Proceedings of the 13th annual congress of the Southern African Society for Veterinary Epidemiology and Preventive Medicine

19-21 August 2015

SOUTHERN
AFRICAN
SOCIETY FOR
VETERINARY
EPIDEMIOLOGY &
PREVENTIVE
MEDICINE

ACKNOWLEDGEMENTS

CONTINUING EDUCATION PRESENTERS

Prof Gavin Thomson
Director: TAD Scientific
Pretoria, South Africa

Dr Louis van Schalkwyk
State Veterinarian: Department of Agriculture, Forestry and Fisheries
Skukuza, Kruger National Park, South Africa

Prof Peter Thompson
Epidemiology Section, Department of Production Animal Studies,
Faculty of Veterinary Science, University of Pretoria, South Africa

SPONSORSHIPS

TABLE OF CONTENTS

CONTINUING EDUCATION PRESENTATION: EPIDEMIOLOGY AND THE COMMODITY-BASED TRADE SAGA

Thomson, G[1]

SUMMARY

No summary available at time of publication.

1. TAD Scientific

Pretoria, South Africa

Email: gavin@tadscientific.co.za

CONTINUING EDUCATION PRESENTATION: COMMUNAL CATTLE DEMOGRAPHICS AT THE WILDLIFE-LIVESTOCK INTERFACE OF THE KRUGER NATIONAL PARK, SOUTH AFRICA

Van Schalkwyk, O. L.[1], De Clercq, E. M., De Pus, C., Hendrickx, G., Van den Bossche, P. & Knobel, L.

ABSTRACT

In South Africa, communal livestock farming is the predominant farming system in the foot-and-mouth disease control zone adjacent to the Kruger National Park (KNP) and its adjoining private and provincial nature reserves (APNR), where persistently-infected African buffaloes (*Syncerus caffer*) roam. During routine veterinary inspections of cattle in this area, a large amount of production and demographic parameters are being recorded. These data were collated for a five-year period (2003-2007) in three study sites, to better understand the temporal dynamics and spatial heterogeneity in this system. A latitudinal gradient in both human and cattle population densities was observed, decreasing from south to north. Rainfall and human population density alone could explain 71% of the variation in cattle density. Over the study period, the northern and central study sites showed an overall decrease in total cattle (15.1% and 2.9%, respectively), whereas a 28.6% increase was recorded in the southern study site. In contrast to cattle numbers, the number of cattle owners remained stable during the study period. Only 4.0% of households in the southern study site own cattle, compared to 13.7% and 12.7% in the northern and central study sites, respectively. The overall annual calving rate was 23.8% (as proportion of the entire herd). Annual mortality rates ranged from 2.4% - 3.2%. Spatio-temporal mortality clusters were characterised by significantly lower normalised difference vegetation index (NDVI) and rainfall values in the preceding season, rather than the current one. The northern study site recorded low calf mortality (2.1%) compared to the southern study site (11.6%). Annual offtake in the form of slaughter averaged 0.2%, 11.7%, and 11.0% in the northern, central and southern study sites, respectively. These figures provide valuable baseline data and demonstrate that there is considerable spatial heterogeneity in cattle demography and production at this wildlife-livestock interface. This is important to take into consideration when performing disease risk assessments or designing disease control systems.

(This work has been submitted for publication in Geospatial Health)

1 Tel.: +27 (0) 13 735 5641

Email: lvs@vodamail.co.za

CONTINUING EDUCATION PRESENTATION:
CHOOSING STATISTICS FOR YOUR WORK - A BRIEF REVIEW

Thompson, P.

SUMMARY

No summary available at time of publication.

1 Epidemiology Section

Department of Production Animal Studies,

Faculty of Veterinary Science,

University of Pretoria,

Onderstepoort, 0110,

South Africa;

*email: peter.thompson@up.ac.za

RAW MILK VENDORS ARE HERE TO STAY – HOW TO DECREASE THE PUBLIC HEALTH RISK?

Woods, P.[a*], Burumu, J.[b], Richardson-Kageler, S.J.[a], & Makaya, P[b].

PURPOSE
Zimbabwe has seen a surge in the last decade of informal roadside milk markets with smallholder and resettled farmers selling milk locally. These "illegal" milk sales occur parallel to existing formal milk marketing and public health systems. Vendor distribution, milk suppliers, and potential hazards posed by informal milk sales in Zimbabwe are not known.

METHODS
All informal milk vendors located along the 7 major roads going into the capital Harare from 110 km radius were interviewed with structured questionnaires about their raw milk sources, management and sales from December 2014 to February 2015. Purchased milk and vendor's site water samples were cultured at Central Veterinary Laboratories, Harare

RESULTS
75 informal milk vendors selling raw milk were interviewed and milk sampled. The average milk volume for sale was 17L +/- SD = 9.7 and was sold in Coke bottles. Most vendors purchased milk for resale, only 28% sold milk from their own farms. 57% milk samples had TBC > 300 cfu/ml and "milk from own farm" related to safe TBC levels (χ^2=10.27, p=0.001). Coliform levels (mean ±SD) of 2±2.11 differed between categories of selling points (F=4.961 DF=5 p<0.001). Transport by bicycle from source was associated with *E.coli* (χ^2=8.46, p=0.01) (prevalence 4%), and by foot together with volume milk for sale (β=4.807 p=0.001 β=0.264 p=0.003) for *S.aureus* (44%). While vendors' knowledge of milk hygiene was low, income from sales was important, especially for women.

CONCLUSIONS
The milk sold by vendors included product that was either risky or possibly safe. Health education of vendors and the consumer would increase public safety.

RELEVANCE
National efforts to increase local milk supplies have also resulted in higher numbers of smallholder and "new" dairy farmers, entrepreneurial vendors and increased public health risks. Public health policies should consider and engage this emerging vendor sector that provides low priced milk and livelihoods.

a University of Zimbabwe, Faculty of Agriculture, P.O. Box MP 167, Mt. Pleasant, Harare.

b Central Veterinary Laboratories, Ministry of Agriculture, Mechanisation and Irrigation Development, Harare, Zimbabwe.

* Tel: +263 773 236 152, Email: pwoods.zim@gmail.com

EMERGENCE OF ANTIGENIC VARIANTS OF SAT2 FOOT-AND-MOUTH DISEASE OUTBREAK VIRUSES AT THE WILDLIFE/LIVESTOCK INTERFACE IN SOUTH AFRICA

Blignaut, B.[1,3], van Heerden, J.[1], Reininghaus, B.[2], Heath, L.[1] & Fosgate, G.T.[3]

ABSTRACT

The South African Territories (SAT) type foot-and-mouth disease viruses (FMDV) are endemic to the greater Kruger National Park (KNP) area in South Africa, where it is maintained through persistent infections of African buffalo. The occurrence of FMDV within the KNP constitutes a continual threat to the livestock industry. To expand on knowledge of FMDV diversity, the genetic and antigenic relatedness of SAT2 type viruses isolated from cattle in 2013/2014 were investigated. Molecular epidemiological relationships of the viruses were determined by sequencing and phylogenetic analysis. Genetically disparate viruses were chosen to determine neutralisation titres between outbreak viruses using virus neutralisation tests (VNT) against four reference sera. Differentiation of variants was determined by nucleotide sequence comparison of the outer capsid proteins to verify amino acids contributing to antigenicity. In addition, the antigenic relatedness (r1-values) of the outbreak viruses and the most suitable vaccine match was determined.

Phylogenetic analysis of the recent outbreak viruses revealed their genetic relatedness to other SAT2 isolates from topotype I (South Africa, Zimbabwe and Mozambique). The SAT2 outbreak viruses (2013/2014) are genetically distinct from previously isolated viruses (2011 and 2012). High neutralisation titres were observed for all outbreak viruses tested against the reference sera representative of viruses from the endemic area in South Africa, as well as Zimbabwe. However, cross-neutralisation data for the outbreak viruses yielded different antigenic profiles. Comparison of the outbreak viruses with reference sera indicated a good vaccine match with 75% (12/16) of r1-values > 0.4, 13% (2/16) of r1-values between 0.3 and 0.4, and 13% (2/16) of r1-values < 0.3. The r1-values for the outbreak viruses were 0.4 and above for the South African vaccine strains. These results confirm the genetic and antigenic variability of SAT2 viruses, emphasising that continuous characterisation of field viruses is important with regards to determining the occurrence of new virus strains, epidemiological surveillance aspects and vaccination.

1 Transboundary Animal Diseases Programme, Onderstepoort Veterinary Institute, Agricultural Research Council, Onderstepoort, 0110, South Africa

2 Mpumalanga Veterinary Services, Orpen, Mpumalanga, South Africa

3 Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Onderstepoort, 0110, South Africa

* Belinda Blignaut Tel +27 12 529 9584/9250 Email: bohmerb@arc.agric.za

SEROLOGICAL SURVEILLANCE OF RABIES VIRUS NEUTRALISING ANTIBODIES IN DOGS FOLLOWING VACCINATION IN LIMPOPO PROVINCE, SOUTH AFRICA

Ngoepe, E.[a], Mathuloe, H.[a], Babi, F.[b], & Sabeta, C.[a]

ABSTRACT

Rabies is a prevalent disease in South Africa and endemic in rural and peri-urban areas with high human and dog population densities. Limpopo province has experienced periodic or sporadic dog rabies outbreaks since the introduction of the disease in the country during the 1950s. The most recent major dog rabies outbreak in the province occurred during 2005/2006 in Vhembe district with at least 22 human deaths. Following the outbreak, dog rabies vaccination campaigns were regularly undertaken and these interventions resulted in a significant reduction of human rabies deaths from 22 in 2005/2006 to 3 in 2010. Rabies can therefore be successfully controlled and prevented through pre-exposure vaccination of the dog population in a given geographic locality.

Pre-exposure vaccination of dogs not only leads to a decline in dog rabies but a rapid reduction in demand for post exposure prophylaxis. However, sufficient rabies virus neutralisation antibodies is the key to herd immunity and controlling of the disease. This study investigated rabies virus neutralising antibody levels in randomly selected or available dogs within Thulamela municipality in Vhembe district, Limpopo province.

It was found that 28% (n=16) of animals had antibody titre above the threshold level of 0.5 IU/ml whereas 72% (n=41) had antibody titres below 0.5 IU/ml, which indicated that 72% of animals included for testing did not have sufficient neutralising antibodies against rabies virus. Therefore, lack of awareness and education in communities about rabies and dog vaccination may results in small numbers of animals being presented for vaccination. Biannual vaccination campaigns repeated every 6-8 months should be considered and encouraged together with serological monitoring to ensure successful vaccination.

a Rabies Unit,

Onderstepoort Veterinary Institute,

Private Bag X05, Onderstepoort, 0110

Pretoria, South Africa

b Limpopo Rabies Advisory Group,

Department of Agriculture: Veterinary Services,

Limpopo province, South Africa

OLD WORLD ALPHAVIRUSES, SINDBIS AND MIDDELBURG AS PATHOGENS IN WILDLIFE AND DOMESTIC LIVESTOCK

Venter, M. [*1,4], Steyn, J, Pretorius, M. [1], van Niekerk, S. [1], Human, S [1], Van Eeden, C. [1,3], Williams, J. [2] & Steyl, J. [2]

BACKGROUND AND AIM

Alphaviruses in the Togaviridae family include important zoonotic vector borne viruses with epidemic potential. Old World alphaviruses were traditionally associated with febrile disease and arthralgia, and thought to be rarely fatal while, New World alphaviruses such as Eastern and Western Equine Enchephalitis viruses are often associated with neurologic disease in horses and potentially severe neurological disease in humans. During a surveillance project in horses with fever of unknown origin and/or neurological disease, between 2008-2013 we identified the Old World alphaviruses, Middelburg (MIDV) and Sindbis (SINV), either as single infections or as co-infections with other arboviruses. SINV cases were mostly mild however of 48 cases of MIDV, 68% displayed neurologic disease, 27% being fatal and several cases detected as single infections in brain tissue of horses with lesions displaying mild to moderate meningoencephalitis. This implicates MIDV in-particular as a neuro-pathogen in horses and suggests possible zoonotic potential. Other equine clinical signs included stiffness, fever, swollen limbs, seizures, paralysis and death.
The equine findings prompted us to similarly investigate cases of undiagnosed neurological disease in other species including livestock and wildlife, as well as to investigate potential reservoirs, the geographic range, seasonality across the country and vectors in areas where cases had been detected.

METHODS

EDTA/clotted blood, cerebrospinal fluid (CSF) and/or post mortem central nervous system (CNS) and spleen tissue from domestic livestock and wild animals (2010-2015) displaying unexplained neurological disease and/or fever submitted to the Zoonoses Research Unit (ZRU), University of Pretoria were screened with an alphavirus family specific RT-PCR and typed by realtime PCR. Differential diagnosis tests included PCRs for flaviviruses (West Nile virus (WNV) and Wesselsbron virus), Shunivirus and equine encephalosis virus (EEV) at ZRU and rabies IFT that was done at Onderstpoort Veterinary institute. All positive cases were confirmed by sequencing and phylogenetic analysis. Histopathology was performed at the Onderstepoort Veterinary Faculty, Section of Pathology. Mosquito vectors were collected at 2 sites in Gauteng where cases in horses had been detected as well as in Lapalala and Marakele game reserves in Limpopo Province where cases in wildlife occurred.

RESULTS

Between 2010 and 2015, 21/359 specimens from species other than horses tested positive for Sindbis (5); Middelburg (12); Shunivirus (4), WNV (3); and EEV (1) representing 6/37 rhinoceros, 3/22 porcine, 4/101 bovine, 1/10 crocodiles, 1/3 giraffe and 4/76 antelope. Co-infections were detected in 4 cases, a Ayrshire calf with MIDV and WNV, a genet found dead in Kruger National Park with MIDV and SINV in brain, liver and spleen, two white rhinoceroses one with MIDV and Shuni and one with MIDV and EEV both in brain. Histopathology of the brain and spinal cord of the wildlife cases were subtle, but were characterised by mild, scattered perivascular lymphocytic cuffing, white matter microgliosis and widespread glial apoptosis in the neuropil. Cases were from wildlife reserves in Limpopo, Mpumalanga, Freestate, Gauteng, Swaziland and North West. Horse cases were from Gauteng, Natal, Limpopo, the Western and Eastern Cape suggesting geographic distribution throughout the country. Mosquitoes collected in Gauteng tested positive from April to June while Middelburg virus was identified in Limpopo in September to October as well.
These results suggest a wide geographic distribution and species range with possible maintenance in different reservoirs and geographic regions year round.

CONCLUSION

Alphaviruses identified in wildlife and farm animals experiencing neurological disease were confirmed by RT-PCR as SINV and MIDV. Isolations directly from the brain and histopathological lesions suggest an association with neurological disease and death in these animals. Cases were severe and due to the zoonotic potential of this family of viruses (these viruses), sero-prevalence and neurological cases should also be investigated in high risk humans to determine the association of MIDV and SINV with human neurological disease as well.

1. Faculty of Health Sciences, University of Pretoria, South Africa;

2. Faculty of Veterinary Science, University of Pretoria, Onderstepoort, South Africa

3. National Institute for Communicable Diseases, Sandringham, South Africa

4. Global Disease Detection Centre, Division of Global Health Protection, US-CDC South Africa office.

* Email: yds8@cdc.gov

REFERENCES

1.   Venter, M., et al., Fatal neurologic disease and abortion in mare infected with lineage 1 West Nile virus, South Africa. *Emerg Infect Dis*, 2011. 17(8): p. 1534-6.

2.   Venter, M., et al., Lineage 2 west nile virus as cause of fatal neurologic disease in horses, South Africa. *Emerg Infect Dis*, 2009. 15(6): p. 877-84.

3.   van Eeden, C., et al., Shuni virus as cause of neurologic disease in horses. *Emerg Infect Dis*, 2012. 18(2): p. 318-21.

THE IMMUNE RESPONSE ELICITED BY INTRACELLULAR BACTERIA WITH SPECIAL REFERAL TO *S. AUREUS* MASTITIS AND THE DANGER OF RESISTANCE AND ZOONOSES OF THIS PATHOGEN GLOBALLY

Kotze, S.M.[*1]

ABSTRACT

S. aureus is known worldwide and varies from symptomless nasal carriers to highly fatal suppurative infection in hospitals (MRSA) and now also in communities (CAMRSA (Bohme et al, 2013). This pathogen has a vast array of virulent factors and is less known as a zoonosis or an intracellular pathogen (Todar, 2008). It is highly feared due to extremely resistant strains that have emerged and a successful vaccine in humans is still to be developed. In animals it is one of the major causes of mastitis and reacts poorly on treatment with resultant culling of cows and vast economic implications (Castagliuolo, I. et al., 2006). This bacterium survives intracellularly and hides from the immune system in various ways. It also controls its display of virulence factors controlled by global regulators and poses a severe challenge in dairies (Knoll et al, 2012). It seems to have the ability to harbour resistant strains in animal species as asymptomatic carriers serving as a potential source of infection for humans. It also poses a risk in food safety being considered a health product. The process of cellular immunity is discussed as well as intracellular survival mechanisms. The process of resistance development is described and the danger thereof. A short overview of the immune response in the cow is discussed with reference to data from a field trial and the extent of resistance in SA herds as determined by a field trial.

1 Head: Kroonstad Provincial Veterinary Laboratory

Department of Agriculture and Rural Development

Free State Province, South Africa

* Tel: 056 212 2671, Email: smkotze@fs.agric.za

MONITORING AND EVALUATING THE ONE HEALTH DETECTION AND RESPONSE TO RABIES, GAUTENG, 2015

Govindasamy, K.[1]*, Harris, B.N. & Mashaole, M.

BACKGROUND

The IHR (2005) identified surveillance and response capacity for emerging infectious diseases (EIDs) as one of the key areas of core capacity development for implementation in South Africa (SA). Establishing mechanisms for detecting and responding to zoonotic events (ZE) and potential zoonoses is set down as indicator 17 of the IHR (2005) selected for reporting to the World Health Assembly. In order to achieve this it is necessary to promote inter-sectorial cooperation between human and animal health sectors.

Rabies is a fatal zoonotic disease of mammals, annually affecting more than 55 000 people globally, many of whom are children. Animal rabies continues to be an endemic disease in SA and even though Gauteng has been the least affected of all provinces from 2006–2010, it experienced an animal rabies outbreak and a human death due to rabies in 2010. Due to a case of animal rabies in Region C of the City of Johannesburg (CoJ) district in April 2015, a vaccination campaign was launched by the Gauteng Department of Agriculture and Rural Development (GDARD). Despite the existence of protocols for inter-sectorial collaboration to control rabies, there is no published data on a descriptive analysis of surveillance and control data being used as evidence of a district's core capacity to meet IHR requirements to detect and respond to a zoonotic event. The City of Johannesburg (CoJ) capacity to detect and respond to a zoonotic event has not previously been evaluated. This study makes use of the IHR evaluation tool to measure the response of CoJ to the 2010 rabies outbreak.

OBJECTIVE

(1) Determine WHO-IHR core capacity score (2010) of district health unit to detect and respond to zoonotic event of PHI. (2) Conduct a descriptive analysis of rabies relevant data in 2010. (2.a) Compare the descriptive analysis reports of 2010 with 2015 to highlight One Health collaborative measures that have been achieved in the interim.

METHODOLOGY

The study was set in the catchment area of the CoJ, Gauteng province. The CoJ is divided into 7 regions (Region A – G). Interviews were conducted with key stakeholders in the Department of Health, Department of Agriculture and laboratory services at the district and provincial level of government using the standardized WHO-IHR questionnaire (in 2010) and the district health unit's core capacity score for the detection and response to a zoonotic event of national or international PHI was calculated using the WHO-IHR rubric . A descriptive analysis was done of data generated by relevant zoonotic surveillance databases over the course of the Rabies 2010 outbreak in Gauteng as well as a descriptive analysis of data generated by CoJ in 2014-2015.

FINDINGS

The WHO-IHR Core capacity-score for 2010 was 89%. However this is a paradox due to the fact that despite this high score, there was a human case of rabies in Gauteng that occurred in Region D (Soweto), reported on the 3 October 2010 occurring in a 2 year old. Animal rabies cases were prominent in the second half of 2010, and began to wane in 2011. The CoJ surveillance for humans bitten by animals and animal rabies began from August 2011 in response to the outbreak of animal rabies in Gauteng. The human rabies case occurred on 3 October 2010. This was also the month with the highest number (12 / 34) of animal rabies cases reported. 76% of all reported animal rabies cases reported to CoJ occurred between August and December of 2010, with no cases reported in 2012. A total of 553 rabies related events were responded to by CoJ from August 2010 to November 2012. Of these events, 94% (n=518) were animal bites of which 77% (n=401) were dog bites. From August 2010 to June 2011, animal bites were differentiated by species responsible for the bite. From July 2012 all animal species bites were no longer specified. Animal rabies cases made up 6% of the total events responded to by the district. Region B is located centrally in the CoJ district and reported the highest number of animal bites (33%) but only 1.1% of all animal rabies cases for the study period. The first cases of animal rabies were detected in June 2010 (State Veterinary and OVI data sets) in this region but the majority of positive animal rabies cases (87%) were reported from the southern regions of CoJ, displaying the area of the greatest impact of the animal rabies outbreak. In 2010 the greatest number of animal bite cases reported occurred in children aged between 0 – 14 years, with a peak in the 5 – 9 year olds. A second peak of animal bites occurred in 30 – 34 year olds. The positive animal rabies cases were reported by adults over 30 years old.

1. Gauteng Department of Agriculture and Rural Development (GDARD) Veterinary Services Animal Health and Epidemiology Directorate

* KRPASHA.GOVINDASAMY@gauteng.gov.za

RECOMMENDATIONS

A collaboration provincial committee should be identified and formed between key stakeholders of the district and provincial zoonotic surveillance system to produce a protocol that defines measurable indicators for selected zoonotic diseases that monitor each attribute identified in the WHO-IHR to attain core capacity to detect and respond to zoonotic events of national and international PHI. A relational one health database management system incorporating animal health and public health variables can be used with the existing WHO-IHR tool as an evaluation tool of the One Health Surveillance and Control System at provincial and district level to monitor the capacity at these levels to detect and respond to ZE of public health importance. Regular descriptive analyses may be done on data generated by this One Health database to produce evidence on which vaccination and awareness campaigns can be based.

CONCLUSIONS

Due to the zoonotic nature of rabies, the protection of public health from rabies is informed by the analysis of surveillance data from human and animal populations. Aggregation of agency-specific data into one database application will enable more comprehensive data analysis and effective communication among participating agencies leading to focussed and evidence based rabies vaccination and awareness campaigns.

ACKNOWLEDGEMENTS

REFERENCES

IHR Monitoring Framework: Checklist and indicators for monitoring progress in the implementation of IHR Core Capacities in State Parties.
http://www.who.int/ihr/Processes_of_IHR_Monitoring_framework_and_Indicators.pdf

World Health Organization. Protocol for assessing national surveillance and response capacities for the International Health Regulations (2005): In accordance with Annex 1. A guide for assessment teams. 2010.
http://www.who.int/ihr/publications/who_hse_ihr_201007_en.pdf

CONTINUING EDUCATION PRESENTATION: FOOT AND MOUTH DISEASE IN SOUTHERN AFRICA: WHAT WE NO LONGER UNDERSTAND

Thomson, G[1]

SUMMARY

No summary available at time of publication.

1. TAD Scientific

Pretoria, South Africa

Email: gavin@tadscientific.co.za

CONTINUING EDUCATION PRESENTATION:
CATTLE MOVEMENT AND DISTRIBUTION PATTERNS IN RELATION TO DISEASE RISK IN AREAS ADJACENT TO THE KRUGER NATIONAL PARK, SOUTH AFRICA

Van Schalkwyk, O. L.[1], De Clercq, E. M., De Pus, C., Hendrickx, G., Van den Bossche, P. & Knobel, L.

SUMMARY

Communal livestock farming makes an important contribution to the livelihoods of a large number of households in South Africa. Current knowledge suggests that there is very little organisation of grazing in these farming areas, with only a few studies that have looked at cattle movement and distribution patterns of these cattle herds. This study investigates the grazing patterns, home ranges and habitat suitability of communally-farmed and smallholder cattle in four study sites along the foot-and-mouth (FMD) infected zone in South Africa, utilising Global Position System (GPS) data from handheld devices and animal collars. Home range was determined with the time-based local convex hull (T-LoCoH) method, whilst habitat suitability was determined through maximum entropy modelling. Daily activity budgets showed walking peaks in the mornings and afternoons, with grazing occurring mostly from late morning to early afternoon. The grazing pattern was also bimodal in sites where no herding of cattle occurred. More grazing occurred during the warm wet season in the northern site and on smallholder farms. Grazing trajectories in the south (where cattle were kraaled daily) were the shortest and significantly longer in the northern site and smallholder farms where animals were often left to roam free. The maximum grazing radius was attained around midday in the communal areas (median ranging from 2-3km). A more pronounced positive relation between a trajectory's grazing radius and its maximum distance from water in the cool dry season, especially in the central site, suggests dependence on water as an important driver of grazing patterns. Utilisation of cultivated fields was significantly elevated during the early dry season. Home range estimates (95%) were larger in the cool dry season, suggesting concentration of animals in specific areas during the warm wet season. Habitat suitability, determined through maximum entropy modelling, echoed this apparent contraction of preferred grazing areas during the warm wet season. Combining these results with similar stray buffalo suitability models and least cost path analyses, shows their application in estimating disease risk at the wildlife-livestock interface, and the importance of better understanding livestock farming systems at such interfaces.

---

1 Tel.: +27 (0) 13 735 5641

Email: lvs@vodamail.co.za

DEMOGRAPHICS OF AN OWNED DOG POPULATION IN BUSHBUCKRIDGE, MPUMALANGA PROVINCE, SOUTH AFRICA

Akerele, O.A.[1*], Knobel, D.L. & van Rooyen, J.

ABSTRACT

Rabies can be controlled and human deaths reduced through the mass vaccination of domestic dogs, as recorded in some parts of the world. However, in sub-Saharan Africa rabies infection is on the increase, largely due to the population dynamics that favour disease transmission. The demographics of the dog population in this study area are unknown. This study describes the demography of owned dogs in a rural sub-Saharan African setting. The study took place in Hluvukani, in the Mnisi area of Bushbuckridge Local Municipality, Mpumalanga Province in South Africa. A full census of the dog population in the study area was conducted at two time points. The first census took place from July through October 2011, followed by a second census from May through October 2013. The first census was accompanied by a house-to-house rabies vaccination campaign.

The demographic surveillance area covered 10.4 km^2 and comprised around 2,000 households, with a mean household size of 4.9, a density of 913 people/km2 and a human:dog ratio of 14:1. Results in the first and second census respectively indicated a dog density of 77 dogs/km^2 and 84 dogs/km^2, and a sex ratio of 1.32 and 1.47 males per female. Household indicators in the first and second censuses respectively showed the number of households as 1,907 and 1,939; and the number of dogs as 799 and 870. The mean number of dogs per household (standard deviation) was 0.41 (1.08) and 0.44 (1.16) and the number of dog-owning households was 393 (20.6%) and 416 (21.5%). The mean number of dogs per dog owning household (standard deviation) was 2.03 (1.56) and 2.09 (1.71). Vaccination coverage against rabies achieved by the campaign during the first census was 68.2% (545/799). Vaccination coverage at the time of the second census was 59% (513/870).

1 Department of Veterinary Tropical Diseases,

Faculty of Veterinary Science,

University of Pretoria,

Onderstepoort, 0110,

South Africa;

*Email: Yemi.akerele@gauteng.gov.za

VALIDATION OF DIAGNOSTIC TESTS FOR WILDLIFE

Michel, A.L.[1*]

SUMMARY

Trade in wildlife, both nationally and internationally, has been hampered by the lack of recognised diagnostic tests able to reliably detect the presence or confirm the absence of trade sensitive pathogens. The absence of validated tests for wildlife is not only a trade barrier but also a serious concern to disease control predominantly at the wildlife-livestock interface. The implementation of a guideline for the validation of diagnostic tests suitable for use in wildlife by the OIE in 2014 has laid the foundation for a much needed test validation strategy in countries with a flourishing wildlife industry such as South Africa.

BACKGROUND

The term 'wildlife' in its broadest sense encompasses captive, free-ranging and feral wild animals. Diseases of wildlife occur in all three groups and have attracted a rapidly increasingly interest worldwide as they can have a negative impact on biodiversity and conservation on the one hand and livestock and human populations living at the wildlife/livestock/human interface on the other hand[1].

Since wild animals species have been shown to be susceptible to many of the pathogens classified as trade-sensitive, zoonotic or as causes of economically important diseases, there is a need for diagnostic tools to detect their presence or, conversely, confirm their absence from wildlife, both at an individual as well as at population level[2].

Wildlife trade has therefore been a matter of growing concern for the OIE and the need for introducing an approach involving diagnostic test validation for wildlife similar to domestic animals was identified. The initiative soon met with challenges as the OIE and its experts have recognised the dichotomy in the stringent requirements for diagnostic test validation and the dire need for validated tests for wildlife which renders the latter entirely unfeasible. Between 2011 and 2013 an *ad hoc* group of experts was tasked to develop validation guidelines for tests used in wildlife which were approved and published by the OIE in May 2014[3].

CHALLENGES

The activity of diagnostic testing including test validation in wildlife populations, regardless of the purpose, starts with accessibility to good quality specimens suitable to detect the pathogen in question. However, for the majority of pathogens affecting wildlife, the pathogenesis is still poorly understood. Relevant samples must be collected from a representative number of animals, sufficient in volume/mass, be accompanied by a detailed history revealing at least the animal species, sex, age, locality, clinical signs and/or post mortem findings.

Many routine diagnostic tests that have been developed and are currently used for detecting or confirming diseases in domestic livestock have generally not been validated for wildlife but many laboratories have accepted these tests assuming their validity based on their performance in a closely related domestic animal species. The question remains as to whether there are any essential differences in diagnostic sensitivity or specificity of these tests when they are applied to wildlife samples[4].

The development of a variety of rapid and easy to perform field tests (animal-side or pen-side tests) for disease diagnosis in domestic animals has been well received by end users and these tests are becoming increasingly popular for use in wildlife. The use and interpretation of field tests is often the sole responsibility of the veterinary personnel attending to cases in the field without laboratory support. The lack of a thorough validation of these tests by the manufacturer is often not disclosed but can be detrimental to the correct interpretation of the test results. Test kits used in the field rather than under laboratory conditions should be evaluated for reproducibility of results under different environmental conditions (temperature, humidity, etc.).

Test validation is a costly process and becomes unaffordable where the throughput of diagnostic does not justify the expenses.

RESULTS AND DISCUSSION

Chapter 1.1.5. 'Principles and methods of validation of diagnostic assay for infectious diseases' of the OIE Manual of Diagnostic Tests and Vaccines for Terrestrial Animals 2013 outlines the underlying principles and stepwise approach to the validation of a diagnostic test in general. In support of this validation standard the World Assembly of Delegates of the OIE adopted the Validation Guideline 3.6.7. in 2014, which provides detailed information with regard to validation of tests for infectious diseases applicable to wildlife[3].

This Validation Guideline is considered a breakthrough in terms of rendering validation in wildlife feasible and affordable. Provisional recognition of a diagnostic test for wildlife is now possible based on the evaluation of test

1* Department Veterinary Tropical Diseases,

Faculty of Veterinary Science, University of Pretoria,

Onderstepoort, South Africa

Tel: 012 5298426, Email: anita.michel@up.ac.za

performance using limited panels of reference samples. This is especially attractive for wildlife species such as the African buffalo (*Syncerus caffer*), where validated tests exist for the closely related domestic cattle. Provisionally recognised tests not only serve the identified purpose for *ad hoc* use but afford the opportunity for longitudinal monitoring and screening of wildlife populations. Such databases are instrumental where countries are required to demonstrate freedom from infection or evidence of trends in disease prevalence and/or spread by monitoring infected wildlife populations and will, in the process, facilitate assay validation and OIE recognition[3].

REFERENCES

1.   Wiethoelter AK, Beltran-Alcrudo D, Kock R, Mor S M 2015 Global trend in infectious diseases at the wildlife-livestock interface Proceedings of the National Academy of Sciences doi 10.1073/pnas.1422741112

2.   Bengis R G 2002 Infectious diseases of wildlife: detection, diagnosis and management (Parts I and II) OIE Scientific and Technical Review 21

3.   http://www.oie.int/fileadmin/Home/eng/Health_standards/tahm/GUIDELINE_3.6.7_WILDLIFE.pdf

4.   Gardner I A, Hietala S, Boyce W M 1996 Validity of using serological tests for diagnosis of diseases in wild animals OIE Scientific and Technical Review 15:323-335

PROVISIONAL VALIDATION OF FOUR SEROLOGICAL TESTS FOR BOVINE BRUCELLOSIS IN AFRICAN BUFFALO (*SYNCERUS CAFFER*)

Dongo, J. C.[*1], Potts, A[2], E. Gorsich[3], A. Jolles[4], & Michel, A. L. M.[5]

ABSTRACT

Bovine brucellosis caused by *Brucella abortus* is a multi-species, zoonotic disease at the wildlife-livestock-community interface in South Africa. Domestic cattle and African buffaloes (*Syncerus caffer*) are known reservoirs of the disease. In South Africa, serological testing for the disease is by Rose Bengal test (RBT), serum agglutination test and complement fixation test (CFT). These tests are validated for use in cattle, a closely related species to the African buffalo. The OIE requires validation of brucellosis serological tests in every species it is used. The study aimed to evaluate the comparative diagnostic performance of the RBT, CFT, indirect enzyme-linked immunosorbent assay (IDEXX) and fluorescence polarisation assay (Diachemix) for bovine brucellosis in African buffalo and followed the OIE pathway for validation in a wildlife species where there is a test validated in a closely related species. Diagnostic sensitivity and specificity were determined after adjustment of cut-off values by receiver-operator characteristics analysis. Repeatability was assessed. The index tests were all found fit to detect or confirm brucellosis in populations and individual animals. The values for DSe and DSp that were estimated will be of use in the interpretation of serological results and determination of diagnostic strategies in different circumstances

*1 Department of Agriculture, Rural Development, Land and Environmental Affairs, Mpumalanga, Department Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, Onderstepoort, South Africa, Tel: 013 766 7336, Email: jcwessels@mpg.gov.za

2 ARC-Onderstepoort Veterinary Institute,

3. Department of Environmental Sciences, Oregon State University, Corvallis OR 97331, USA

4. College of Veterinary Medicine, Oregon State University, Corvallis OR 97331, USA

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

FIELD APPLICATION OF IMMUNOASSAYS FOR THE DETECTION OF *MYCOBACTERIUM BOVIS* INFECTION IN THE AFRICAN BUFFALO (*SYNCERUS CAFFER*)

van der Heijden, E.M.D.L.[a, b], Jenkins, A.O.[a, b], Cooper, D.V.[c], Rutten, V.P.M.G.[a, b] & Michel, A.L.[b]

ABSTRACT

The African buffalo (*Syncerus caffer*) is considered the most important maintenance host of BTB (bovine tuberculosis) in wildlife in Southern Africa. The diagnosis of *Mycobacterium bovis* infection in this species mostly relies on the SICTT (single intradermal comparative tuberculin test). As an alternative, the BOVIGAM® 1G, an IFN-γ (interferon-gamma) release assay, is frequently used. The objective of this study was to compare the test performance of CMI- (cell-mediated immunity) and HI- (humoral immunity) based assays for the detection of *M. bovis* infections in buffaloes for fitness of the test purpose. Buffaloes were sampled during the annual BTB testing in the Hluhluwe-iMfolozi-Park (KwaZulu-Natal, South Africa) during June 2013. A total of 58 animals were subjected to the SICTT, 17 of these tested positive and 1 showed an inconclusive reaction. CMI based assays (B1G (BOVIGAM® 1G) and B2G (BOVIGAM® 2G)) as well as a serological assay (IDEXX TB ELISA) were used to further investigate immune responsiveness of these 18 animals and 40 SICTT negative animals. Seventeen SICTT positive and suspect buffaloes were slaughtered and a PM (post-mortem) examination was conducted. Test results of individual assays were compared with serial and parallel test interpretation. Post-mortem examination was used to confirm BTB. Lesions characteristic of BTB were found in 9 animals (52.9%). The B1G assay showed the highest individual sensitivity (85.7%) followed by the B2G assay (75%) and the IDEXX TB ELISA (43.8%). Using in parallel interpretation, the combination of the SICTT and the BOVIGAM® assay or the combination of the BOVIGAM® assay and the IDEXX TB ELISA showed the highest sensitivity (100%). In conclusion, this study has shown that the BOVIGAM® IFN-γ assay has the highest test performance and when used alone or in conjunction with the IDEXX TB ELISA it is fit for the diagnosis of BTB in free-roaming African buffaloes.

(This work has been submitted for publication)

a Division of Immunology, Department of Infectious Diseases and Immunology, Faculty of Veterinary Medicine, Utrecht University, Yalelaan 1, 3584 CL, Utrecht, The Netherlands

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

c Ezemvelo Kwazulu-Natal Wildlife, Private bag 01, St. Lucia, 3936, South Africa

*Corresponding author: Elisabeth van der Heijden, 0765906817, e.m.d.l.vanderheijden@uu.nl.

A DIRECT PCR ASSAY FOR THE DETECTION OF CONTAGIOUS EQUINE METRITIS

Jambwa, K.[*], Lee, I., Gelaw, A. & Gcebe, N.

ABSTRACT

Contagious equine metritis (CEM) is an acute, highly contagious venereal disease of horses caused by *Taylorella equigenitalis*. It is characterized by a profuse, mucopurulent vaginal discharge and early return to oestrus in most affected mares. It is spread during breeding. Undetected infected mares and stallions are the source of outbreak. CEM have a negative impact on fertility in both mares and stallions. CEM is considered to be high economic significant due to its devastating effect on the reproductive system of infected equines. These losses result due to loss of fertile in mares, embryonic loss and costs related to repeated breeding and treatment, CEM is a listed disease on the OIE list and affects a country's ability to trade. CEM was first confirmed in South Africa in April 2011 and reported to the OIE in May 2011. Before this period South Africa was regarded as a CEM free country.

The commonly used methods for diagnosis of the disease include culture, serology, Polymerase Chain Reaction (PCR) and test breeding. In this study we optimised and validated a direct PCR assay for detection of *Taylorella equigenitalis* from 245 swab and semen specimens following the Office International des Epizooties (OIE), 2013 guidelines. Cultured bacterial cells were also included in the validation. DNA extracted either directly from swabs taken from the mare's clitoral fossa, cervix and endometrium as well as from the stallion's penile sheath, penis and urethral fossa and semen, or from cultured cells was used as a template for the amplification of a 585-bp fragment of the 16S rDNA. Comparison of the PCR assay to the culture results showed that PCR was more sensitive than culture with the estimated sensitivity and specificity values of 100% each for PCR and 88% and 100% for culture, respectively. The kappa coefficient value was also estimated at 0.93 suggesting a strong agreement between the two tests. Sequencing of the PCR products confirmed that the amplified DNA was indeed *Taylorella equigenitalis* MCE9 16S rDNA. The PCR assay was therefore proven to be an alternative test for the screening, surveillance and monitoring of the disease.

*Agricultural Research Council, Onderstepoort Veterinary Institute

Corresponding Author: Ms N. Gcebe

Telephone number: 012 529 9138/140

Email: GcebeN@arc.agric.za

EFFICIENCY INDICES AND INDICATORS OF POOR PERFORMANCE AMONG EMERGING SMALL-SCALE PIG FARMERS IN THE LIMPOPO PROVINCE, SOUTH AFRICA

Mokoele, J.M., Spencer, B.T., van Leengoed, L. & Fasina, F.O.

ABSTRACT

Limpopo is a very important area for pig production in terms of animal populations and contributions to transboundary animal disease spread. Emerging small-scale pig farmers (ESSPF) are being encouraged to establish operations and spread in South Africa; however, for these farmers to perform optimally, they need to understand the basics of animal agriculture and contribute to enhancing biosecurity and efficient production systems. In the present study, the limitations to efficient production amongst ESSPF were evaluated and some improvements were suggested. It was found that the ESSPF are dominated by males and include a large percentage of older persons. A total of 26.54% of these farmers have post-matriculation qualifications. Undefined and indigenous breeds still dominate their animal genetics. The animal health technicians are the preferred channels by which farmers report diseases to the authorities (52.47%) and only one out of five (20.37%) will preferably report a disease situation direct to a veterinarian. These farmers do not vaccinate their stock, and knowledge of biosecurity is poor. Antimicrobials, especially tetracyclines, are abused. Animals that are slaughtered within the community or sold at local sale points, pension pay stations and auction markets are likely candidates for disease spread. It is recommended that the younger generations are retained and incentivised in animal agriculture. Improved training on management, health, biosecurity and better market access must be provided for the ESSPF, whilst efforts should made to consolidate these farmers into small cooperatives. The current government agricultural support system will need to be reworked to benefit the resource-poor farmers. Collaborative efforts in disease reporting and management among veterinarians, animal health technicians and extension officers will become necessary. Finally, the creation of a progressive quality grading system for ESSPF should be planned by the industry and this should be attached to a reward system that will encourage these farmers to target good farming practice.

* Tel: 073 449 6119, Email: japhta.mokoele@gmail.com,

THE AFRICAN SWINE FEVER CONTROL ZONE IN SOUTH AFRICA AND ITS CURRENT RELEVANCE

Magadla, N.R.[1, 2], Vosloo, W.[4], Heath, L.[5] & Gummow, B.[2,3]

ABSTRACT

African swine fever (ASF) has been reported in South Africa since the early 20th century. The disease has been controlled and confined to northern South Africa over the past 20 years by means of a well-defined boundary line with strict control measures and movement restrictions north and across this line. In 2012 the first outbreak of ASF outside the ASF control zone since 1996 occurred. The objective of this study was to evaluate the current relevance of the ASF control line to determine whether there was a need to re-align its trajectory given the recent outbreak and global climate and developmental changes since the line's inception. A study of ASF determinants was conducted in an area 20 km north and 20 km south of the line in Limpopo, Mpumalanga, North West and Gauteng Provinces between May 2008 and September 2012. The study confirmed that warthogs, warthog burrows and the soft tick reservoir, *Ornithodoros moubata*, are present south of the ASF control line, but no virus or viral DNA was detected in these ticks. There appears to be an increasing trend in the diurnal maximum temperature and a decrease in humidity, with no discernible changes in minimum temperatures and average rainfall along the disease control line between 1992 and 2014. The impact of these changes is uncertain. Even though the reservoir was found south of the ASF control line, the study concluded that there was no need to realign its trajectory, with the exception of Limpopo province. However, the provincial surveillance programs for both the reservoir, vector and ASF virus south of this line needs to be maintained and intensified as changing farming practices seem to favour the southwards spread of ASF virus.

1 Veterinary Services, Gauteng Department of Agriculture and Rural Development, PO Box 8769 Johannesburg 2000

2 Department of Production Animal Medicine, Faculty of Veterinary Science, University of Pretoria

3 Discipline of Veterinary Science, James Cook University, Townsville, Australia

4 CSIRO-Australian Animal Health Laboratory, Geelong, Australia

5 Agricultural Research Council, Onderstepoort Veterinary Institute, Private Bag X05, Onderstepoort, 0110

USE OF A RHVT-NDV VECTOR VACCINE IN BACKYARD CHICKENS IN NEWCASTLE DISEASE ENDEMIC AREA, GAUTENG, SOUTH AFRICA, 2014-2015

Geertsma, P.[*] & Govindasamy, K.

PURPOSE

Vectormune ND®, Ceva-Biomune, USA (VM), a rVHT-NCD vector vaccine, has been used in commercial chickens and a vaccine recovery rate of more than 80% is expected. However it has not been used in backyard chickens in Gauteng before. A study was conducted in Tarlton where numerous NCD outbreaks in both commercial and backyard sectors occurred over the last 3 years. Water-based NCD vaccine in this population has been unsuccessful. This study aimed to (1) determine the association of the VM vaccine in backyard chickens to NCD anti-body titres (2) determine the protective efficacy of VM.

METHOD

81 Boschvelders (BV) were introduced into 13 Sites (S1-S13) in 14/07. 61 of the BVs and 45 local breed (LB) chickens were vaccinated, in 14/10, with VM after baseline blood samples were taken. All birds were tagged (61 BVs and 130 LBs). The cohort was sampled monthly and Haemagglutination Inhibition (HI) tests were done. Data was captured into MS ACCESS 2013, cleaned and analysed using EXCEL and RStudio. Univariate analysis was done and an ordinal logistic regression model (Epicalc) used.

RESULTS

An outbreak of virulent NDV was confirmed on 14/12/11 in (S2). 50 birds died. A total of 21 of the study cohort were reported dead on 15/02/24. Of these 86% (18/21) were not vaccinated. 10/12 VM birds on S2 survived.

The RR of VM vaccinated (exposed) chickens dying to chickens of unknown vaccine status dying was 0.17 (95% CI = 0.06–0.5) in this endemic NCD area (when all other causes of death are ruled out) i.e. the vaccine had a protective efficacy of 83.5% (95% CI = 50.38 - 94.18). The conclusion from the ordinal logistic regression model is that the increase in titre levels to NCD significantly increases with vaccination: OR 2.2 (CI:1.2 - 4.1, p-value 5.68e-03) and some locations: (S10) OR:5.0 CI: 1.2 - 22.2 , p-value 1.47e-02 2; (S2) OR 4.4, CI- 1.2 - 17.3, p-value 1.52e-02.

CONCLUSION

Chicken deaths were significantly associated with an unknown vaccine status. The vaccination is associated with increased titre levels indicating seroconversion. The use of VM prevented 84% of deaths in the vaccinated flock.

*Department of Agriculture, Gauteng Province, Pretoria, South Africa. Email: peter.geertsma@gauteng.gov.za. Tel: 0824550835

COMPULSORY COMMUNITY SERVICE FOR VETERINARIANS IN SOUTH AFRICA 2016

Mathonsi, M.[*]

ABSTRACT

The primary objectives for Compulsory Community Service(CCS) is to promote accessibility of veterinary services particulary in under-served and resource poor areas, to distribute the veterinary profession in an equitable manner and to provide an opportunity for CCS veterinarians to acquire knowledge, critical thinking and problem-solving skills that will help their professional development.

The implementation of CCS required four phases namely: - The feasibility study which was concluded in 2007, legislative framework started in 2008 to date with significant challenges regarding difference in legal opinions, infrastructural development began in 2013 to date and lastly the deployment of CCS veterinarians in all areas of need throughout the country should begin in 2016.

*Department of Agriculture, Forestry and Fisheries

USING HEXAGON GRIDS FOR DATA COLLATION IN GEOGRAPHIC INFORMATION SYSTEMS

Grewar, J. D.[1]

INTRODUCTION

Hexagons are common in nature, and even the humble honey bee has realised that if you want to store something properly then a hexagon is the way to go. It is common practice in mapping to display collated data on a square grid background. One of the major reasons for this is that square grids form the intrinsic backdrop to most imagery, given that pixels are generally square. If seen from far enough away (or at a high resolution) square grid imagery blends away and data is seen as continuous. In general in the veterinary epidemiology context disease occurrence mapping has a relatively low resolution, and interpolating this information into a continuous raster is often not possible or useful. On the other end of the scale is when we use layers to collate data that are just too varying or have too low a resolution, an is where disease is collated based on the local municipality in which it falls. The major advantage of doing this is that people relate to local municipality collation well.

The actual point data is often used but the major disadvantage of this is that technically these point data can be 'reverse-engineered' in software to establish the location of an event, and this does bring client privacy into question. The purpose of this presentation is to show the advantage of using hexagonal instead of square grids to collate and visualise data on maps using an example of Rift Valley Fever (RVF) that occurred during 2010 in South Africa. The comparison between a hexagon grid collation versus square grid collation and finally local municipality collation is made showing the differences, advantage and disadvantages of each method.

WHY HEXAGONS WORK WELL

Simply put hexagons link well and are easier on the eye, with the major advantage of not creating horizontal and vertical lines when zooming out as is evident with square grids. Hexagons also flow over irregular surfaces better than squares do. Square grids also can create visualisation irregularities, a common one being enclosure of space where because the points of diagonally placed squares touch they can create an illusion of an enclosed space[1].

EXAMPLES OF USING HEXAGONS IN VETERINARY EPIDEMIOLOGY

Hexagon use in mapping has been performed for some time now, but a brief search of its use in veterinary medicine showed very few results. A good example of its use is in McGrath et al. (2009) on the mapping of bovine tuberculosis in Ireland[2] where both a kernel smoothing raster was created and then a second method was explored using a hexagonal grid. A review of the use of hexagonal grids in an ecological setting showed that its use is rare, but that even just for visualisation purposes, authors should consider it more often[3].

THE DISADVANTAGES OF HEXAGONS

One of the issues with hexagon collation is that further analysis is more difficult compared to square grid data - for instance in ArcGIS® there is a raster calculator which can query/compare multiple raster (which are essentially square grids) layers, and this would be difficult if data was in a hexagonal grid. Another down side of hexagons is their intrinsic incompatibility with the basic points of the compass insomuch that they can have North and South directions but their East and West directions must contain a North or South vector ending up with NE, SE, SW and NW directions which make up the six sides of the hexagon. A final drawback is that you cannot subdivide hexagons like you can with squares. This may however be an advantage as researchers can 'create' data by increasing the raster resolution beyond the resolution at which their data was collected.

MAKING YOUR OWN HEXAGONAL GRID

There are a number of ways to create a hexagon layer of the size that is appropriate for your work. Examples can be found in the following article: http://blogs.esri.com/esri/esri-insider/2015/04/08/thematic-mapping-with-hexagons/

* Western Cape Department of Agriculture, Elsenburg, 7607

Email: johng@elsenburg.com Tel: 021 808 5056

REFERENCES

1 http://gis.stackexchange.com/questions/82362/what-are-the-benefits-of-hexagonal-sampling-polygon

2 McGrath, G., Abernethy, D., Stringer, L., & More, S. J. (2009). An all-island approach to mapping bovine tuberculosis in Ireland. Irish veterinary journal, 62(3), 192.

3 Birch, C. P., Oom, S. P., & Beecham, J. A. (2007). Rectangular and hexagonal grids used for observation, experiment and simulation in ecology. Ecological Modelling, 206(3), 347-359.

CONTROL OF OVINE JOHNE'S DISEASE IN THE NORTHERN CAPE PROVINCE: A CASE REPORT

Matekwe, N.[*]

ABSTRACT

A farm in the Northern Cape Province was suspected of having been infected with vvine Johne's disease (OJD) when the owner of the farm bought 406 sheep at an auction. The sheep came from a known OJD infected farm in a neighbouring province. The farm was immediately put under quarantine and disease control measures were put in place. Serological tests (ELISA) were performed on serum samples from all the 406 bought in sheep and 18 (4.43%) tested positive. All the sheep (406) were slaughtered at a registered abattoir and 20 tissue samples (ileocaecal valves and mesenteric lymph nodes) were collected for histopathology using the immunoperoxidase staining technique and 10 (50%) of them tested positive. Following the successful slaughter of all the 406 bought in sheep, OJD sero-surveillance was done on the farm as well as 17 contact farms. Random samples were taken from sheep that were at least 24 months old. 7 samples (1.3%) from 5 farms tested positive for OJD using ELISA, however, tissue samples from the positive animals were negative for OJD on histopathology. The sample size was increased and the five positive farms were retested and only one sample (0.4%) tested positive for OJD on ELISA but was negative on histopathology. In addition to the serological and histopathological tests done, as a way of assessing a risk factor associated with the survival and propagation of OJD in the environment, soil samples for pH determination were taken from the infected farm. The results showed that the pH of the soil does not favour the prolonged survival of OJD's causative agent in the environment. Subsequent serological and histopathological retests were carried out on the farm at intervals determined by the provincial veterinary services and the farm was finally removed from quarantine when the provincial veterinary authority was satisfied that the farm had attained freedom from OJD.

* Northern Cape Veterinary Services
Email: rutego@yahoo.com>

AN OUTBREAK OF AN INFECTION WITH *APHANOMYCES INVADANS* (EPIZOOTIC ULCERATIVE SYNDROME) IN SHARPTOOTH CATFISH (*CLARIAS GARIEPINUS*) IN THE NORTH WEST PROVINCE: A CASE REPORT

Mlilo, T.[*]

ABSTRACT

Epizootic ulcerative syndrome (EUS) is an infection caused by an invasive aquatic oomycete, *Aphanomyces invadans*, and causes focal necrotising granulomatous dermatitis and myositis and subsequent mortalities in catfish. It has been previously diagnosed in the Western Cape Province in February and October 2011 and this was the first occurrence in the North West Province.

Heavy catfish mortalities were reported in a private farm dam in the Bokfontein area in Brits, North West Province. On disease investigation randomly caught fish (n=5) were physically examined and found to have focal reddish to white mycotic granulomas on the entire length of their bodies. After euthanasia by severing the spine samples were taken from the edge of the lesions from each fish and preserved in 10% formalin for histopathology and 90% alcohol for polymerase chain reaction (PCR) testing.

Histopathology results were inconclusive for confirming EUS infection but PCR results came out positive for all the samples submitted (100%) thereby confirming an infection with EUS. The farm was then quarantined and fishing activities halted and movement of fish both in and out of the farm stopped and an SR1 form issued for disease notification.

It would have been helpful to test the water quality of the dam during the outbreak to see if it did not predispose to the fish getting infection but we were unable to do that due to lack of resources. We suspect the infection could have been introduced by contaminated fishing equipment as the farm offers recreational catch and release fishing activities.

* Tel: 0810314716; Email: thethelanimlilo@yahoo.co.uk

THE DROMEDARY CAMEL: AN OASIS OF ZOONOTIC PATHOGENS?

Bastos, A.*

ABSTRACT

No abstract available at time of publication.

* Mpumalanga Veterinary Services

Email: johann.vet@gmail.com

ELIMINATION OF RABIES FROM AN ENDEMIC AREA BY TARGETING STRATEGIC KEY POINTS

Kotze, J.*

PURPOSE

Canine rabies is controlled mainly through the vaccination of dogs. It is generally accepted that a herd immunity of 70% would result in its elimination but is seldom achieved due to poor resource allocation. The objective of this study was to determine if the strategic application of vaccinations could eliminate rabies from an endemic area since the 1950's.

METHODS

Beginning in 2009, rabies vaccinations were focused at strategic points along the borders between sub-populations of the study area. The rationale was to prevent the spread of infection between the sub-populations and allowing natural extinction of the virus in the smaller sub-populations. Phylogeographic analysis of rabies virus have shown that regional variants arise and disappear with time. In 2012 the last positive case was diagnosed in the study area whilst a maximum of only 45% population immunity was achieved. To determine if the strategy was responsible for the success, a logistic regression model was developed using data from 2002 to 2014. The strategic application of vaccinations and the total number of vaccinations were included as determinant variables with elimination as the response variable.

RESULTS

The model showed the strongest association in two areas of the meta-population that were amenable to strategic application due to their specific topography. These had p-values lower than 0.001 associated with the strategy and no significant association with the number of vaccinations. Another two areas of commercial farmland showed no significant association with any of the study variables.

CONCLUSIONS AND RELEVANCE

It is concluded that strategic placement of rabies vaccination campaigns can isolate sub-populations and assist to eliminate rabies within a meta-population. This requires fewer resources and is highly applicable in resource poor countries.

* Mpumalanga Veterinary Services

Email: johann.vet@gmail.com

SOUTHERN
AFRICAN
SOCIETY FOR
VETERINARY
EPIDEMIOLOGY &
PREVENTIVE
MEDICINE

Proceedings of the 13th annual congress of the Southern African Society for Veterinary Epidemiology and Preventive Medicine

OBP
ONDERSTEPOORT
BIOLOGICAL PRODUCTS