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
  o Chronic infections in livestock rarely show any signs
  o 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

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

<table>
<thead>
<tr>
<th>Variables</th>
<th>Levels</th>
<th>Odds Ratio</th>
<th>Z</th>
<th>P&gt;Z</th>
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<td>Estimate</td>
<td>SE</td>
<td>95% CI</td>
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<td>0.18</td>
<td>0.11</td>
<td>0.05 – 0.59</td>
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<td>Adult</td>
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<tr>
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<td>2.57</td>
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<td>Hola</td>
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<td>Constant</td>
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<td>0.01</td>
<td>0.01</td>
<td>0.01 – 0.04</td>
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<td><strong>Random effects</strong></td>
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<tr>
<td>Herd ID</td>
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<td>1.13</td>
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<td>0.40 – 3.21</td>
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<td>0.82</td>
<td>0.19 – 5.04</td>
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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 | Estimate | SE  | 95% CI      | z    | P>|z| |
|------------|-------|----------|-----|-------------|------|-----|
| Fixed effects |       |          |     |             |      |     |
| Herd size  |       | 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

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<th>P&gt;z</th>
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<td>Village ID</td>
<td>1.08</td>
<td>0.40</td>
<td>0.52 – 2.24</td>
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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)
  o Livestock: household and village levels: 0.39 vs 0.18
  o 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
Acknowledgements

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better lives through livestock