A sero-survey of rinderpest in nomadic pastoral systems in central and southern Somalia from 2002 to 2003, using a spatially integrated random sampling approach


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Summary

A cross-sectional sero-survey, using a two-stage cluster sampling design, was conducted between 2002 and 2003 in ten administrative regions of central and southern Somalia, to estimate the seroprevalence and geographic distribution of rinderpest (RP) in the study area, as well as to identify potential risk factors for the observed seroprevalence distribution. The study was also used to test the feasibility of the spatially integrated investigation technique in nomadic and semi-nomadic pastoral systems. In the absence of a systematic list of livestock holdings, the primary sampling units were selected by generating random map coordinates. A total of 9,216 serum samples were collected from cattle aged 12 to 36 months at 562 sampling sites. Two apparent clusters of RP seroprevalence were detected. Four potential risk factors associated with the observed seroprevalence were identified: the mobility of cattle herds, the cattle population density, the proximity of cattle herds to cattle trade routes and cattle herd size. Risk maps were then generated to assist in designing more targeted surveillance strategies. The observed seroprevalence in these areas declined over time. In subsequent years, similar seroprevalence studies in neighbouring areas of Kenya and Ethiopia also showed a very low seroprevalence of RP or the absence of antibodies against RP. The progressive decline in RP antibody prevalence is consistent with virus extinction. Verification of freedom from RP infection in the Somali ecosystem is currently in progress.

Keywords
Introduction

Rinderpest (RP) is currently the subject of a major international eradication effort, coordinated by the Food and Agriculture Organization (FAO) of the United Nations through the Global Rinderpest Eradication Programme, in conjunction with the World Organisation for Animal Health (OIE). A target date for the worldwide eradication of RP was set for the year 2010 (15).

Until 1994, when a mild form of RP was detected and diagnosed in cattle in the Tsavo East National Park (in Kenya, close to the Tanzanian border), and subsequently in Nairobi National Park (1994 to 1996), the main endemic infected area in East Africa was believed to be southern Sudan. All virus isolates recovered from southern Sudan and the neighbouring areas since 1983 have been of the African type 1 lineage (8).

Initially, the Tsavo RP outbreak was thought to have originated from southern Sudan but the molecular evidence clearly showed that the Tsavo virus and the isolates from the Nairobi National Park were completely different, genetically, and fell into the African type 2 lineage. Isolates of this lineage had been recovered from West Africa as late as 1983 but not since 1962 in East Africa. Thus, a second main focus of RP was revealed in East Africa, after having remained un-reported throughout the period of the Joint Project 15 campaign (the first major programme to eradicate rinderpest that began in 1961) and eight years of the Pan-African Rinderpest Campaign. The exact location of this focus was uncertain but surveillance had concentrated on north-eastern Kenya and southern Somalia (8) (Fig. 1). Between October and November 2001, an outbreak of RP was again detected and confirmed in buffalo in the Meru National Park (Kenya). The same lineage was implicated in the outbreak (Fig. 1).

Up until 2001, only limited information had been gathered on the extent of virus circulation in Somalia, due to widespread insecurity in the country since the collapse of the government in 1991. The mild clinical reaction induced by the RP African type 2 lineage in cattle posed additional challenges in detecting the disease. Kock observed that, in cattle populations, disease due to a strain of this lineage is often missed and is thus considered of no economic importance to herders (23).

A large-scale, cross-sectional sero-survey was therefore conducted from 2002 to 2003 in ten administrative...
regions of central and southern Somalia (346,501 km²). The aim of this survey was to estimate the seroprevalence and geographic distribution of RP in the study area, as well as to identify potential risk factors for disease maintenance and spread. In the absence of a systematic list of livestock holdings, the primary sampling units were selected by randomly generating the necessary number of map coordinates. This study was also used to test the feasibility of the spatially integrated investigation technique.

Materials and methods

Survey design and implementation

Ten administrative regions from central and southern Somalia were included in the survey:

- Bakool
- Bay
- Galgadud
- Gedo
- Hiran
- Lower Juba
- Lower Shabele
- Middle Juba
- Middle Shabele
- Mudug, south of Galkayo.

The study area was selected for its cattle density (16, 37), as well as on evidence of RP virus (RPV) activity in the past two decades. Less than 10% of the cattle population of Somalia is found in the northern regions (16, 37). The study area is shown in Figure 2 and the identified sampling locations in Figure 3.

The study consisted of a cross-sectional sero-survey. The sample size was calculated for a two-stage, cluster-sampling design, and the primary sampling units were randomly generated as geospatial (map) coordinates. The between-cluster variance in the study area was calculated according to Thrusfield (46), using data collected from previous pilot studies (40, 41), then used to compute the final sample size for each administrative region. The sample-size calculations assumed:

- an expected prevalence of 50% (as the worst-case scenario, since no precise prevalence estimates were available for the study area)
- a confidence level of 95%
- 5% absolute precision.

A total of 9,000 targeted samples (15 per sampling location) were assigned to 600 randomly selected locations (identified by random map coordinates), which were proportionally allocated, according to the presumed density of the cattle population in each region of interest. Ten spare coordinates for each sampling team (10% of the target number of sampling locations) were also generated to allow for the possibility of not reaching a specific sampling site or not finding animals in it.

The survey was implemented by 20 contracted investigation teams (two per administrative region). Each team, composed of a team leader, an assistant and a monitor, operated under the close field supervision of permanent staff of the Pan-African Programme for the Control of Epizootics (the Somali component). When a specific target site was reached, using a hand-held global positioning system (GPS), the investigating teams found the herd that was closest to the target coordinates. The distance around the target site in which animals could be bled was set at a 10-km radius. If no
animals were found within the set radius, or the site was not able to be reached, then a spare site was used instead. When the herd was identified, the coordinates of the actual sampling site were recorded, and a total of 16 to 17 eligible animals (i.e. from 12 to 36 months) were bled (to allow for spoilage of samples).

The ages of the cattle were determined by inspecting their teeth, and double-checked against the knowledge of the local pastoralists. Animals between 12 and 36 months old were selected with the purpose of identifying relatively recent circulation of RPV and to avoid sampling animals that still possessed maternal antibodies or had been vaccinated during previous RP vaccination campaigns. The last official RP vaccination campaigns were carried out in Somalia in 1998 and 1999, in the Trans-Juba regions (i.e. Lower Juba, Gedo and part of Middle Juba) (40), and in the neighbouring north-eastern region of Kenya in 2000.

At each sampling site, specifically designed questionnaires were given to the livestock owners of the sampled herds. The information collected through the questionnaire included:

- the livestock species owned (e.g. cattle, sheep, goats and camels)
- the herd or flock size of each livestock species
- the location of the cattle herd during the previous two years
- the RP vaccination history

All herds that were reported to have received RP vaccination within the four-year period preceding the survey were excluded from the study, to avoid the inclusion of vaccinated animals. All questionnaires were translated into Somali (the national language spoken in Somalia) and administered to livestock keepers by trained Somali veterinary professionals. The information collected through the questionnaires was validated by interviewing three members of the same family independently. The veterinary professionals were trained in data collection using questionnaires over a period of three years, by an independent programme. Only those veterinary professionals from the area under investigation participated in the survey, to guarantee accessibility to the area as well as good interaction with the pastoralists belonging to the same clan. All collected sera were tested for the presence of antibodies against RP at the Kenya Agricultural Research Institute – Veterinary Research Centre in Muguga, Kenya, using an RP competitive enzyme-linked immunosorbent assay, directed against the haemagglutinin protein of the virus (1). All samples with a percentage of inhibition of 50 were retested. The specificity and sensitivity of the test were 99.9% and 98.5%, respectively (2).

**Data analysis**

The observed between-cluster variance was taken into account when analysing the data to calculate the standard error used in the construction of the confidence intervals. The observed seroprevalence was adjusted, using the method described by Rogan and Gladen (31).

The global spatial autocorrelation of the observed seroprevalence was tested using a Moran’s I statistic (28) and visualised in the form of a Moran scatter plot (5, 6, 7). A fourth-order rook contiguity weight matrix, which included all lower-order contiguities, was used for the analysis. Since significant global spatial autocorrelation was detected, a local indicator of spatial autocorrelation (LISA) was used to detect the local spatial dependency of the observed seroprevalence (4).

Logistic regression analysis was used to identify potential risk factors that could explain the observed distribution of seroprevalence (20, 25). The explanatory variables of the model were selected according to their potential to influence maintenance and spread of the disease in the study area. The data collection teams were also included as an explanatory variable, to assess bias due to collection practices. The explanatory variables included in the study are provided in Table I.

A ‘design-based’ analysis, which considered stratification, clustering and statistical weights, was used (24, 30, 36, 45). According to the survey design, the strata in the model were considered to be the ‘Administrative regions’ and the primary sampling units were the ‘Sampling locations’.

**Table I**

<table>
<thead>
<tr>
<th>Code</th>
<th>Variable description</th>
<th>Variable unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hr</td>
<td>Home range of the herd calculated with the minimum convex polygon method</td>
<td>km²</td>
</tr>
<tr>
<td>MDens</td>
<td>Mean cattle population density of the herd locations over the two-year period before the time of the survey</td>
<td>Head of cattle /km²</td>
</tr>
<tr>
<td>MDist</td>
<td>Mean distance of the herd locations from cattle trade routes over the two-year period before the time of the survey</td>
<td>km</td>
</tr>
<tr>
<td>HSC</td>
<td>Cattle herd size</td>
<td>Number of animals</td>
</tr>
<tr>
<td>FSS</td>
<td>Size of the sheep flock belonging to the owner of the cattle included in the survey</td>
<td>Number of animals</td>
</tr>
<tr>
<td>FSG</td>
<td>Size of the goat flock belonging to the owner of the cattle included in the survey</td>
<td>Number of animals</td>
</tr>
<tr>
<td>Team_ID</td>
<td>Identification code of the data collection teams</td>
<td>Categorical</td>
</tr>
</tbody>
</table>

Team_ID Identification code of the data collection teams 1 to 20 entered in the model as dummy variable.
The home range of each herd included in the study was estimated by first obtaining the geographic coordinates of the locations of the herds (according to the reports of the pastoralists) during the different seasons (e.g. Jiilaal: December to March; Gu`: April to June; Xagaa: July to September and Dayr: October to November) of the two years prior to the survey. The geographic coordinates of each location were obtained from databases for Somalia, Kenya and Ethiopia (22, 48, 52). If a particular reported location was not included in the available databases, then the location was visited and the geographic coordinates were recorded.

The home range for each herd was then calculated, using the minimum convex polygon (MCP) method (51), and a buffer of 5 km around the MCP was created, to account for the reported daily mobility of the herds. The buffer radius reflects the estimated average mobility of the herds in the study area. The area of the home range polygon was then extracted and used as an explanatory variable for the mobility of each herd. Figure 4a provides the location of the herd (during different seasons), used as an example, while Figure 4b shows the method used to calculate the home range of the individual herd.

The mean population density of the cattle at the herd locations, over the two years before the survey, was calculated by generating a cattle density map. The cattle population density for each administrative region was derived by projections of cattle population growth (16), based on the 1989 livestock census for Somalia (37). A neighbourhood analysis (moving average) (27) was performed on the available data (Fig. 5).
The spatial autocorrelation of the observed and predicted prevalence and the residuals of the model were tested. For the spatial autocorrelation analysis, an inverse-distance, spatial-weight matrix was created. The geographic location used for the construction of the matrix was considered to be the centroid of the home range polygon of each individual herd. The ‘global spatial autocorrelation’ of the data was tested, using a Moran’s I statistic (28).

First-order interactions were also tested for significance at $\alpha = 0.05$. The ‘goodness-of-fit’ of the model (containing only the significant variables, each at the correct power, and the significant first-order interaction) was then assessed using the Hosmer-Lemeshow (19) and Brown (10) goodness-of-fit tests.

The model was then adjusted via the ‘bootstrap’ method (13, 14), in which the model parameters were reassessed by re-sampling the available data and then used to predict the spatial risk of RP occurrence in the study area. The model parameters were re-estimated by re-sampling the available data set 1,000 times. At each cycle, 90% of the primary sampling unit was randomly re-sampled and the model was refitted. The best model coefficients were then derived from the distribution of the model coefficients’ population obtained from the bootstrap.

To use the identified risk factors in a geospatial analysis environment, a distribution map was created for each of the four main effect variables and the three interactions. The distribution maps for cattle herd mobility (home range) and cattle herd size were generated using kriging techniques (11, 29, 38, 50). The final risk map was created using the reassessed multiple linear regression (MLR) model by back-transforming the estimated logit (20) values, as follows:

$$p = \frac{e^{g(x)}}{1 + e^{g(x)}} \quad [1]$$

where:

- $p$: is the probability of disease (RP)
- $g(x)$: is the final logistic regression model.

The risk map was then reclassified to identify low-, medium- and high-risk areas for RP occurrence, according to expert opinion.

The logistic regression analysis was carried out in STATA® 8.0 SE, while the MCPs were obtained using the Hawthorne’s Analysis Tool extension of ArcGIS 8.3. The cattle density and distance maps were created using the Spatial Analyst extension of ArcGIS 8.3. The analysis of
the spatial autocorrelation of the residuals of the model was carried out in GeoDa 0.9.5-i-β.

**Results**

The field operations lasted 42 days, from the first day of training to the last day of sample collection in the field. All herds were sampled within Somali territory. However, it was reported that a few herds (4%) crossed the country’s borders and that, during certain seasons, herds were grazed in neighbouring areas of Kenya and Ethiopia. A total of 9,216 serum samples (102.4% of targeted samples) were collected from cattle aged 12 to 36 months at 562 sampling sites (93.6% of the target sites). Some 6.4% of the target sampling sites could not be reached, because of prevailing insecurity in the area or inaccessibility of the location, due to lack of road networks. The number of locations where antibodies against RP were detected in at least one of the animals sampled was 206 (36.6%), with a mean prevalence among these positive locations of 18.2% (range: 5.8% to 82.4%). Table II summarises the RP seroprevalence, along with corresponding 95% confidence intervals by region.

<table>
<thead>
<tr>
<th>Region</th>
<th>Cattle aged 12 to 36 months</th>
<th>Prevalence (%)</th>
<th>95% CI (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bakool</td>
<td>0.6</td>
<td>(0.2; 1.5)</td>
<td></td>
</tr>
<tr>
<td>Bay</td>
<td>0.7</td>
<td>(0.3; 1.7)</td>
<td></td>
</tr>
<tr>
<td>Galgadud</td>
<td>1.4</td>
<td>(0.5; 2.3)</td>
<td></td>
</tr>
<tr>
<td>Gede</td>
<td>17.7</td>
<td>(15.2; 20.6)</td>
<td></td>
</tr>
<tr>
<td>Hiran</td>
<td>4.1</td>
<td>(2.8; 6.1)</td>
<td></td>
</tr>
<tr>
<td>Lower Juba</td>
<td>16.8</td>
<td>(14.7; 19.7)</td>
<td></td>
</tr>
<tr>
<td>Lower Shabele</td>
<td>2.5</td>
<td>(1.8; 3.9)</td>
<td></td>
</tr>
<tr>
<td>Middle Juba</td>
<td>16.1</td>
<td>(13.9; 18.5)</td>
<td></td>
</tr>
<tr>
<td>Middle Shabele</td>
<td>0.5</td>
<td>(0.4; 1.4)</td>
<td></td>
</tr>
<tr>
<td>Mudug</td>
<td>0.3</td>
<td>(0.2; 1.2)</td>
<td></td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>6.7</strong></td>
<td><strong>(5.7; 7.9)</strong></td>
<td></td>
</tr>
</tbody>
</table>

CI: confidence interval

The global spatial dependency of the data was tested using a Moran’s I statistic (Fig. 7). The significance of the Moran’s I was tested against a reference distribution, obtained from 999 random permutations (Fig. 8).

The Moran’s I indicated a significant global spatial dependency ($p < 0.001$) (Fig. 8) of the RP seroprevalence in the study area. The local spatial dependency was tested using a LISA statistic. Figure 9 shows the LISA cluster map of the local spatial associations for the observed seroprevalence. The significance levels of the individual spatial associations are given in Figure 10. Their significance was tested against reference distributions obtained from 999 random permutations.

The summary statistics of the explanatory variables considered in the study are provided in Table III.
Four main effect variables and three interactions had statistically detectable associations ($\alpha = 0.05$), with differences in seroprevalence (Table IV). The four main effect variables were:

- cattle home range ($Hr$)
- mean distance to cattle trade routes ($MDist.$)
- mean cattle density ($MDens.$)
- cattle herd size ($HSC$).

### Table III

Summary statistics of the explanatory variables considered in the logistic regression model for identifying potential risk factors associated with differences in rinderpest seroprevalence

<table>
<thead>
<tr>
<th>Variable</th>
<th>Mean</th>
<th>Std dev.</th>
<th>Minimum</th>
<th>Maximum</th>
<th>Unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>$Hr$</td>
<td>2,300.9</td>
<td>2,990.2</td>
<td>79.2</td>
<td>29,732.8 km²</td>
<td></td>
</tr>
<tr>
<td>$MDens.$</td>
<td>13.4</td>
<td>6.8</td>
<td>4</td>
<td>24</td>
<td>Head of cattle/km²</td>
</tr>
<tr>
<td>$MDist.$</td>
<td>43.8</td>
<td>46.3</td>
<td>0.5</td>
<td>190.5</td>
<td>km</td>
</tr>
<tr>
<td>$HSC$</td>
<td>46.7</td>
<td>42.4</td>
<td>11</td>
<td>364</td>
<td>Number of animals</td>
</tr>
<tr>
<td>$FSS$</td>
<td>32.5</td>
<td>32.0</td>
<td>0</td>
<td>253</td>
<td>Number of animals</td>
</tr>
<tr>
<td>$FSG$</td>
<td>48.8</td>
<td>52.4</td>
<td>0</td>
<td>407</td>
<td>Number of animals</td>
</tr>
<tr>
<td>Team_ID</td>
<td>Categorical variable (1 to 20)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### Table IV

Logistic regression model for identifying potential risk factors associated with differences in the seroprevalence of rinderpest

The odds ratio values are provided in square brackets.

<table>
<thead>
<tr>
<th>Variables</th>
<th>Coefficient/ [odds ratio]</th>
<th>Standard error</th>
<th>P</th>
<th>95% Confidence interval</th>
</tr>
</thead>
<tbody>
<tr>
<td>Constant</td>
<td>–1.89</td>
<td>0.12</td>
<td>&lt;0.001</td>
<td>–2.14; –1.64</td>
</tr>
<tr>
<td>$Hr$</td>
<td>0.57</td>
<td>0.08</td>
<td>&lt;0.001</td>
<td>0.40; 0.74</td>
</tr>
<tr>
<td>$MDens.$</td>
<td>–2.77</td>
<td>0.69</td>
<td>&lt;0.001</td>
<td>–4.14; –1.40</td>
</tr>
<tr>
<td>$HSC$</td>
<td>–0.19</td>
<td>0.04</td>
<td>&lt;0.001</td>
<td>0.28; –0.09</td>
</tr>
<tr>
<td>$MDist.$</td>
<td>–4.37</td>
<td>1.37</td>
<td>&lt;0.001</td>
<td>–7.07; –1.67</td>
</tr>
<tr>
<td>$MDens. \times HSC$</td>
<td>0.27</td>
<td>0.07</td>
<td>0.002</td>
<td>0.13; 0.41</td>
</tr>
<tr>
<td>$MDist. \times Hr$</td>
<td>–0.99</td>
<td>0.39</td>
<td>0.011</td>
<td>–1.76; –0.23</td>
</tr>
<tr>
<td>$MDens. \times MDist.$</td>
<td>3.56</td>
<td>1.57</td>
<td>0.024</td>
<td>0.46; 6.65</td>
</tr>
</tbody>
</table>

P: probability

$Hr$: home range
$MDens.$: mean cattle density
$MDist.$: mean distance of the herd locations from the cattle trade routes
$HSC$: herd size, cattle
$FSS$: flock size, sheep
$FSG$: flock size, goats
The three interactions were:
– MDens. × HSC
– MDist. × Hr
– MDens. × MDist.

Both the Hosmer-Lemeshow (number of groups: 10; \( \chi^2: 8.13 \); degree of freedom: 8; \( p: 0.42 \)) and the Brown (\( \chi^2: 1.254 \); degree of freedom: 1; \( p: 0.263 \)) goodness-of-fit tests indicate that the final fitted MLR model had a good fit.

The residuals of the final model were then tested for spatial autocorrelation using a Moran’s I statistic. No spatial autocorrelation was detected (Table V).

The model parameters reassessed via the bootstrap method are given in Table VI.

The risk – probability: \( p(x) \) – distribution maps generated (using the reassessed MLR model and the reclassified risk map) are given in Figures 11 and 12, respectively. Based on expert opinion, the following risk levels were considered for the reclassification:

i) low risk: \( p(x) < 0.005 \)
ii) medium risk: \( 0.005 \leq p(x) \leq 0.03 \)
iii) high risk: \( p(x) > 0.03 \).

**Discussion and conclusion**

This work represents the first structured, large-scale, cross-sectional study carried out in the cattle-rearing areas of Somalia over the past two decades. The prevailing conditions of insecurity that have characterised Somalia since 1991 were one of the primary obstacles preventing the implementation of epidemiological investigations in the country. The absence of Veterinary Services since the government collapsed and the lack of qualified veterinary professionals were also important factors that negatively affected the ability to implement a structured survey. Moreover, the husbandry system of Somalia is characterised by the high-to-moderate mobility of the Somali herds and/or flocks, which further complicated the ability to perform a survey using traditional sampling strategies. These facts have made the application of a randomised survey to collect statistically valid data a challenge for decades.

**Table V**

<table>
<thead>
<tr>
<th>Variables</th>
<th>Moran’s I</th>
<th>Pseudo-significance level (p)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Observed prevalence</td>
<td>0.339</td>
<td>&lt; 0.001</td>
</tr>
<tr>
<td>Predicted prevalence</td>
<td>0.610</td>
<td>&lt; 0.001</td>
</tr>
<tr>
<td>Model residuals</td>
<td>0.012</td>
<td>0.178</td>
</tr>
</tbody>
</table>

**Table VI**

<table>
<thead>
<tr>
<th>Variables</th>
<th>Coefficient</th>
<th>Standard error</th>
<th>95% Confidence interval</th>
</tr>
</thead>
<tbody>
<tr>
<td>Constant</td>
<td>–1.89</td>
<td>0.13</td>
<td>–2.16; –1.62</td>
</tr>
<tr>
<td>Hr</td>
<td>0.57</td>
<td>0.09</td>
<td>0.40; 0.80</td>
</tr>
<tr>
<td>MDens.</td>
<td>–2.72</td>
<td>0.72</td>
<td>–4.29; –1.41</td>
</tr>
<tr>
<td>HSC</td>
<td>–0.19</td>
<td>0.05</td>
<td>–0.29; –0.09</td>
</tr>
<tr>
<td>MDist.</td>
<td>–4.56</td>
<td>1.48</td>
<td>–7.70; –1.88</td>
</tr>
<tr>
<td>MDens. × HSC</td>
<td>0.26</td>
<td>0.11</td>
<td>0.02; 0.48</td>
</tr>
<tr>
<td>MDist. × Hr</td>
<td>–0.97</td>
<td>0.34</td>
<td>–1.63; –0.28</td>
</tr>
<tr>
<td>MDens. × MDist.</td>
<td>3.37</td>
<td>1.55</td>
<td>0.45; 6.38</td>
</tr>
</tbody>
</table>

Hr: home range
MDens.: mean cattle density
MDist.: mean distance of the herd locations from the cattle trade routes
HSC: herd size, cattle
FSS: flock size, sheep
FSG: flock size, goats

Fig. 11
Risk \( p(x) \): logit of the logistic regression model map for the seroprevalence of rinderpest in central and southern Somalia, calculated using the logistic regression model, reassessed by the bootstrap method.
This study is a unique example of the adaptation and application of conventional investigation methodologies to investigate diseases in the absence of a list or other structured sampling frame, in nomadic and semi-nomadic husbandry conditions, and in areas of prevailing instability. The involvement of well-trained Somali veterinary professionals significantly aided access to all areas, including insecure areas. Only 6.4% of the target sampling sites could not be reached, and more samples were collected than required for the target quota using this methodology.

Varying RP seroprevalences were observed in the investigated areas. The highest values were detected in three administrative regions (Lower Juba, Middle Juba and Gedo) that border Kenya to the west (Table II). Intermediate seroprevalence was identified in Hiran and in Lower Shabele, while the remaining regions had negligible seroprevalences (Table II).

The spatial analysis has highlighted a significant global spatial dependency in the observed seroprevalence (Figs 7 & 8). The local high-to-high and high-to-low spatial dependencies detected by the LISA test suggested the existence of two potential seroprevalence clusters in the country (Lower Juba, Middle Juba, Gedo and part of Lower Shabele as Cluster 1; and Hiran as Cluster 2) (Fig. 9).

The serological tests available for RP antibody detection do not allow for differentiation between antibodies against the RP virus, vaccination strains or maternal antibodies. During the survey, measures were taken to prevent the inclusion of animals that might possess maternal or vaccination-induced antibodies against RP (e.g. only sampling animals 12 to 36 months old and excluding herds with a vaccination history within the four years before the survey). Well-trained Somali veterinary professionals were recruited to conduct the survey. The teeth of the animals were assessed to establish their age, in addition to gathering this information from the pastoralists. It has been noted that pastoral communities in the Somali ecosystem of the Horn of Africa are livestock specialists and local knowledge has been used to estimate population structure, life expectancy and disease incidence in several pastoral communities (26). However, despite these preventive measures, the authors cannot exclude the possibility that a few animals bearing maternal or vaccination-induced antibodies were included in the survey.

The application of multivariate logistic regression analysis (adjusted using the bootstrap method, which allows the refining of the model coefficients from a coefficient population) identified and quantified the magnitude of four main risk factors (Table IV) for the observed seroprevalence of RP in central and southern Somalia, namely:
- herd mobility
- cattle density
- cattle herd size
- distance from cattle trade routes.

These findings are not surprising since RP is mainly transmitted by close contact between susceptible and infected animals. The transmission is believed to be by droplet, either in the breath of an infected animal or in its secretions and excretions (34), but close contact is required for effective contagious spread. All the identified risk factors contribute to the increase of the contact rate between individuals in the population.

Additional methods of contagious spread, such as airborne transmission, have also been investigated. Experimentation has shown that airborne transmission is a theoretical possibility over several hundred metres (21), but circumstantial evidence does not support the hypothesis that this type of transmission plays a role in the spread of the disease under natural conditions. Furthermore, the fragile nature of the virus ensures that most infectivity survives for only a few hours outside the host, though some may persist, under favourable conditions, for up to two to four days (35, 47). Carcass decomposition inactivates the virus within one to three days (12).

The ease with which the disease is transmitted depends upon the strain of the virus (34). Virulent strains induce a severe clinical manifestation in the host which, during the...
earliest stages of clinical disease, excretes infectious virus in its ocular, nasal, oral and vaginal secretions and faeces (12, 17, 18, 34).

For mild forms of RP, where few clinical reactions (discharges) are induced, a high contact rate between individuals may be necessary to allow effective virus transmission. Using serological data collected in the Lower Juba and Gedo regions, during a preliminary study conducted under a similar framework in 1998 to 1999 (40), Mariner et al. (26) estimated a basic reproductive number \( R_0 \) for the lineage 2 virus in the Somali ecosystem (Somalia and its neighbouring areas of Kenya and Ethiopia) of between 1.2 and 1.9. The basic reproductive number is a feature of transmissibility of an agent in a totally susceptible population and encompasses the characteristics of both the infectious agent and the host population in which transmission occurs (3). The model for the lineage 2 virus was validated using a subset of samples (from Lower Juba and Middle Juba) (39) generated under the study presented in this paper. No differences between the test prevalence and the model estimated prevalence were found (26). In the same study, Mariner et al. estimated an \( R_0 = 4.4 \) for the southern Sudan lineage 1 virus. The estimated \( R_0 \) for the lineage 2 virus is less than half the \( R_0 \) for the lineage 1 virus. When the \( R_0 < 1 \), the infection will die out in the long run, provided that infection rates are constant (3). More sedentary husbandry systems, low cattle density and small herd sizes may considerably reduce the chances of transmitting the virus. This may explain the absence or very low levels of RP antibodies in certain zones of the study area, even though there were no physical barriers, movement restrictions, quarantine or vaccination interventions in the country at the time of the survey.

Proximity to cattle trade routes can considerably increase the risk of contracting the disease. Trade herds are normally large, move quickly, may pass through infected areas and are grazed alongside the trade routes, often using the same pastures as nomadic herds. The animals that are moved for export could therefore play an important role in spreading the disease over long distances in a short time.

Sheep and goats are known to be susceptible to RP, and may transmit the disease to cattle (9, 33). In Somalia, herd diversification (in terms of livestock species) is a common feature, since it allows pastoralists to exploit the natural resources available in different environments more effectively. It is not rare for sheep and goats to be herded alongside cattle by the same family. However, the size of the herds or flocks and their relative composition, in terms of livestock species, may vary considerably from area to area. Sheep and goat flocks herded with cattle were considered a potential risk factor in the study, but neither of these two variables was found to be significant in the model. These results are consistent with experience in northern Tanzania, where small ruminants did not seem to be important in RP transmission of lineage 2 (49). The data collection team variable was also not found to be significant in the model, suggesting that no bias was introduced into the study by sampling practices.

Three out of six first-order interactions were significant in the model:

- cattle density × cattle herd size
- distance from cattle trade routes × herd mobility (home range)
- cattle density × distance from cattle trade routes.

The transmission of the virus is likely to occur efficiently within a herd. Large herds can maintain the disease more efficiently than small herds and produce a large number of infectious animals that, in turn, may infect other herds. Transmission between herds may be facilitated in highly populated areas. Similarly, it can be argued that infection contracted through contact with trade cattle can be spread across the resident population more efficiently in areas where the herd mobility is elevated and/or in highly populated areas. No spatial autocorrelation was detected for the residuals of the model, meaning that the explanatory variables accounted for the spatial dependence identified for the observed and predicted prevalences.

The integration of spatial and logistic regression analysis enabled the production of risk maps, which can be used to formulate more focused surveillance strategies. Similar serological studies later conducted in the study area detected antibodies against RP in the high-risk areas identified in this study. However, the reported seroprevalence in these areas was observed to decline over time (42, 43, 44). Similar seroprevalence studies conducted in neighbouring areas of Kenya and Ethiopia in subsequent years also showed a very low seroprevalence or the absence of RP antibodies (1). The progressive decline in RP antibody prevalence is consistent with virus extinction. The verification of freedom from RP infection in the Somali ecosystem is currently in progress.

Although considerable progress has been achieved on RP eradication in the study area since this study was conducted, the value and applications of the applied methodology remain of interest for investigating other livestock diseases in nomadic and semi-nomadic pastoral systems.

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Enquête sérologique conduite en 2002 et 2003 sur la peste bovine dans les systèmes pastoraux nomadiques du centre et du sud de la Somalie, basée sur une méthode d’échantillonnage intégrant les données spatiales


Résumé
Une enquête sérologique transversale basée sur une méthode d’échantillonnage en grappes à deux étapes a été menée pendant les années 2002 et 2003 dans dix régions administratives du centre et du sud de la Somalie dans le but d’estimer la prévalence sérologique et la distribution géographique de la peste bovine dans les zones étudiées et d’identifier les facteurs de risque potentiels pouvant expliquer la distribution constatée de cette prévalence. L’étude a également permis de tester la faisabilité d’une technique intégrant les données spatiales dans les enquêtes portant sur les systèmes pastoraux nomadiques et semi-nomadiques. En l’absence d’une liste complète des élevages, les unités primaires d’échantillonnage ont été établies en utilisant des coordonnées spatiales déterminées de manière aléatoire. Pour cette étude, 9 216 sérums ont été prélevés sur des bovins âgés de 12 à 36 mois provenant de 562 sites différents. L’analyse de la prévalence sérologique a permis de constater l’existence de deux grappes distinctes d’infection de peste bovine. Quatre facteurs de risque ont été associés à la prévalence sérologique constatée : la mobilité des troupeaux, la densité de la population bovine, la proximité des troupeaux avec les routes commerciales où transitent des bovins et la taille des troupeaux.

Une cartographie des risques a été établie afin de contribuer à la mise au point de stratégies de surveillance ciblées. La prévalence sérologique constatée dans ces régions a progressivement diminué. Lors des années qui ont suivi, des enquêtes sérologiques similaires réalisées dans des zones voisines du Kenya et d’Éthiopie ont révélé une prévalence sérologique très faible, voire l’absence totale d’anticorps dirigés contre la peste bovine. Cette diminution progressive est cohérente avec la disparition du virus. Le statut indemne de peste bovine de l’écosystème somalien est actuellement en cours de confirmation.

Mots-clés
Aplicación a sistemas de pastoreo nómadas de un método de muestreo aleatorio con integración espacial: estudio serológico de la peste bovina en el centro y sur de Somalia de 2002 a 2003


Resumen
Utilizando un método de muestreo por conglomerados en dos etapas, de 2002 a 2003 se llevó a cabo en diez regiones administrativas del centro y el sur de Somalia un estudio serológico transversal para estimar la seroprevalencia y la distribución geográfica de la peste bovina en el área de estudio y detectar eventuales factores de riesgo ligados a la distribución de la seroprevalencia observada. El estudio también sirvió para ensayar la aplicación de la técnica de investigación espacialmente integrada a los sistemas de pastoreo nómadas y seminómadas. A falta de un repertorio sistemático de las explotaciones ganaderas, las unidades primarias de muestreo se eligieron generando coordenadas cartográficas aleatorias. Tras extraer un total de 9.216 muestras séricas de bovinos de entre 12 y 36 meses de edad de 562 lugares diferentes, se observaron dos aparentes conglomerados de seroprevalencia de peste bovina y se determinaron cuatro posibles factores de riesgo ligados a la seroprevalencia observada: la movilidad de los rebaños, la densidad de la población bovina, el tamaño de los rebaños y su proximidad a las rutas de comercio ganadero. A continuación se elaboró una cartografía de los riesgos como elemento auxiliar para la concepción de estrategias de vigilancia más específicas. Con el paso del tiempo se observó una caída de la seroprevalencia en las zonas en cuestión. En los años subsiguientes se llevaron a cabo estudios similares en áreas contiguas de Kenia y Etiopía, que también pusieron de manifiesto una seroprevalencia nula o muy baja de anticuerpos contra la peste bovina. El progresivo descenso de la prevalencia de anticuerpos apunta a la extinción del virus. Actualmente se están realizando estudios para comprobar que el ecosistema somalí esté libre de la infección por el virus de la peste bovina.

Palabras clave

References


