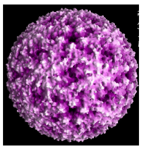
Epidemiological patterns of foot-and-mouth disease in livestock-wildlife interface areas of northern Tanzania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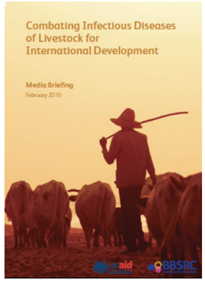
CIDLID INITIATIVE

BBSRC bioscience for the future

DFID Department for International Development

The Scottish Government



BBSRC-DFID-Scottish Government CIDLID: bringing together expertise in FMD, livestock health and wildlife

- University of Glasgow
- Tanzania Wildlife Research Institute
- Institute for Animal Health, Pirbright
- Central Veterinary Laboratory, Tanzania
- Sokoine University of Agriculture, Tanzania
- University of Edinburgh

Thanks!

Glasgow University, UK
- S. Cleaveland
- D. Haydon
- R. Reeve
- H. Auty

IAH-P, UK
- D. King
- D. Paton
- S. Parida
- T. Knight-Jones
- N. Knowles
- K. Parekh

Washington State University, USA
- J. Yoder
- T. Marsh

Directorate Veterinary Services, Tanzania
- F. Kivaria

Central Veterinary Laboratory, Tanzania
- M. Yongolo
- C. Ngeleja
- R. Sallu

Veterinary Investigation Centre-Arusha, Tanzania
- D. Msahanga

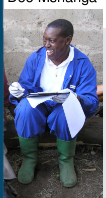
Tanzania Wildlife Research Institute
- R. Fyumagwa
- J. Keyyu
- R. Hoare

Sokoine University of Agriculture, Tanzania
- R. Kazwala
- C. Kasanga
- E. Kamani

Onderstepoort Veterinary Institute
- F. Maree

Field team

Deo Mshanga



Enos Kamani

Robert Fyumagwa

Mahemba Shabani and Paulo Tango

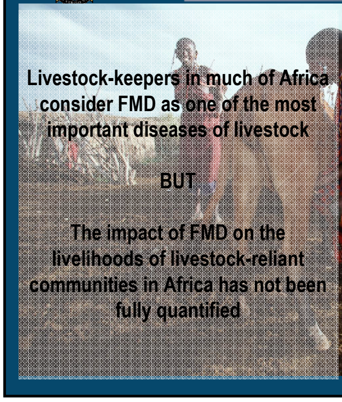
Ahmed Lugelo

Machunde Bigambo

Problems of endemic FMD in Africa

- Calf mortality
- Loss of condition
- Loss of milk production
- Lameness – difficulty moving to grazing/watering points
- Abortion
- Loss of draught power
- Loss of trade opportunities
- Lack of effective vaccines

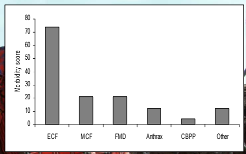

Poverty impacts in Africa



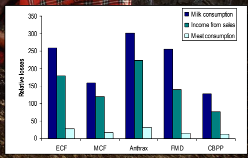
Livestock-keepers in much of Africa consider FMD as one of the most important diseases of livestock

BUT

The impact of FMD on the livelihoods of livestock-reliant communities in Africa has not been fully quantified



Jost et al. (2010) Am. J. Trop. Med. Hyg. 83: 65-72



Bedelian et al. (2007) Prev. Vet. Med. 78: 296-316

Risk factors in Africa

- Frequent, recurrent outbreaks
- Seasonality
- Risk factors: transhumance, buying cattle from markets, mixing of herds at watering points, contact with buffalo *(Bronsvoort et al. (2004) Prev. Vet. Med. 66: 127-139).*

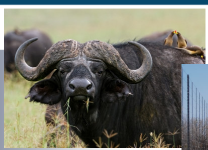
TABLE 4A

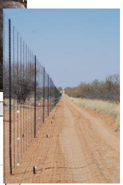
Proportions derived from simple matrices constructed with Somali pastoralists in North Eastern Province, Kenya, ranking five livestock diseases with respect to their perceived strength of association with selected risk factors ($N = 3$)*

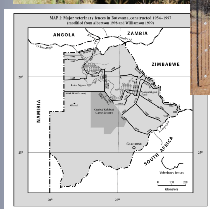
	Median (10th percentile, 90th percentile)‡				
Risk factor†	RVF	Trypanosomosis	Gastrointestinal parasitism	FMD	Anthrax
Biting flies	5.0 (4.2, 6.6)	11.0 (8.6, 12.6)	0 (0, 0)	0 (0, 0)	4.0 (0.8, 7.2)
Contact with wild animals	0 (0, 3.2)	10.0 (8.4, 10.8)	0 (0, 0)	6.0 (3.6, 8.4)	4.0 (0.8, 7.2)
Wet grass	0 (0, 0)	0 (0, 0)	12.0 (8.0, 12.0)	0 (0, 0)	8.0 (8.0, 12.0)
Mosquitoes	13.0 (10.6, 18.6)	0 (0, 1.6)	0 (0, 0)	0 (0, 0)	7.0 (1.4, 7.8)
Abnormally heavy rains	20.0 (8.0, 20.0)	0 (0, 0)	0 (0, 0)	0, (0, 8.0)	0 (0, 4.0)
Soil and dust	0 (0, 0)	0 (0, 0)	0 (0, 8.0)	8.0 (1.6, 15.2)	10.0 (4.4, 11.6)
Stagnant water	0 (0, 0)	7.5 (1.5, 8.5)	17.3 (4.3, 16.3)	0 (0, 0)	0 (0, 6.4)
Ticks	10.0 (2.0, 10.0)	0 (0, 8.8)	0 (0, 0)	0 (0, 0)	10.0 (9.2, 10.0)
Wind	0 (0, 7.2)	0 (0, 0)	0 (0, 0)	20.0 (12.8, 20.0)	0 (0, 0)

Catley (2003)

The role of wildlife in FMD epidemiology







Buffalo maintain SAT serotypes of FMDV

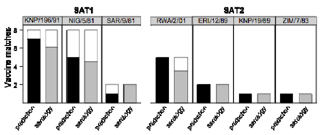
Veterinary fences built to control FMD by restricting movement of wildlife

How much cattle infection is associated with spill-over from wildlife?

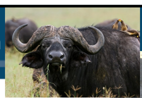
How can we best control FMD adjacent to wildlife protected areas?

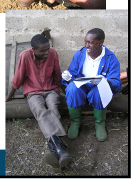
Vaccine-based control strategies

- Vaccination provides a potential solution for controlling disease in sub-Saharan Africa
- To select effective vaccines, we need to understand which genetic strains of virus occur in different parts of Tanzania
- We need to understand the relationship between cross-reactivity and cross-protection for better prediction of vaccine efficacy
- We need to understand how to optimize vaccination strategies to provide economic benefits across different sectors



Key areas of research

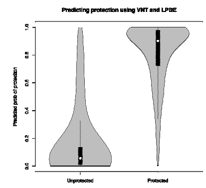




- BASIC EPIDEMIOLOGICAL QUESTIONS:
  - Role of livestock and wildlife in disease maintenance and how common the carrier state is in livestock and wildlife
  - Temporal / spatial infection patterns
  - Risk factors for infections and outbreaks in livestock (e.g. associated with livestock management and movement patterns, and contact with wildlife)
  - Spatial distribution of antigenic / genetic variation and origin of locally occurring antigenic novelty
- SOCIO-ECONOMIC IMPACTS AT HOUSEHOLD AND NATIONAL LEVELS:
  - Identify and quantify production losses due to FMD infection and individual outbreaks

Key areas of research - continued

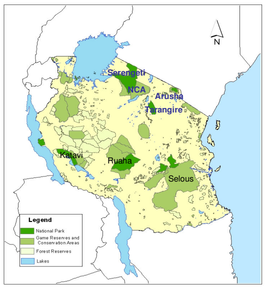
- CONTROL STRATEGIES:
  - Contribute data on circulating serotypes responsible for outbreaks for vaccine selection
  - Develop serological and genetic models for cross protection and therefore vaccine selection and outbreak prediction
  - Develop mathematical models to explore potential local, national and regional control strategies (e.g. vaccination, buffer zones around wildlife areas, market controls, movement restrictions, etc.)



Timeframe and study design

- Project time scale: August 2010 to August 2014, but project duration depending on funds
- Set-up phase and training of field personnel completed
- Fieldwork started February 2011
- Two components:
  - Cross-sectional livestock and wildlife surveys
  - Investigation and sample collection from livestock outbreaks followed by longitudinal sampling of outbreak herds

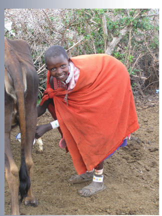
Cross-sectional surveys - study sites



- Original plan - Serengeti, Ngorongoro, Tarangire, Arusha, Ruaha, Selous, Katavi
- Current plan – Serengeti, Ngorongoro, Tarangire, Arusha (northern ecosystems)

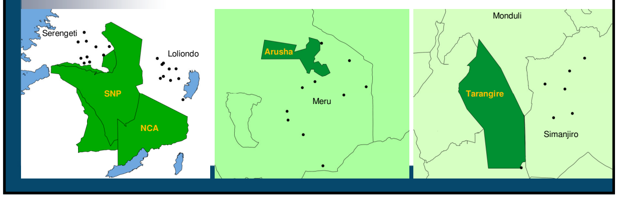
Cross-sectional surveys – objectives

- Sampling of livestock and buffalo to obtain data on:
- Antigenic and genetic diversity, seroprevalence and prevalence, prevalence of carriers, disease impacts at the household level and risk factors for livestock outbreaks

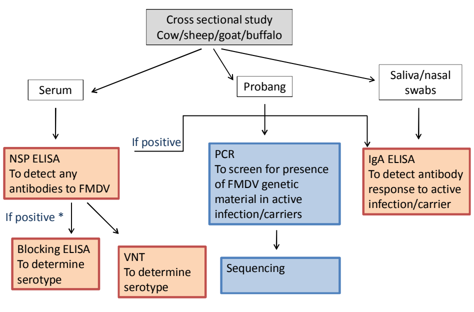


Cross-sectional surveys - progress

- Livestock surveys:
  - Ten villages selected at different distances from park boundaries and two households in each village
  - In each household: 30 – 40 livestock (cattle, sheep, goats) sampled (serum, probang, nasal / saliva samples) and questionnaire conducted
- Buffalo surveys: 25 animals per ecosystem from a range of herds
- Livestock and buffalo surveys completed in all northern ecosystems

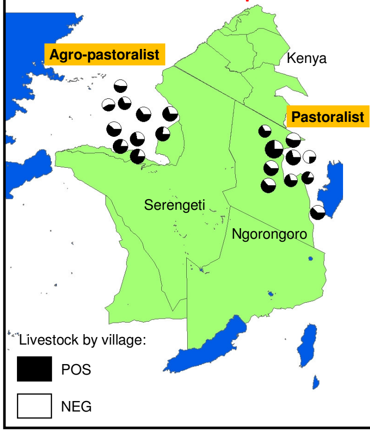


Cross-sectional surveys - laboratory analysis



* On a subset of serum samples

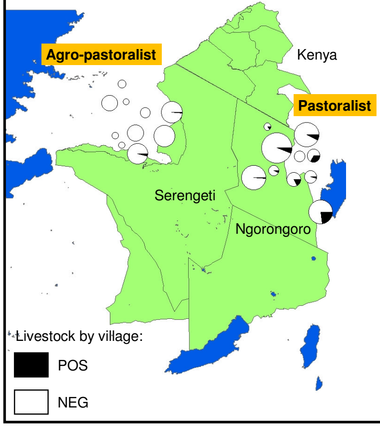
Livestock NSP ELISA seroprevalence – Serengeti & Ngorongoro



Ngorongoro (pastoralist):
Overall - 64% (n = 750)
Cattle – 76% (n = 380)
Sheep – 48% (n = 135)
Goats - 54% (n = 235)

Serengeti (agro-pastoralist):
Overall - 68% (n = 725)
Cattle – 77% (n = 411)
Sheep – 47% (n = 94)
Goats – 59% (n = 220)

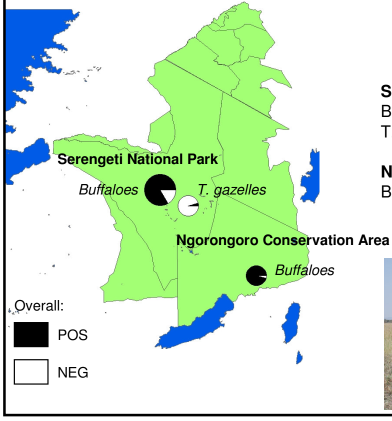
Livestock RT-PCR prevalence – Serengeti & Ngorongoro



Ngorongoro (pastoralist):
Overall - 10% (n = 445)
Cattle – 15% (n = 237)
Sheep – 3% (n = 69)
Goats - 5% (n = 139)

Serengeti (agro-pastoralist):
Overall - 1% (n = 274)
Cattle – 2% (n = 158)
Sheep – 0% (n = 28)
Goats – 0% (n = 88)

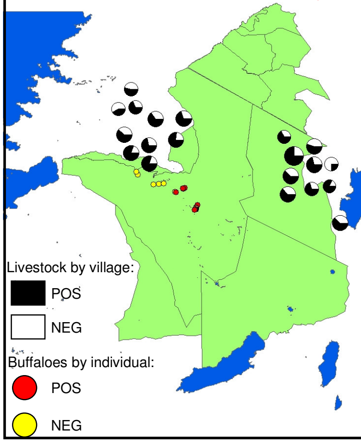
Wildlife NSP ELISA seroprevalence (archived sera)



Serengeti:
Buffaloes - 83% (n = 54)
T. gazelles – 4% (n = 23)

Ngorongoro:
Buffaloes – 96% (n = 23)

Livestock and buffalo NSP ELISA seroprevalence and RT-PCR prevalence

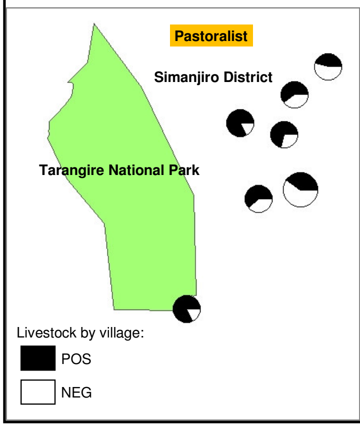


Buffaloes – overall:

NSP ELISA 59% (n=17)

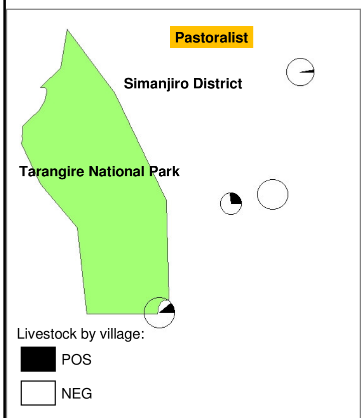
RT-PCR 35% (n=17)

Livestock NSP ELISA seroprevalence – Tarangire



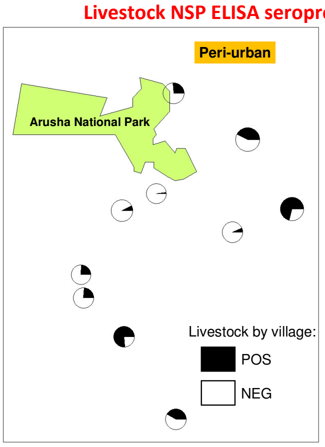
Seroprevalence:
Overall - 68% (n = 419)
Cattle – 78% (n = 210)
Sheep – 48% (n = 64)
Goats - 61% (n = 145)

Livestock RT-PCR prevalence – Tarangire



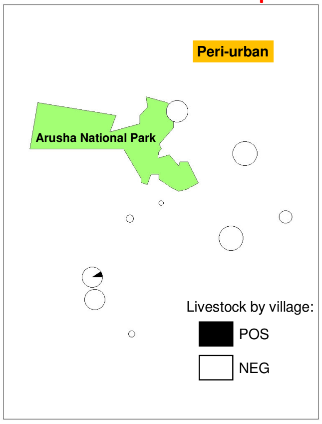
Prevalence:
Overall - 8% (n = 175)
Cattle – 9% (n = 90)
Sheep – 10% (n = 30)
Goats - 5% (n = 55)

Livestock NSP ELISA seroprevalence – Arusha



Seroprevalence:
Overall - 33% (n = 634)
Cattle – 36% (n = 302)
Sheep – 36% (n = 112)
Goats - 28% (n = 215)

Livestock RT-PCR prevalence – Arusha



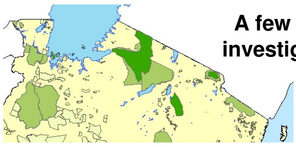
Prevalence:
Overall – 1.4% (n = 140)
Cattle – 0% (n = 64)
Sheep – 0% (n = 25)
Goats - 3.9% (n = 51)

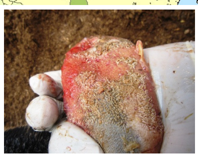
Outbreak investigations and longitudinal sampling

- Four main objectives:
  - Determine temporal infection patterns, risk factors for outbreaks, impacts of individual outbreaks at the household level, etc.
  - Quantify carrier animals
  - Vaccine matching studies
  - Evaluate serological correlates of cross-protection
- Focus on 2 ecosystems (Serengeti and Tarangire). Others as opportunities arise.
- Cattle only
- Pre-outbreak (cross-sectional), outbreak, and post-outbreak sampling
- If no outbreaks in 6 months after post-outbreak sampling, routine sampling

A few outbreaks investigated so far

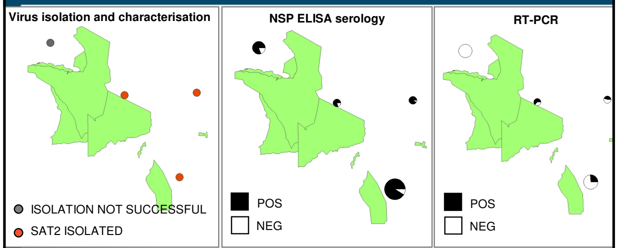
University of Glasgow





SAT2 LIVESTOCK OUTBREAKS

UNIVERSITY of GLASGOW



- Outbreaks occurred close in time
- SAT-2 viruses isolated across three ecosystems were closely related

Conclusions so far

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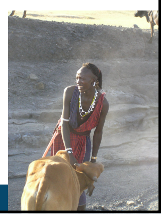
- Seroprevalences and probang PCR-positivity in livestock variable across ecosystems
  - High levels of exposure in pastoralist and agro-pastoralist communities, lower in peri-urban communities
- High seroprevalence and RT-PCR prevalence also in buffaloes, but low in non-buffalo species
- FMD ranked amongst most important diseases by livestock keepers with multiple outbreaks a year reported in pastoralist and agro-pastoralist herds
- Closely related viruses isolated from 3 outbreaks suggest that livestock contact patterns may be an important source of outbreaks

THANKS FOR FUNDING AND PERMISSION

UNIVERSITY of GLASGOW

- Combating Infectious Diseases of Livestock for International Development (BBSRC – DfID – Scottish Government) for funding
- COSTECH, MoLFD, TAWIRI, TANAPA, NCAA, and WD for permission
- All livestock owners for participating in the study with great patience and enthusiasm!



Thanks for getting us all here!