Brucellosis in the Southern Cape

BACKGROUND
A dairy farm in the Southern Cape area just north-east of George tested positive to brucellosis (B. abortus) on serum samples taken in late May 2014 (farm C - Fig 2). This was the first positive test for this farmer with the previous negative test event occurring in May 2013. An outbreak investigation took place and a further two farms (farms A and B - Fig 2) in contact were also found to be positive with high prevalences (see Fig 1).

CURRENT SITUATION
ANIMAL DEMOGRAPHICS
See the top section of Fig 2 for the total cattle population density in the Southern Cape. This area is a highly dense cattle farming area and is dominated by dairy farming, given the availability of pastures and the generally year-round rainfall patterns in the area. The dairy herd affected has approximately 900 cows in milk (two milking’s per day) at any given point in time and is a Jersey and Jersey cross herd. The herd is unvaccinated against brucellosis, making every animal on the property a susceptible animal. The farmer uses artificial insemination on the farm. Farms A and B had approximately 431 and 20 cows respectively prior to control slaughtering.

SPATIAL ASPECTS
See the bottom section of Fig 2 for a view of the affected farms. The affected dairy has over-the-fence and road contact with farm A and B. It also has a common water source in the form of a shared dam with farm A. The dairy farmer uses maternity camps for calving cows. In our opinion this outbreak has shown the ability of brucellosis to spread easily laterally between farms.

CLINICAL PRESENTATION
The dairy farmer has experienced abortions on the farm since the first positive results were found and, in his opinion, they are above the baseline of what he normally experiences. About ten abortions have occurred in the last two months, with half of those occurring within the past two weeks.

TEST RESULTS

<table>
<thead>
<tr>
<th>Farm</th>
<th>April ’13</th>
<th>May ’14</th>
<th>June ’14</th>
<th>July ’14</th>
<th>Aug ’14</th>
<th>Sept ’14</th>
</tr>
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<tbody>
<tr>
<td>Farm A</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>37%</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Farm B</td>
<td>-</td>
<td>-</td>
<td>-</td>
<td>40%</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Farm C</td>
<td>0%</td>
<td>1%</td>
<td>-</td>
<td>3%</td>
<td>-</td>
<td>8%</td>
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</table>

Fig 1: Test prevalences for the three affected farms. On Farm A 219 animals were tested with 80 positives. Farm B had 8 positives out of the entire herd of 20 while farm C has had over 1220 animals tested on all three occasions during 2014 with a total of 50 reactors on CFT.

Test results are shown through tested prevalences in Fig 1. The dairy farmer involved has maintained negative milk ring tests throughout the outbreak thus far and this is likely as a result of the dilution factor, given the high numbers of animals being milked. The dairy had Brucella isolated after culture at the Stellenbosch Veterinary Laboratory.

SOURCE
None of the positive farms can be considered as closed herds. The dairy farm (farm C) is the only one that could attain this status but this has not occurred. The farmer had sent some heifers to be raised on a family farm in the Eastern Cape and in Aug 2013 they had returned. The farmer as also brought in small numbers of bulls from stud breeders over the past few years with the latest movement in December 2013. Given the prevalence information in Fig 1, however, we get the impression that the infection is now picking up steam and that both farm A and B were likely to have been infected prior to the dairy.

FOLLOW UP AND CONTROL
Private vets have been informed of the outbreak and are busy testing the surrounding herds. Two herds (one beef and one dairy replacement herd) have already been tested negative (see the blue squares in Fig 2). Slaughter of reactors has occurred on all three positive farms so far. Farm B has slaughtered out all 20 animals on the farm, farm A has slaughtered 144 of the 431 cows on the farm and will be slaughtering the rest which will attain appropriate slaughter weight in December this year. The dairy (farm C) has been slaughtering all reactors and thus far has slaughtered 50 animals.

Control of the bacteria on the dairy farm has been attempted through the collection and burning of all post-partum material left in the maternity camps, including the aborted material.

CONCLUSIONS AND REMARKS
It is important for positive identification of Brucella to occur on the dairy farm and therefore it is imperative that all abortions are tested for the bacterium prior to the aborted material being destroyed. This dairy farmer has not been vaccinating against the disease. Unfortunately, even if a farmer maintains excellent biosecurity the lateral transmission of the disease from neighbouring farms always will be a risk. If the dairy farmer had been vaccinating, the number of susceptible animals would have been significantly less, making the likelihood of successful intra-herd transmission very low and even if infection did occur the control thereof would have been easier and the impact the disease would have made would have paled in comparison to what this farmer must now deal with in the coming months.

There is a risk of abortions occurring after vaccination of pregnant animals with RB51. This risk may be increased with certain breeds, including Jersey cattle. The risk of abortion is increased further if vaccination is performed in an unvaccinated herd. Unfortunately the dairy farmer involved has Jerseys and his herd is unvaccinated, making this control measure difficult to proceed with, but in our opinion the only option going forward.

continued on Page 2
The dairy farmer involved also now needs to consider removing all calves born to positive reactors over the past three months. Many farmers that have strict biosecurity principles in place on their farms will only integrate new animals into their existing herd after thorough testing, depending on the source of the animals. The dairy farmer now involved sits between a rock and a hard place since commercially it becomes extremely difficult to slaughter out positives while trying to maintain milking numbers, and bringing unvaccinated animals onto the farm just increases the risk of disease continuation.

This outbreak illustrates the need for extremely strict biosecurity measures coupled with a well devised and carried out vaccination and testing protocol against Brucellosis. Not maintaining these two principles is a recipe for disaster.

Brucellosis is a very important zoonotic disease. The dairy farmer must take the necessary precautions for himself and his workers to ensure that they are protected from infection. This includes the management of post partum materials and especially aborted materials as well as management of raw milk in the parlour and the access workers and their families have to this milk. It is also important to inform the abattoir where positive reactors are slaughtered of the status of the animals.

We visited more farms in the area and discovered that the farmer knowledge of brucellosis is not complete. Several farmers, including large dairy farmers, do not vaccinate against the disease. Brucellosis must not become a forgotten disease and information about its prevention must be carried across to farmers.

**Fig 2:** Map showing the overview of the Southern Cape (top) with the associated cattle farms as captured in the last 3 years by our Animal Health Technicians. The bottom map shows the affected farms as a result of the outbreak with farm C being the dairy farm detailed in this report. Shown in red lines are potential lateral spread mechanisms of the bacteria between properties with a common source dam being highlighted by the black arrow. All roads shown are dirt roads and are secondary and tertiary roads. Small rivers in the area are shown in blue. Blue squares indicate negative tested farms during this outbreak.
On 3 September a farm in the Klein Karoo area (showed as Farm A in Fig 3) tested ELISA positive for avian influenza (AI). Tracheal swabs were collected for PCR testing during the follow-up investigation and H9 AI was identified. Although the N-type was not determined by PCR, the serology results suggest the involvement of a N2 virus. There were no movements of ostriches to this farm in the 3-months prior to sampling.

On 30 September, during routine pre-slaughter sampling, Farm B tested ELISA positive to AI as well. On this farm there is a clear geographical distinction between the older slaughter birds and the chicks as shown on the map. The slaughter birds, which are kept in camps neighbouring Farm A (although divided by a dirt road and so no over-the-fence contact possible), had a high ELISA prevalence (87%), while all the chicks, which are further away, tested negative. All haemagglutination inhibition (HI) tests (to H5, H6 and H7) were completely negative. Further investigation is ongoing to determine the virus type although H9 is strongly suspected given the proximity to Farm A. Interestingly Farm B was also tested on the 3rd of September with negative results, indicating that Farm A was indeed first infected.

Both this farm and the slaughter bird section of Farm B were affected by an incident during August (and again later) when the water canals overflowed, causing muddy conditions which attracted a lot of sacred ibis and other birds. This occurrence considered together with the movement history, leads to the conclusion that the virus was most likely introduced via wild birds.

This is the first report of an H9N2 virus for the Western Cape over the past few years. Clinically there have been no indications of disease on either farm affected.
**Outbreaks and Surveillance**

**Outbreak events**

- Over and above the H9N2 AI farms in the Oudtshoorn area another H5N2 ostrich farm has been identified in the Oudtshoorn/George area with serological results on follow up testing confirming the subtype. PCR results have stayed negative throughout and this farm is currently classified as a LPAI farm.

- Orf was reported in two herds of goats on the Cape Flats in Cape Town.

- A wool farm near Riversdale was confirmed positive for ovine Johne’s disease. They had been experiencing an increased incidence of emaciation in their ewes for approximately six months.

- Salmonella enteritidis was detected from routine environmental swabs on several poultry farms surrounding Malmesbury. Affected houses are managed according to the salmonella reduction protocol, including treating chickens with enrofloxacin and disinfecting the houses after slaughter.

- Two sheep farms in the Beaufort West area tested positive for *Brucella ovis* on routine ram testing. Slaughter out of the affected rams and retesting was recommended.

- An atypical case of sheep scab occurred in a communal farming area near Ceres. Sheep were losing wool and had pustules on their bodies, but no pruritis was observed.

- A breeder of exotic birds in Cape Town noticed a dead African Grey parrot in its outdoor housing facility in June this year, but took no further actions. When a second African Grey died acutely in August, he submitted the carcass to the Stellenbosch Provincial Veterinary Laboratory. On post-mortem, peritonitis and multifocal areas of necrosis were seen. PCR testing on the spleen was positive for *Chlamyphila psittaci*, but not before a second...
Outbreak events continued

mortality of an African Grey. The property was placed under quarantine in September and all birds on the property are being treated with doxycycline. The owner has disinfected the property and all equipment and his family has visited their local GP and are taking prophylactic antibiotics. The most recent introduction of a new bird (a Senegal parrot— see fig 5) occurred in March 2014, so it is suspected that the infection was introduced by wild birds, which have access to the outdoor, open-topped cages.

- An angora kid on a farm near Prince Albert showed abnormal behaviour when it began nibbling at the ears of other kids as well as nibbling and licking people with whom it came into contact with on the farm. Later, it became aggressive, causing the farmer to suspect rabies and have it killed. After positive laboratory results for rabies were received, all goats on the farm as well as a small herd of dairy cattle were vaccinated.

A vaccination campaign for dogs and cats in the area was also held. The people who had had contact with the rabid goat, including one who had been licked in an area of broken skin, received rabies post-exposure prophylaxis at a local health clinic.

Fig 6 and 7 show the locations and vaccination totals performed by AHT Cobus Ferreira during the outbreak response. A total of 1394 animals were vaccinated with the majority being the goat herd on the affected farm.

Fig 5: A Senegal parrot

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<th>Total OIE logs</th>
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Epidemiology Report
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Web based event logging AHT leader boards

Disclaimer: This report is published on a monthly basis for the purpose of providing up-to-date information regarding epidemiology of animal diseases in the Western Cape Province. Much of the information is therefore preliminary and should not be cited/utilized for publication.
Univariate analysis - Chi²

Lab #5 requirements

- R - http://cran.r-project.org/bin/windows/base/
- R Studio - www.rstudio.com/ide/download/desktop
- Internet connection
- epicalc package (download info in code below)
- Internet connection

The code

# In this lab we are going to look at some very basic evaluation of data. Firstly we download the cleaned SASVEPM data which we performed last month if you haven't done that lab yet then go to http://www.elsenburg.com/vetepi/BPEL/  
#BPEL_2014_08_EvalData_Clean1.pdf
#Here we download the cleaned data and put it into a data frame called 'sasvepmdataclean'
sasvepmdataclean<-read.csv('http://www.jdata.co.za/backpagelabs/backpagelabs_jdg_sasvepmclean.csv', header=T)
#to remind you of the data and its content
summary(sasvepmdataclean)
#for some reason - can't quite figure it out - R sometimes adds an additional X column with the same data as the id field into the data frame - so let's just 
#remove that if it's there...if not don't worry
sasvepmdataclean$X<-
#Before we get started we are just going to take a detour and use a very cool function in the epicalc package
#if you haven't installed the epicalc package yet then type this into your R console
install.packages("epicalc")
#activate the library after it has been installed (you can also tick it in R Studio's package window)
library("epicalc")
#note above how I needed to refer to the X column in the sasvepmdataclean data set by typing in sasvepmdataclean$X. This was of doing things is 
#very pedantic and thorough but ultimately not necessary. In R there is a way to essentially attach your data frame that you are working with that it 
#recognises column names without you having to refer to them explicitly. The epicalc package has a function that has simplified this so let's try it.
#first we see what is attached in your environment
search()
#these are all packages and data that is attached, so the epicalc package should be there
#if you want to attach sasvepmdataclean - the epicalc function is "use"
use(sasvepmdataclean)
#now try
search()
#again - you'll see a "data" listed in the attached data and packages - this is your dataset you have now attached
#now instead of referring to say the participation field in sasvepmdataclean (sasvepmdataclean$participation) you could just type in participation
#and get the same result
#ok to get back to our analysis - you'll remember that the summary command is a general one
summary(sasvepmdataclean)
#the epicalc package has some of its own summaries which are also useful - codebook is the first
codebook(sasvepmdataclean)
#this takes a look at each variable and does a frequency count for categorical variables (like most of the data in this example) or measures of centrality and spread for the continuous data - like id in our case - (which is meaningless) Another epicalc summary is:
summary(sasvepmdataclean)
#this seems more useful for continuous data so is not so worthwhile in our example. In this lab we are going to do some univariate analysis so we are 
#going to try answer one question for now

###Q1: Were presenters more likely to be from an academic institute?

#First we need to create a two by two table to evaluate all participation by whether the participant was an academic or not. To do this we use a table 
#command.
table(participation,institute)
#note this gives us categories of all participation by all institutes - but some categories are poorly represented and out

So last month we imported some SASVEPM congress attendance data and found that it needed some cleaning up. This month we start to analyse some of it for a bit of fun and this lab is focussed on two aspects - the first is an introduction to the use of a very cool package for epidemiologists called "epicalc". We use some of its summary functions as well as an attach function which helps in decreasing command input time in R. (as always, remember to hit TAB in R-Studio when typing in commands - it will help a lot!) The second aspect of the lab is to start analysis. In this case we are asking one question - Was there an association at the congress of academics attending and whether they presented a talk or not compared to non-academic attendees. We might be interested in this to determine whether a group of attendees like State officials are over represented in attendance but under represented in presenting - this may be something worthwhile knowing for the society when they advertise and call for papers for the next congress...
Univariate analysis - Chi2

The output

The input and observed table

The expected values if null hypothesis was true

The chi squared test result

The actual p-value for the result

The chi squared statistic

The degrees of freedom

The chi squared test result

The result

Attendees that are from an academic background were associated (p<0.05) with being presenters at the 2014 SASVEPM congress

References

