Bovine tuberculosis surveillance system evaluation - Greater-Accra Region, Ghana, 2011

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Background: Bovine tuberculosis (BTB) is caused by Mycobacterium bovis. Developed countries have succeeded to control BTB infections and reduced its transmission to humans through the enforcement of meat inspection laws, test and slaughter/segmentation of positive reactors, and milk pasteurisation. This was paralleled by a concomitant decrease in human tuberculosis infections (HTBI) from 5%-20% to 0.5%-1% in the past five decades. In developing countries, an estimated 10-15% of HTBI are attributed to M. bovis, however, weak control measures and under reporting of BTB may grossly underestimate this. Surveillance by the Veterinary Services Directorate (VSD) through meat inspection, voluntary reporting and periodic cattle screening with the objective to early detect and monitor trend for rapid intervention are the mainstay of control. Controlling BTB in cattle results in its reduction in humans; hence, we evaluated the BTB surveillance system in the Greater-Accra Region of Ghana to determine its performance and assessed the system’s attributes.

Methods & Materials: We interviewed stakeholders, reviewed veterinary monthly reports of all ten districts in the region, laboratory and screening records, and extracted surveillance data from national electronic database for the period 2006-2011 using the CDC Guidelines for Evaluation of Public Health Surveillance Systems.

Results: From 2006-2011, 284/244,576 (0.12%) cattle slaughtered were suspected to have BTB; of which 7/284 (2.5%) were submitted and all laboratory-confirmed positive by Ziehl-Neelsen acid-fast stain test; predictive value positive (PVP) being 100%. From the suspected carcasses, there were 91 partial and 8 total condemnations. BTB detected at slaughter rose from 13 in 2006 to 78 in 2010, then dropped to 48 in 2011. Interviews suggest that about 50% of carcasses slip through inspection. Out of 3,367 cattle screened with tuberculin from eight farms, 97 (2.9%), tested positive and were culled. Ninety percent (9/10) of districts consistently submitted reports late to the region whereas 70% (7/10) made no reference to BTB. Regional and district data were manually stored with no electronic backups.

Conclusion: The BTB surveillance system is sensitive, useful and monitors trend, however, timeliness, representativeness, completeness of reporting, and data quality need improvement. Non-reporting districts are now reporting following training.

Tracking the inter-epidemic activity of Rift Valley fever (RVFV) virus in RVF outbreak hotspots in Kenya: Determination of biotic and socio-economic drivers

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Background: Rift Valley Fever is a mosquito-borne viral zoonosis that affects humans and livestock occurring in periodic epidemic hotspot areas in Africa and the Middle East mostly during periods of heavy sustained rainfall. RVFV transmission is a complex process involving vectors which emerge in large numbers during flood- ing and involving livestock, wildlife, and humans. The livelihoods of communities in arid N.E Kenya depend on nomadic pastoralism where large livestock herds are moved in search of pasture and water all year round. It is hypothesized that ecological, climatic, human/mosquito behavioral determinants contribute to the virus spread and the burden of human and animal disease due to RVFV remains undetermined during inter-epidemic periods hence missed opportunities for prevention. To improve our understanding of how these factors influence virus activity between epidemics and how these can be exploited to reduce epidemics, we attempted to understand the spatiotemporal dynamics of the virus, determine how nomadic pastoral lifestyle and the vector response to environmental dynamics.

Methods & Materials: Five livestock herds were selected in North Eastern Kenya (RVF hotspot areas) and tracked using GPS collars. Tracking data was imported into a GIS system to provide mapping. Periodic sampling of 10% of each selected herd was screened for antibody to RVFV after each rainy season. Vector sampling, speciation and virus screening along the same route was also analyzed. Participatory mapping was used to understand the underlying dynamics that guide the decision-making process of the livestock owners.

Results: The map generated from animal tracking demonstrated pattern of animal movement in search of pasture largely driven by availability of pasture/water and avoidance of diseases like trypanosomiasis. There was increased virus activity (animal seroprevalence) after the rains as animals emerged from forested high vegetation areas which provide pasture during extended drought. This was strongly supported by the distribution and abundance of primary and secondary vectors of Rift Valley Fever, principally Aedes mcintoshi, Aedes ochraceus, Culex poicilipes and Anopheles squamosus.

Conclusion: These findings demonstrated how the spatial distribution patterns of RVF was influenced by the nomadic pastoral system and provided information that could be helpful in guiding interventions for RVF control.