Seroepidemiology of *Brucella* spp. in humans and livestock in eastern Kenya: Opportunities for One Health interventions

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Introduction

- Brucellosis - zoonotic disease caused by gram-negative coccobacillus in the genus *Brucella*
    - *B. melitensis*, *B. abortus*, *B. suis*, *B. ovis*, *B. canis* -- classical species affecting livestock
    - *B. melitensis*, *B. abortus*, *B. suis* – zoonotic species
    - Most widespread zoonotic infection

- Risk factors – sub-Saharan Africa
    - Large herd sizes and land holding
    - Nomadic pastoralism

- Impacts on livestock production and trade
    - Longer calving intervals
    - Reduced growth
    - Increased incidences of abortion, infertility and calf mortality
    - Trade restrictions

- Disease in humans -- prolonged fever, body aches, arthralgia and weakness

Challenges with brucellosis control in SSA

- Endemic in a wide range of hosts – livestock and wildlife -- which share grazing/watering points

- Clinical signs often not discernible
  - Chronic infections in livestock rarely show any signs
  - Humans – disease often misdiagnosed for febrile infections e.g. malaria

- Limited access to veterinary/health services in endemic areas

- Deep-rooted socio-cultural practices which enhance exposure

Objectives

- Determine seroprevalences of *Brucella* spp. in livestock and humans in eastern Kenya

- Estimate the proportion of human exposure attributable to livestock infection

- Examine patterns of occurrence (clustering) of exposures at various levels of subject aggregation – i.e., individual-herd-village levels
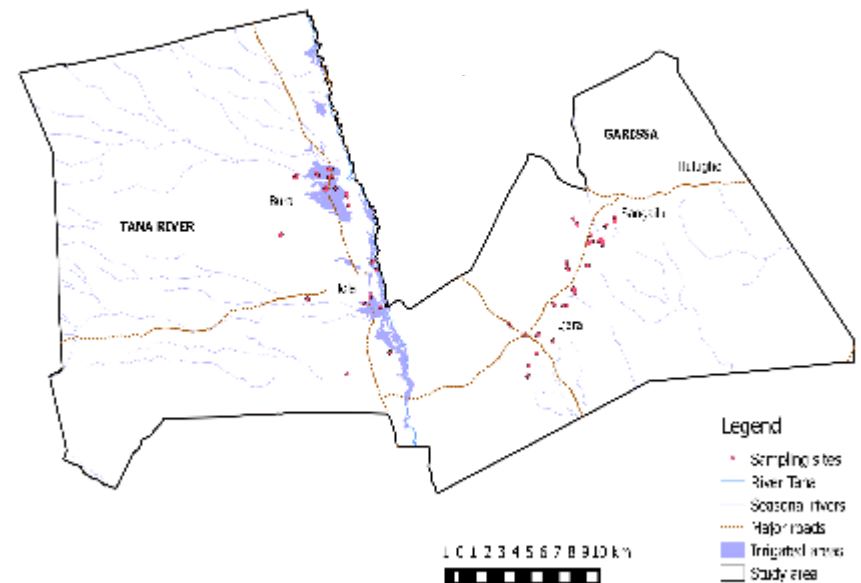
Methods – study design

Study site:

- Arid/semi-arid region in eastern Kenya

Study design

- Cross sectional design
- Humans and livestock within households
- Power sample size estimation techniques – 220 households and 550 subjects
- Sampling frame constructed with local leaders

Methods – sampling and analysis

- Livestock sampled by officers from DVS while humans MoH

- Activities
  - Blood collection
  - Serum extraction and storage
  - Sample screening using ELISA kits

- Ethical review – AMREF and IACUC – ILRI

- Statistical analysis –multilevel mixed effects logistic model in STATA

A typical sampling unit, B. Bett, ILRI

ELISA Kits used

Animal samples –
    Brucella competitive ELISA (Svanovir® Brucella-Ab C-ELISA)

Human samples
    Brucella IgG in vitro ELISA
    (Demeditec Diagnostics GmbH)

Results – livestock (animal level)

- 2,017 animals sampled comprising: 460 cattle, 927 goats, 630 sheep
  Mean seroprevalence: 3.47% (95% CI: 2.72 – 4.36%)

Mixed effects logistic regression model showing risk factors for livestock exposure

Variables	Levels	Odds Ratio			Z	P>Z
		Estimate	SE	95% CI		
Fixed effects						
Age	Kid/lamb/calf	0.13	0.13	0.02 – 1.00	-1.96	0.05
	Weaner	0.18	0.11	0.05 – 0.59	-2.83	0.01
	Adult	1.00				
Area	Bura	3.73	2.57	0.96 – 14.43	1.90	0.06
	Hola	1.00				
Constant		0.01	0.01	0.01 – 0.04	-8.57	0.00
Random effects						
Herd ID		1.13	0.60	0.40 – 3.21		
Village ID		0.99	0.82	0.19 – 5.04		

Log likelihood -202.49, number of observations 1,503

Results – livestock (herd-level)

- Herd-level seroprevalence: 60.16% (54.93 – 65.23%)

Mixed effects logistic regression model showing risk factors for livestock exposure at the herd level

Variable	Level	Odds Ratio			z	P>z
		Estimate	SE	95% CI		
Fixed effects						
Herd size[1]		1.03	0.02	1.00 – 1.08	2.11	0.03
Area	Bura	0.14	0.13	0.03 – 0.84	-2.16	0.03
	Hola	1.00				
Constant		4.60	7.00	0.23 – 91.03	1.00	0.32
Random effect						
Village ID		1.54	1.32	0.29 – 8.23		

Log likelihood -52.41, number of observations 119
[1]Herd size divided by 100 to stabilize its odds ratio

Results – humans

- ## 1,022 humans sampled

  mean seroprevalence -- 35.81% (32.87 – 38.84%)

Mixed effects logistic regression model showing risk factors for human exposure

Variable	Levels	Odds Ratio			Z	P>z
		Estimate	SE	95% CI		
Fixed effects						
Age (years)	≤17	0.31	0.07	0.20 – 0.47	-5.34	0.00
	18 - 40	1.00				
	>40	2.00	0.42	1.32 – 3.01	3.30	
Gender	Male	3.23	0.60	2.24 – 4.66	6.25	0.00
	Female	1.00				
Land use	Irrigation	0.15	0.07	0.06 – 0.36	-4.31	0.00
	Pastoralism	1.00				
Constant		0.58	0.16	0.35 – 0.98	-2.03	0.04
Random effects						
Household ID		0.57	0.29	0.21 – 1.55		
Village ID		1.08	0.40	0.52 – 2.24		

Log likelihood -501.60, number of observations 1,016

Results - livestock/human interactions

- Odds of human exposure in household with at least one seropositive animal:

  3.34 (95% CI: 1.48 – 7.57)

- Intra-cluster correlation coefficients (ICC)
  - Livestock: household and village levels: **0.39 vs 0.18**
  - Humans: household and village levels: **0.33 vs 0.22**

Discussion and conclusions

- Brucella infections in human and livestock cluster at households and villages.

- Challenges and opportunities associated with these occurrence patterns:

  o For epidemiological surveys, we need high number of households and villages to obtain reliable measures of burden or demonstrating absence

  o Risk-based surveillance e.g. using human cases identified in hospitals to locate infected livestock

- Cases in livestock increases risk in people 3 fold – interventions at the animal-level can greatly minimize risk of exposure

- Observations on risk factors corroborate published findings – age, herd size in livestock, and age and sex in people

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better lives through livestock