was 6.3%, Lokaleng 3.7%, Ramatlabama 4.5%, Masutlhe 4.5%, Makgobistad 2.2%, Dithakong 1.5%, Tlapeng 1.1%, Modimola 0.7%, Majemantsho 2.6, Magogoe 0.7%, Bodibe 4.8% and Sunny side 2.7%. The presence of Streptomycin residues was 5.3%. Tsetse 1.1%, Lokaleng 1.8%, Ramatlabama 0.3%, Makgobistad 1.1%, Masutlhe 0.3%, Majemantsho 0.3% and Tlapeng 0.4% respectively, while Tetracycline, Sulfamethazine and Erythromycin were detected below MRL as prescribed by the European Union and Codex Alimentarius.

Discussion and Recommendations

The negative value of MRL obtained in this study was lower compared to those reported by Layada *et al.* (2016) .The results obtained revealed that farmers are having access to antibiotics over the counter and can use them at anytime. The presence of these antibiotics in milk is of concern as these populations due to their life standard drink daily this milk and might be developing resistance to the antibiotics because of residues. In light of these results there is a need for the state to look into the issue of antibiotic accessibility over the counter and regulation of who is able to use them in addition to training of farmers

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Assessment of microbial quality of dried fish sold in the informal market around Johannesburg and, its public health implications in South Africa

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Fish is one of the most important sources of animal protein available in the tropics and has been widely accepted as a good source of protein and other elements for the maintenance of healthy body in many African countries.

The objectives of the study were mainly to microbiologically evaluate the quality of dried fish sold in informal markets in Johannesburg. In addition, to study the antimicrobial resistance profile of the isolated bacteria as well as to assess the public health risk exposure for consumers.

In this study, fifty (50) dried fish samples were purchased from informal markets and shops in the CBD; Hilbrow; Berea and Yeoville in Johannesburg using the convenient sampling method.

Samples were cultured on different medium and identification of isolated bacteria was done using the biochemical tests and molecular techniques such as DNA extraction, PCR, Amplification of 16S rDNA. Sequencing was used for identification and confirmation (Ngoma *et al.*, 2013).

In addition, isolated bacteria were evaluated for their antibiotic resistance profiles against four common antibiotics using the disc diffusion method as described by Ajayi & Akonai (2003) and the interpretation of the break point zone as specified in the guideline of clinical laboratory institute (Wayne, 2007).

The isolated bacteria were Enterobacter Sakanakii (20%), Staphylococcus aureus (17%), Staphylococcus xylosus (11%) Staphylococcus lentus (11%), Staphylococcus epidermis (7%), Listeria Monocytogenes (7%), Serrati liquefaciens (6%), Bacillus subtills (6%), Salmonella Typhi (7%) and Enterobacter clloaclae (4%). It was also found that about 23% of isolated bacteria were strongly resistant to amoxicillin, oxytetracycline, norfloxacin and ciprofloxacin. While, 29% of isolates had an intermediate resistance and 48% were susceptible to antibiotics tested.

The dried fish from the markets are contaminated with food pathogens that are of public importance and expose consumers to food borne diseases risks. The contamination could be poor hygiene during processing, transportation, preparation, storage or at the market since they are sold in an open area market. In Addition, there is a need of hygiene education of food handlers and further analysis on the dried fish.

In conclusion, due the occurrence of foodborne diseases outbreaks in South Africa neighbouring countries, there is a need of regular monitoring and strict control measures to ensure the safety of consumers.

Key words: informal markets, dried fish, Food borne pathogens and antibiotic residence

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Molecular Characterization and Antibiotic Resistance of Foodborne Pathogens in Street Vended Ready -to -eat Meat in South Africa

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Co-author(s): Lubanza, N.1, Adetunji, M.C.1 & Mwanza, M.1

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Background

The consumption of contaminated food with microbial population remains a key way of foodborne infection in developing countries and a serious public health burden among population.

Objective(s)

This study aimed at identifying food borne pathogens and their antibiotics resistance in ready-to-eat meat sold in public eateries around Johannesburg, South Africa

Method and Materials

A total of 115 samples were examined for the incidence of bacteria pathogens and their antibiotic resistance profiles against commonly used antibiotics (Ampicillin, Tetracycline, Chloramphenicol, Erythromycin, Ciprofloxacin, Streptomycin and Sulphonamides) using the molecular methods and the disc diffusion methods.

Results

Fifteen bacteria spp. were detected in the samples with *Staphylococcus aureus* having the highest prevalence (25%) among others while 53.33% of the isolates exhibited multidrug resistance to the antibiotics tested

Discussion and Recommendations

This study revealed a wide diversity of bacteria spp. contaminating the street meat, consumers of ready-to-eat meat sold in public eateries is at risk of food poisoning. Hence strict intervention strategies should be put in place by government agencies to reduce the menace of food poisoning in the country.

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Effect of protein supplements on reproductive performance

<u>Speaker / Author: Tsheole, M.S¹</u> Co-author(s): Mwanza, M.^{1,2}

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Production of meat from goats and sheep plays an important role in the supply of animal protein for the people in North West. Goat production in the villages is mostly done through the traditional husbandry system using the extensive system without any supplementation. This is characterised by poor growth rate, high mortality and low reproductive rates. This study evaluated the impact of protein supplements on the reproduction performance of female Tswana goats. In an internally controlled environment, twenty-four female weaner goats with similar body weights and age (3 months old and 10.56±1.28 kg BW) were used to evaluate the effect of protein supplements on reproduction and reproductive parameters. Animals were grouped into three treatments of eight in a completely randomised block design (CRD) according to live weight. Goats were supplemented with concentrate mixtures consisting of maize, grass and soybean meal once daily (at 09:00 hours) informed based on their weight and later given grass ad libitum and had 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. Blood was collected at 08:00 for further measurement of reproductive hormones as treatment group 1 to 3. Observations on reproduction performances were made by following planned standard procedures. The procedures used for supplementing goats were reviewed and approved by the Animal Research Ethics Committee, North-West University, Mafikeng Campus (AREC-MC) (approval no. NWU-00019-14-S9). The results are that feeding of goats with high protein diet significantly increases reproduction. Goats that received high concentrations of protein gave birth to twins as compare to others. It is also concluded that protein supplementation effectively influences twinning. Finally, the study revealed that survival rate of kids correlated with protein supplementation to the extent that the highest survival rate was observed among kids born from animals supplemented compared to control treatment.

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The study of poisonous plants of veterinary significance in the Rooigrond area, North West Province.

<u>Speaker / Author: Maseko, F.M</u> Co-author(s): Verster, R. & Ndou, R.V.

Background

Poisonous plants are plants that contain substances that are capable of producing a variety of discomfort and adverse physical or chemical effects or even death to human and animals through consumption and contact. The direct costs of poisonings and mycotoxicosis to the livestock industry in South Africa have been conservatively estimated to be more than one hundred million rand per year.

Objective

This study was focused on documenting the poisonous plants in the Rooigrond area of the North West province.

Method and Materials

The study used a quantitative observational method to document the poisonous plants in the area according to their names (scientific and common). Field data were also collected including plant growth patterns and characteristics. Furthermore, the location of the plants were plotted on maps using GPS coordinates.

Results

The only extremely dangerous plant found in Rooigrond was *Lantana camara*. They tend to grow next to dirt roads as thick impenetrable bushes with a lot of dust on the leaves from bypassing vehicles. Other plants have toxicity such as *Opuntia* and *Agave*, while *Solanum* and *Cucumis* grow flat on the ground and less likely to be eaten by cattle which tend to be high grazers. Some *Datura* plants were found on rubbish dumps, but the difficult terrain (high heaps) should make leisurely grazing improbable. Some plants occur everywhere and they were not plotted on maps, because they are not limited or specific to the study area. Example such as *Argemone*, which could be seen especially on newly ploughed lands after the first rain.

Discussion and Recommendations

This study recommends knowledge extension to farmers about poisonous plants in their area especially *Lantana camara*. In addition, better fencing of some plots may certainly help to prevent cattle access to poisonous plants and also zero grazing the livestock during drought.

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Development of indicator cells for virus detection

Speaker / Author: Nogwebela, T.

Supervisor: Weidmann, M. email m.w.weidmann@stir.ac.uk

Background

Teleost fish are armed with an innate antiviral defence system which is based on the production of interferon (IFN). This represents the first line of defence against viral agents. Mx-gene has an interferon -induced gene promoter structure which can be stimulated in RTG cells by poly I: C (polyinosinic: polycytidylic acid) which is a mimic of viral dsRNA.

Objective(s)

We needed to develop an Mx-promoter controlled luciferase expressing EPC cell line (Fathead minnow derived cell line) which will be useful for viral disease detection in cold blooded animals.

Method and Materials

Cellular and molecular laboratory activities used focused on plasmid pGL3-pomMx1 acquired from Dr Collet, containing an Mx-Promoter fused to a firefly Luciferase gene. The experiments propagated the plasmid, tested G418 susceptibility of the EPC cells that were to be used, optimised transfection with Fu-Gene and pGL3-pomMx1 to develop of a stable cell line of EPC cells.

Results: These cells needed to be propagated until they show full healthy growth to be able to give an indication of whether they can stably express the firefly luciferase gene activity.

Discussion and Recommendations

If their luminescence activity were shown to be triggered by virus replication a cell line would have been developed. This would be expected to help diagnose viral diseases of cold blooded vertebrates. Fish farmers and fish health practitioners will benefit from quick and reliable disease diagnosis. This new type of cell line will help to optimize virus identification and possibly response to virus outbreaks. The research took four months to complete and will probably need 2-3 more months to complete.

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Food safety knowledge, perceptions and practices among students at the North-West University (Mafikeng Campus)

Speaker / Author: Rendani Victress Ndou, R.V1

Co-author(s): Ramafoko, L.O¹

Background

Each year more than one-third of the total population in developing countries are affected by foodborne illness. Furthermore, the emergence of resistant and extremely virulent strains of foodborne microorganisms could lead to major outbreaks with calamitous consequences. Therefore, it is crucial to determine if there is a need for food safety education amongst consumers in different communities.

Objective(s)

This study investigated the food safety knowledge, perceptions and practices amongst students at the North West University (Mafikeng Campus).

Method and Materials

The study used the cluster sampling method to collect data from 375 students from five Faculties using a self-administered questionnaire. The questionnaire contained three sections which included knowledge, perceptions and practices. The data was analysed using IBM Statistical Package for Social Sciences (SPSS) version 24 statistical package.

Results

The study determined that most students had a poor knowledge of food safety with an overall score of 39.6%. Whilst, the score for good food safety practices was an overall low of 40,4%. On the other hand, a moderately high percentage of the students had positive perceptions about food safety at 64.1%. Chi-square test revealed a significant relationship between gender and food safety perceptions at p=0.005.

Discussion and Recommendations

The findings in this study revealed a low level of knowledge and poor practices of food safety among students, which may be indicative of a poor or non-existent food safety education during the primary and secondary school years of these students. Therefore, this study recommends the evaluation of food safety education at primary and secondary schools and also food safety education programmes aimed at institutions of higher learning students and other consumers.

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Field Epidemiology in Action

Prevalence of leptospirosis in donkeys and associated risk factors in the South Africa

Speaker / Author: Daddy, K.K.1

Co-author(s): Mwanza, M^{1,} & Ngoma, L. ^{1,}

Abstract

Leptospirosis is a neglected zoonosis of global importance with a complex epidemiology that affects humans, domestic and wild mammals. Several studies have addressed *Leptospira* seroprevalence and risk factors in horses worldwide, including South Africa. Nevertheless, seroprevalence of *Leptospira* spp. in donkeys around Ngaka Modiri Molema district (NMMD), North West Province is unknown. The aim of this study was to estimate the seroprevalence of eight Leptospira serovars in donkey in the NMMD and to identify factors associated with Leptospira infection.

Three Hundred and Sixty-Five donkeys' sera were collected between March 2017 and October 2018. Sera were tested with live antigen suspensions of leptospiral serovars including serovars Canicola, Bratislava Hardjo, Grippotyphosa, Icterohaemorrahagiae Szwajizak, Tarassovi and Pomona using the microscopic agglutination test (MAT).

In addition, structured interviews using a questionnaire were conducted to gather information on the risk factors for *Leptospira* sero-status. This included demographic, geographical, environmental and livestock management information.

Cross-sectional study shows that antibodies against *Leptospira* were found in 42 of 365 (11.5%) in apparently healthy donkeys. The common leptospiral serovar against which serum antibodies were detected was serovar Bratislava 34 (81%) followed by Serovars Tarassovi 8 (19.04%) respectively. Pearson Chi square test and logistic regression analysis shows that age and agricultural activity in the vicinity of donkey premises were positively associated with *Leptospira* sero-positivity. Donkeys with fruits and vegetables farming in vicinity as the main agricultural activity were nearly four times at high risk of being seropositive (Odds=3.8; 95% CI:0.08-16.67) than those surrounded with other agricultural activities. In addition, donkeys with ages between 0-5 years old were two times at high risk of being seropositive than donkeys of others age group (Odds=2.05; 95% CI: 0.34-12.29).

This study also shows that donkeys in the NMMD are routinely infected by *Leptospira interrogans* serovars Bratislava and Tarassovi, and these rural areas may be seen as reservoir for the bacteria. Furthermore, the age and donkeys being surrounded with fruits and vegetables farming were also found to be at risk for *Leptospira* infection.

Keywords: Rural communities Ngaka Modiri Molema district, leptospirosis, prevalence, risk factors

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Investigating *Campylobacter* species diversity in slaughter age broiler chickens in Ngaka Modiri Molema District, North West Province, South Africa

Speaker / Author: Mileng, K.1

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Background

Infections with *Campylobacter* species have gained recognition as the most frequent cause of food-borne bacterial gastroenteritis overtaking those of *E.coli* and *Salmonella spp* in humans worldwide. Consequently, understanding the mechanism leading to *Campylobacter* human infections has become very crucial. Most these infections are known to occur as a result of consumption of contaminated meat and other animal products, such as unpasteurised milk and chicken products.

Objective

This study investigated the species diversity and seasonal variations of *Campylobacter* found in slaughter age broiler chickens in Ngaka Modiri Molema District (NMMD), North West Province

Method and Materials

Using convenience sampling methods, 2064 chicken faecal samples were collected between July 2017 and May 2018. Genoemic DNA was extracted directly from faecal samples using Qiagen Amp mini Stool kit (Qiagen Inc). The genomic DNA was then used to identify Campylobacter species through PCR and Maximum likelihood (ML) phylogenetic methods.

Results

The investigations showed that 336 of 2064 samples were positive for Campylobacter. After sequencing of PCR amplicons, *Campylobacter jejuni* (*C jejuni*) was the only species identified in this study. In addition, positive samples were more prevalent in summer than in other seasons. The 26 sequences obtained were further used for phylogenetic analysis, which consisted of the genera Campylobacter. All C. jejuni gene sequences generated in this study clustered with corresponding congener in the tree topologies monophly within Family Campylobacteracae was well supported.

Discussion and Recommendations

The findings of this study exposed chickens as a reservoir of *C jejuni* which can be a considerable risk for human infections through consumption. The findings also suggest a need for public awareness about food safety and a review of standards of hygiene at commercial poultry production plants.

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Seroprevalence of *Toxoplasma gondii* in communal livestock at Ratlou Local Municipality in the North West Province, South Africa

Speaker / Author: Mosikidi, K.N.¹
Co-author(s): Ndou, R.V.¹, Dada, T.A.¹

Background

Toxoplasma gondii (T. gondii) is a zoonotic microscopic protozoan parasite that causes toxoplasmosis and is wildly prevalent in warm blooded animals worldwide. Whilst toxoplasmosis causes abortion, stillbirth and fatal death in animals, it is also a significant zoonotic diseases causing encephalitis, abortions in pregnant women, hydrocephalus in infants and fatality in some cases especially in immune suppressed individuals. Therefore, it is imperative to determine the prevalence of *T. gondii* amongst animals as a risk assessment for human infections.

Objective

The study aimed at determining the seroprevalence of *T. gondii* in different animal species at Ratlou Local Municipality, in the North West Province, using the enzyme-linked-immunosorbent assay (ELISA).

Method and Materials

The study employed the convenience sampling method. A total number of 357 blood samples from free-range chickens, goats, sheep and cattle were collected at different communal grazing communities. The samples were analysed using the ID screen toxoplasmosis indirect multi- species ELISA test kit. In addition, a baseline questionnaire was also used collect data on awareness of *Toxoplasma gondii* and other zoonotic diseases among the participating farmers.

Results

Overall, 0.02% seropositivity was found in this study. Among those, cattle had the highest seropositives at 3.26% followed by sheep at 3.1%, while goats and chickens were both seronegative (0%). In additions, the questionnaire data determined that farmers had either no or very poor knowledge of zoonotic diseases including *Toxoplasma gondii*.

Discussion and Recommendations

The low prevalence of *Toxoplasma gondii* was attributed to the dry and very hot climatic conditions in the study area which is not favourable for the survival of oocyst. Nevertheless, this study recommends knowledge extension to farmers that will assist them to practice proper herd health management and food safety as to prevent human infections with *T. gondi* and other zoonotic diseases.

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Identification and characterisation of viral bloody diarrhoea aetiology in puppies, presented to the Animal Health hospital, North-West University

Speaker / Author: Ntumba, K1

Co-author(s): Mwanza, M. 1,2 & Ngoma, L1,2

Diarrhoea is a complex condition mostly encountered in small animal practices incriminating enteric pathogens including viruses, bacteria, parasites, as well as lifestyle and diet. CPV, CCoV and CRV are the main viral enteric pathogens responsible for severe gastroenteritis in puppies; whereas CPV-2 is the cause of high morbidity and high mortality in dog populations.

This study aimed to determine the epidemiology of bloody diarrhoea, to identify and discriminate viral enteric pathogens circulating among puppies presented to the Animal Health Hospital, North-West University. In this study, two diagnostic methods: immunochromatography assay (IC) for antigen detection and conventional PCR for Characterisation were used to confirm the clinician diagnostic. Demographic information and faecal samples of 84 diarrhoeic young dogs aged between 3 weeks to 9 months were collected on presentation at the NWU hospital. For IC assay, rapid diagnostic kits of CPV, CCoV and CRV antigen (Quicking) were used; and for conventional PCR, primers set forward and reverse were used.

Results obtained showed that IC assay detected 66/84 (78.6%), 2/84 (2.4%) and 2/84 (2.4%) positive CPV-2, CCoV and CRV antigens respectively. While conventional PCR revealed 80/84 (95.2%), 0/84 (0%) and 12/84 (14.3%) positive CPV-2 DNA, CCoV RNA and CRV RNA respectively.

The sequence analysis of 80 CPV-2 strains and 12 CRV strains confirmed that the predominant circulating variant was CPV-2c followed by CPV-2b (minor), and G3 rotavirus serotype. The phylogenetic analysis were performed for CPV-2 and CRV, thus demonstrated that there is similarity with variants from Korea, Peru, China, India, Nigeria for CPV and Japan for CRV.

In conclusion, this study revealed that the majority of animals presented with gastroenteritis to the animal Health Hospital at the North-West University, Mafikeng campus are predominantly affected by CPV-2 virus. Furthermore some animals had a co-infection of CPV and CRV viruses. There is a need of more awareness for pet owners on the issue of vaccination in order to reduce the prevalence of the diseases in the Area. Keywords: Gastroenteritis, IC, PCR, Canine parvovirus, Canine coronavirus, Canine rotavirus

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Influence of human factors in the transmission of *taenia solium* cysticercosis in villages of Alfred Nzo and OR Tambo districts of the eastern cape province, South Africa

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Taenia solium is an emerging and expanding zoonosis in Africa leading to human cysticercosis. The prevalence in pig populations is often underestimated. The higher prevalence of porcine cysticercosis is known to be accompanied by frequent *T. solium* tapeworm infections in man. Within the sub-Saharan region, South Africa has the highest reported prevalence of cysticercosis as a result of its large number of pigs. A large proportion of farming is done by resource-poor farmers in the Eastern Cape Province. These pigs are mostly of indigenous breed and kept as free ranging. In terms of the Meat Safety Act 40 of 2000 (South Africa, 2000), the Directorate: Veterinary Public Health (VPH) has the responsibility to provide measures that promote meat safety and the safety of animal products in order to ensure the safe consumption of meat, meat products and as well as animal products. However informal and illegal slaughter are often unknown to provincial veterinary officials and are mostly identified after complaints from the public which makes it difficult for the Department Agriculture, Forestry and Fisheries (DAFF) to determine whether people who are infected with *T. solium* get their meat from registered or unregistered facilities.

Information regarding the study was obtained through the analysis of meat inspection and Ag-ELISA against dissection (N=180) carcasses as the "gold standard" to determine the prevalence and the spread of cysts in the carcasses, questionnaire responses from rural pig owners (N=180) on the pig keeping/husbandry and consumers (N=361) on knowledge and food safety practices followed.

The pig keeping practices were not always supporting the control of pig cysticercosis. Pigs were often free range and were exposed to human and animal (especially) dog faeces. Although sanitation was available in most of the villages, these were not always used due to certain practical reasons. Furthermore, it was evident that cysts were not only limited to the conventional areas checked during primary meat inspection but that they could be found in areas which are of economic importance and would preferably not be cut during inspection.

Preliminary results showed that areas of pig keeping need to be improved on and that the pig owners need to be educated about the possible risks of the disease. Furthermore, it was evident that, in addition to normal primary meat inspection, additional measures might be required to prevent the transmission of this zoonotic disease to consumers of pork.

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The geographical distribution of *R* (*B*) decoloratus and *R* (*B*) microplus in cattle herds in KwaZulu Natal

Speaker / Author: Ms Maphalala, M

Co-author(s): Shacklock, C.

Background

Ticks are external parasites of economic importance that affect livestock health and production all over the world. KwaZulu Natal is an area of South Africa where the one host ticks, *Rhipicephalus (Boophilus) microplus* and *Rhipicephalus (Boophilus) decoloratus*, have a high impact on livestock farming, as they are responsible for the transmission of *Babesia bigemina* and *Babesia bovis* in cattle. The African Blue tick, *R (B) decoloratus*, is widely distributed throughout KwaZulu Natal where the temperature and rainfall are high during the summer months. The Asiatic blue tick, *R (B) microplus*, was introduced fairly recently to Africa via cattle brought from Madagascar, and has encroached on territories previously occupied by its African counterpart. Research shows that the exotic Asiatic blue tick is slowly displacing the native African blue tick in parts of South Africa.

Objective

The purpose of the study is to plot the geographical distribution of *R.B microplus and R.B decoloratus* in cattle herds in KwaZulu Natal, based on the data collected by Afrivet laboratory over the past three years.

Method and Materials

Ticks were collected from cattle at communal dip tanks or from commercial cattle herds in rural areas of KZN. Engorged female blue ticks were collected off the animals before dipping for the purposes of acaricide resistance testing at Afrivet laboratory. Ticks were identified (where possible) as either, *Rhipicephalus* (Boophilus) microplus or Rhipicephalus (Boophilus) decoloratus using a light or stereo microscope. The mouthparts of female ticks and the anal plates of any male ticks collected were used as differentiation features. GPS co-ordinates were recorded at each sample site and the distribution points of each tick species was plotted on a map of KZN.

Results and discussion

The study will give a good indication of the distribution of these two tick spec<mark>ies, and ascertain whether the postulated displacement of R. decoloratus by R. microplus is occurring in certain areas of KwaZulu Natal.</mark>

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Laboratory & Diagnostics

Prevalence of pathogens causing subclinical mastitis and drugs resistance in small ruminants in Mafikeng

Speaker / Author: Mmutle, K.1

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Three hundred and twenty (320) of milk samples were collected from goats at the different zones of Mafikeng area, collected in two seasons which is winter and summer where hundred and sixty (160) samples were collected during summer and the other half in winter.

Background

Goat milk is a major source of dietary protein among the rural residents of the Ngaka Molema District, North West Province, South Africa. Mastitis is a clinical or subclinical condition that could affect the quality of milk and health of community.

Objective(s)

Determine the occurrence of bacterial-associated with subclinical mastitis infections in small ruminant and conduct phylogenetic analysis in order to compare nucleotide sequences identified in this study with isolates previously identified elsewhere.

Method and Materials

The quality of milk and biochemical and molecular techniques were employed for discrimination of isolates, And cultured of Nutrient agar for 24-48 hours at 37°C. DNA was isolated from the isolates and 16S rDNA was amplified and send to Inqaba Analytical laboratory for sequencing. The antibiotic susceptibility profiles of the isolates together with virulence genes were investigated

Results

Location and season of milk collection influenced the quality of milk samples while the identified potential cause of mastitis includes; Bacillus spp., Clostridium spp., Pseudomonas spp., Enterococcus and Staphylococcus spp were dominating cultures of milk samples. Out of 320 milk samples that were collected California Mastitis Test (CMT) was performed and the results shows that the presence of subclinical mastitis the prevalence of healthy, subclinical mastitis and clinical mastitis during summer season was 56.26, 20.01, and 23.76% and in winter season was 45.63, 18.75 and 35.64%.

Discussion and Recommendations

The reported prevalence rate could be very important from the economic loss and public health point of view of the rural communities. The presence of antibiotic and multidrug resistant bacterial strain is also reported as a serious problem. Therefore, the responsible authorities should take the necessary actions to control the undiscriminating and lengthy use of antibiotic in the study area in particular; therefore, it is also important to have regulation and guidelines on the use of antibiotics at country level.

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Assessment of bacteriological quality and handling of bovine raw milk collected from communal areas in Mahikeng, SA

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The consumption of raw bovine milk is gradually increasing worldwide due to various reasons including its health properties, nutritional benefits and affordability. The aim of this study was to investigate the occurrence and antibiotic resistance profiles of pathogenic bacteria in raw bovine milk obtained from communal farms in Mahikeng, North-West Province of South Africa. The study also investigated milk handling practices at farm level. A total of 168 raw milk samples were collected from communal farms/households in 8 selected villages in Mahikeng between September 2017 and January 2018. All raw milk samples tested had total bacterial count ranging from 1.94 x 10⁷ and 4.36 x 10⁷, which was higher than the acceptable level of 5.0 x 10⁴ cfu/ml. A total of 56 bacterial species including Staphylococcus aureus, Staphylococcus equorum, Enterococcus sp., Enterobacter sp., Clostridium sp., Salmonella Typhimurium, Escherichia coli, Shigella species, Bacillus sp., Alcaligenes faecalis, Citrobacter braakii, Proteus hauseri, Providencia species, Lactococcus garvieae, Lactococcus lactis and Weissella cibaria were isolated from all the milk samples tested. Disc-diffusion method was used to determine antibiotic resistance profiles of the isolates against 8 commonly used antibiotics and it was found that only 1 out of 56 isolates (Weissella cibaria) was resistant to one antibiotic while the rest were resistant to more than one antibiotic. Moreover, most (46.4%) of the bacterial isolates were susceptible to Norfloxacin while most (53.6%) were resistant to Streptomycin. It was observed that milk handling practices at farm level were poor with lack of proper hygiene practices in most farms, example being that only 3% of the respondents indicated that they wash their hands without using soap or disinfectants before milking and the rest of the respondents reported not to wash their hands at all. Based on the results of this study which demonstrated poor quality of raw milk produced by communal dairy farmers in Mahikeng, it was therefore concluded that such milk is not safe for human consumption.

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Serum biochemical parameters and possible correlations between different cow reproductive conditions

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Background

In veterinary medicine, the analysis of biochemical blood parameter is an important metabolic profile test in cows [1] Serum metabolic profile have been widely used in animal health as a predictive tool for abnormalities in the reproductive system and in risk assessment of cattle metabolic disorders [2].

Objective(s)

The aim of this study was to determine cow serum metabolites in cases of dystocia, downer cow syndrome, abortion, retained placenta and vaginal prolapse.

Method and Materials

The study was conducted in Mafikeng area of the North West Province of South Africa. An overall blood sample of 179 was collected from cases of cows experiencing dystocia (n=50), downer cow syndrome (n=34), retained placenta (n=13), vaginal prolapse (n=16) and abortions (n=69) during the reports the North West University animal hospital in Mafikeng Campus. Convenient sampling method was employed where by sample collected following reports of cases. Biochemical metabolites tested in this study were total protein, AST, Urea, Chloride, Potassium, Sodium, Lipase, Cholesterol, Ammonia, Uric acid, Triglycerides and Creatinine kinase, Calcium. The data were analysed using SPSS version 25.

Results

Significant differences were seen in the concentrations of Urea/BUN, Total bilirubin, Aspartate aminotransferase (AST), ammonia and lipase. During the occurrence of abortions, retained placenta, vaginal prolapse, dystocia and downer cow syndrome the serum biochemistry is significantly altered. The result also suggests that adequate energy supply during and after gestation is important in reducing the incidences of reproductive conditions.

Discussion and Recommendations

The incidences of reproductive conditions in communal areas are linked to poor nutrition during the transition based on the abnormal serum metabolite assessment of the current study. Adoption of a regular metabolic profiling can be a useful method that can assist to alter the status of reproductive performance in rural farm by enabling early detection of possible calving and post calving disorders.

References

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Pre and post ovariohysterectomy study of haemopoetic cell profile of bitches presented at Dale Beighle Veterinary Hospital (NWU, Mafikeng Campus)

Speaker / Author: Pule, L.P.¹ Co-author(s): Mefane, M.¹

Background

Haemopoetic cells perform a diverse range of functions from the transport of gases and nutrients to acting as a buffer, stabilizing body temperature and defending against pathogens. At Dale Beighle Veterinary Hospital, ovariohysterectomy is one of the most frequently performed surgical operations in dogs for different reasons

Objective(s)

To calculate the percentages of haemopoetic cell pre- and -post ovariohysterectomy. To evaluate the accepted level of platelets, red blood cell, white blood cell count found per slide of animal that goes through surgery

Method and Materials

Five bitches were randomly selected and have their haemopoetic cells evaluated via a blood smear

Results

The study revealed that all the bitches haemopoetic cell were within normal limits except that bitches (P1 and P2) had a mild lymphocytosis that could have been due to the effects of catechol amine/epinephrine release (fear or excitement) thus lymphocytosis

Discussion and Recommendations

Mild lymphocytosis have no effect unto the outcomes of the surgery other than having a look unto ways that can be instituted to further improve handling of patients prior and post-surgery. Evaluation of the blood smear is the least costly exercise which every clinician should execute pre and post any surgery to combat pre or post-surgery complication.

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The impact of storage facilities on animal feed quality with reference to mycotoxin contamination around Ngaka Modiri Molema District, North West Province of South Africa

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Background

The improper storage system of feed is a major factor influencing the presence of fungi and mycotoxin contamination.

Objective(s)

To assess the effects of these storage facility type on fungal contamination and mycotoxins accumulation in animal feed collected from farmers and commercial feed suppliers

To quantify the fungi and mycotoxin contamination in animal feed in different storage conditions in the Ngaka Modiri Molema District

Method and Materials

The moisture content was determined using the oven drying method, and fungal isolation and identification were performed using serial dilution and cultured on malt extract agar (MEA), potato dextrose agar (PDA), and Sabouraud dextrose agar (SDA) media. Isolated fungi were confirmed using the molecular techniques and Polymerase Chain Reaction (PCR). The mycotoxins extraction, determination, and quantification were done using the ELISA and HPLC and TLC methods.

Results

It was noted that major challenges faced by emerging farmers versus feed commercial suppliers were that they were not knowledgeable about proper feed storage, effects of mycotoxin contamination on feed and, not educationally trained. It was also found in this study that participated farmers mainly used two types of storage systems, about 41.7% used open storage system and 58.3% used closed storage systems and their animal feeds were preserved in bags or dustbin, whilst feed commercial suppliers mainly used closed storage.

Discussion and Recommendations

The study clearly showed that both closed and open storages had fungal and mycotoxin contamination. Although the closed storages showed high contamination with fungi and mycotoxins, the study noted that this was due to improper control of the environment in the storage. Feed quality regarding fungi and mycotoxin remain primarily a training issue for farmers so they can be able to control the storage and reduce the risk of contamination. Therefore, environmental control is the key to fungal and mycotoxin control

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A case control study of risk factors for bovine brucellosis in KwaZulu-Natal, South Africa

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Background

Few epidemiological studies of brucellosis have been undertaken in South Africa and consequently, little is known about the drivers of infection.

Objective(s)

A case-control study was undertaken to address this gap.

Method and Materials

73 case and 102 control herds were recruited from the northern part of KwaZulu-Natal. These district municipalities were chosen because six had experienced cases of brucellosis, either in communal or commercial herds. Livestock owners or employees were interviewed using pre-tested questionnaires. A range of risk factors were identified and assessed including herd characteristics, management factors and knowledge of farm personnel.

Results

The risk factors identified were the herd size (a risk), with the odds increasing with increase in herd size up to 26 cattle, the number and proportion of heifers, being government sponsored was found to be protective, presence of sheep and goats (risk), number of sheep and goats (risk), knowing the status of neighbouring farm (protective), presence of wild ruminants in the neighbouring farm (risk), brucellosis clinical signs in cattle and owners receiving training in the control of brucellosis.

Discussion and Recommendations

The study provided valuable information on drivers for brucellosis and will assist owners and programme managers in the control of bovine brucellosis and thus contribute to the on-going eradication programs in KwaZulu-Natal.

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The use of bulk tank milk testing as an adjunct to other udder health evaluation methods

Speaker / Author: Schmidt, T.1

Co-author(s): Nienaber, J.¹ and van der Leek, M.²

Background

Routine bulk tank (BT) milk testing can be used as an adjunct to other methods to monitor milk quality and herd udder health. Total bacterial counts combined with the enumeration of psychotropic and thermoduric bacteria in tank samples can provide useful information on the cleanliness of milking procedures and equipment, the effectiveness of milk cooling and system sanitation. Species- or group-specific differential counts can provide further information on the occurrence of mastitis pathogens. The purpose of this investigation is to evaluate the usefulness of routine BT testing under local conditions.

Materials and Methods

Four herds are enrolled in this study which commenced in September 2018. Bulk tank samples are collected every second week and tested following guidelines issued by the College of Veterinary Medicine (Cornell University). In addition to BT analysis, herd tests are carried out quarterly and all cases of clinical mastitis are being cultured. Dairy parlour audits and questionnaires covering herd management practices were completed.

Results and Discussion

For each herd, test data is being collated and temporal trends monitored. Vast differences in overall milk quality is evident between herds. Whilst the two high-producing herds in this study are consistently producing quality milk with low SCC (< 200,000 cells/ml) and total bacterial counts, the other two herds are struggling with high BTSCC (> 300 000 cells/ml) and total bacterial counts (> 20 000 cells/ml). Psychrophile counts, when interpreted in conjunction with total bacterial counts, are exceptionally high in all study herds. In at least one herd (Herd C) the high psychrophile count is attributable to the high incidence of environmental sub-clinical mastitis in the herd. In the other herds the problem appears to be multifactorial being influenced by poor udder preparation practices (Herds B and D), problems with cleaning of equipment (Herd A) and adequate cooling of milk in tanks (Herd D).

Conclusions

The use of bulk tank milk analysis as an adjunct to existing udder health monitoring tools should be a consideration in the quest to produce milk of the highest quality.

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