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Epidemiologic and Genomic Characterization of an Outbreak of Rift Valley Fever Among Humans and Dairy Cattle in Northern Tanzania

Deng B. Madut[1], **Matthew P. Rubach**[1], **Kathryn J. Allan**[2], **Kate M. Thomas**[3], **William A. de Glanville**[2], **Jo E. B. Halliday**[2], **Cristina Costales**[1], **Manuela Carugati**[1], **Robert J. Rolfe**[1], **John P. Bonnewell**[1], **Michael J. Maze**[4], **Alex R. Mremi**[5], **Patrick T. Amsi**[5], **Nathaniel H. Kalengo**[5], **Furaha Lyamuya**[5], **Grace D. Kinabo**[5], **Ronald Mbwasi**[5], **Kajiru G. Kilonzo**[6], **Venance P. Maro**[6], **Blandina T. Mmbaga**[6], **Bingileki Lwezaula**[7], **Calvin Mosha**[7], **Annette Marandu**[7], **Tito J. Kibona**[8], **Feng Zhu**[9], **Tanu Chawla**[9], **Wan Ni Chia**[9], **Danielle E. Anderson**[9], **Lin-Fa Wang**[9], **Jie Liu**[10], **Eric R. Houpt**[11], **Roosecelis B. Martines**[12], **Sherif R. Zaki**[12,a], **Austin Leach**[13], **Aridth Gibbons**[13], **Cheng-Feng Chiang**[13], **Ketan Patel**[13], **John D. Klena**[13], **Sarah Cleaveland**[2], **John A. Crump**[3]

[1]Division of Infectious Diseases and International Health, Department of Medicine, Duke University, Durham, North Carolina, USA;

[2]Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow, Glasgow, United Kingdom;

[3]Centre for International Health, University of Otago, Dunedin, New Zealand;

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Correspondence: Deng B. Madut, MD, Division of Infectious Diseases, Duke University, 315 Trent Drive, Hanes House, Room 253, Durham 27710, NC (deng.madut@duke.edu).

[a]S. R. Z. deceased.

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Supplementary Data

Supplementary materials are available at *The Journal of Infectious Diseases* online (http://jid.oxfordjournals.org/). Supplementary materials consist of data provided by the author that are published to benefit the reader. The posted materials are not copyedited. The contents of all supplementary data are the sole responsibility of the authors. Questions or messages regarding errors should be addressed to the author.

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[4]Department of Medicine, University of Otago, Christchurch, New Zealand;

[5]Kilimanjaro Christian Medical Centre, Moshi, Tanzania;

[6]Kilimanjaro Christian Medical University College, Moshi, Tanzania;

[7]Mawenzi Regional Referral Hospital, Moshi, Tanzania;

[8]Nelson Mandela African Institution of Science and Technology, Arusha, Tanzania;

[9]Programme in Emerging Infectious Diseases, Duke-National University of Singapore Medical School, Singapore, Singapore;

[10]School of Public Health, Qingdao University, Qingdao, China;

[11]Division of Infectious Diseases and International Health, Department of Medicine, University of Virginia, Charlottesville, Virginia, USA;

[12]Infectious Diseases Pathology Branch, Centers for Disease Control and Prevention, Atlanta, Georgia, USA;

[13]Viral Special Pathogens Branch, Centers for Disease Control and Prevention, Atlanta, Georgia, USA

Abstract

Background. A periurban outbreak of Rift Valley fever virus (RVFV) among dairy cattle from May through August 2018 in northern Tanzania was detected through testing samples from prospective livestock abortion surveillance. We sought to identify concurrent human infections, their phylogeny, and epidemiologic characteristics in a cohort of febrile patients enrolled from 2016 to 2019 at hospitals serving the epizootic area.

Methods. From September 2016 through May 2019, we conducted a prospective cohort study that enrolled febrile patients hospitalized at 2 hospitals in Moshi, Tanzania. Archived serum, plasma, or whole blood samples were retrospectively tested for RVFV by PCR. Human samples positive for RVFV were sequenced and compared to RVFV sequences obtained from cattle through a prospective livestock abortion study. Phylogenetic analysis was performed on complete RVFV genomes.

Results. Among 656 human participants, we detected RVFV RNA in 4 (0.6%), including 1 death with hepatic necrosis and other end-organ damage at autopsy. Humans infected with RVFV were enrolled from June through August 2018, and all resided in or near urban areas. Phylogenetic analysis of human and cattle RVFV sequences demonstrated that most clustered to lineage B, a lineage previously described in East Africa. A lineage E strain clustering with lineages in Angola was also identified in cattle.

Conclusions. We provide evidence that an apparently small RVFV outbreak among dairy cattle in northern Tanzania was associated with concurrent severe and fatal infections among humans. Our findings highlight the unidentified scale and diversity of interepizootic RVFV transmission, including near and within an urban area.

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Keywords

Africa; zoonoses; Rift Valley fever; Crimean-Congo hemorrhagic fever; Tanzania

Rift Valley fever virus (RVFV) is a zoonotic pathogen that belongs to the Phenuviridae family within the order Bunyavirales and causes Rift Valley fever (RVF) in animals and humans. The disease was first described in the Rift Valley of Kenya in 1912, and the etiologic agent was first isolated in 1931 [1]. The geographic range of the virus is now understood to include most of the African continent and more recently the virus emerged in the Arabian Peninsula [2]. There is concern for further expansion into naive regions given changing global climatic patterns and the widespread distribution of competent vectors and susceptible hosts. Due to its epidemic potential and lack of countermeasures, RVFV, along with Crimean-Congo hemorrhagic fever (CCHF) virus and others, are listed by the World Health Organization and other global bodies as priority pathogens that need further research and investment [3].

The epidemiology of RVF is characterized by periodic epizootics and epidemics that occur in cycles of 5–15 years, generally following periods of heavy rainfall that favor breeding of mosquito vectors [4]. Infected mosquitoes transmit the virus when taking a blood meal, potentially infecting a wide range of vertebrate hosts. Ruminant livestock are particularly susceptible to RVFV, leading to epizootics with high mortality among young ruminants and large numbers of near-simultaneous abortions among pregnant ruminants, sometimes referred to as “abortion storms” [5]. Infections in humans typically follow those in livestock, and humans are presumed to be exposed to RVFV through the handling of tissue from infected livestock or less commonly via bites from infected mosquitoes [4]. Most human infections are asymptomatic or manifest as a mild febrile illness [5]. However, some infected persons develop severe manifestations, including multiorgan failure and hemorrhagic complications.

Epizootics and epidemics are followed by lengthy interepizootic and interepidemic periods (IEP) where clinical disease among animals and humans is often not apparent. For this reason, early studies hypothesized that the virus was principally maintained by vertical transmission within infected *Aedes* mosquito species [6]. However, this assumption has been challenged due to the demonstration of clinical disease in livestock or humans during the IEP through active surveillance studies and the observation that vertically acquired infections are rapidly diluted in each mosquito generation unless regular amplification between vectors and hosts occurs [7–9]. Numerous modeling studies now suggest that RVFV maintenance is likely a delicate balance of environmental stochasticity, vertical transmission among mosquitoes, and horizontal transmission between mosquito species and susceptible mammalian hosts [10–12].

In 2018, testing of samples collected from a prospective livestock abortion study detected RVFV infections among 14 dairy cattle in northern Tanzania [13, 14]. This outbreak occurred outside a major epizootic and was undetected by local surveillance systems. Notable epidemiologic features of this outbreak included detecting infections within a periurban environment and RVFV nucleic acids in the milk of aborting cattle. We

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hypothesized that RVFV in cattle may have been associated with undetected spillover infections in humans that could shed light on transmission during the IEP.

To investigate the epidemiology of RVFV transmission during the IEP and the human health implications of the 2018 cattle outbreak, archived blood samples from participants enrolled in a prospective hospital-based febrile surveillance study in northern Tanzania from 2016 through 2019 were tested for RVFV. We sought to describe any contemporaneous infections in humans and characterize RVFV sequences from cattle and humans. Simultaneous with our evaluation of RVFV IEP infection in humans, we also tested for another arthropod-borne viral zoonosis, CCHF.

METHODS

Study Setting

Participants were enrolled in a prospective cohort study to understand the etiologies of febrile illness, including febrile deaths, among hospitalized patients at Kilimanjaro Christian Medical Centre (KCMC) and Mawenzi Regional Referral Hospital (MRRH) in Moshi, Tanzania from 7 September 2016 through 31 May 2019. Some results from this study have been previously published [15–20]. Moshi (population, >180 000) is the administrative center of the Kilimanjaro Region (population, >1.6 million) and is situated at an elevation of approximately 890 meters above sea level. Typical annual precipitation patterns are characterized by a semiarid climate with a long rainy period from March through May and a shorter rainy period from November through December.

Study Procedures

From Monday through Friday during the study period, all pediatric and adult patients presenting to the medical wards of KCMC and MRRH were screened within 24 hours of hospitalization. Patients presenting with a fever were eligible for enrollment if they had a tympanic temperature ≥ 38.0°C or a subjective report of fever within the previous 72 hours. After obtaining informed consent, a trained study team member completed standardized case report forms that included age, sex, and village of residence. Participants were also asked to self-report cattle contact based on the question “In the past 30 days, have you lived or worked in close contact with cattle?” Venous whole-blood samples were collected from participants into ethylenediaminetetraacetic acid (EDTA)-preservative tubes and serum separator tubes, and blood specimens were processed, aliquoted, and archived at −70°C as EDTA whole blood, EDTA-derived plasma, and serum.

In addition to febrile illness surveillance, decedents with a recorded temperature ≥ 38.0°C at any time during hospitalization or a subjective report of fever within the 72 hours before hospital admission to KCMC or MRRH were eligible for postmortem examination. Complete diagnostic autopsy was performed upon written authorization by the decedent’s family. After obtaining informed consent, a trained study team member administered a standardized questionnaire to the decedent’s next of kin to collect age, gender, village of residence, and history of contact with cattle for the decedent. Autopsies were performed by trained pathologists (C. C., A. R. M., P. T. A.) and all were considered infectious

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regardless of the clinical history. As such, all personnel participating in autopsies wore protective equipment, including scrub suits, protective coveralls, shoe covers, face shields or other protective eyewear, N95 masks, and 2 pairs of gloves. At autopsy, venous blood was collected, processed, and archived similar to that for blood specimens collected antemortem. Pathologists collected tissue samples from the brain, heart, lungs, liver, spleen, and kidneys.

Sample Processing

As part of the original study protocol, participant samples were evaluated for a range of infectious diseases, and this has been described in detail elsewhere [15–18]. To determine the human health implication of the 2018 cattle outbreak, archived human whole blood, serum, and plasma from participants with sufficient samples were shipped on dry ice from Moshi to the Viral Special Pathogens Branch of the United States Centers for Disease Control and Prevention (US CDC) to test for RVFV by reverse transcription-quantitative polymerase chain reaction (RT-qPCR) and serology (Figure 1). Decedent tissue samples were also available for RVFV testing by RT-qPCR if RVFV was detected from whole blood, serum, or plasma. To examine the phylogenetic relationship of RVFV detected in humans to that of the contemporaneous cattle outbreak, RNA was extracted from vaginal swabs from the dam, fetal swabs, or placental tissues of the 14 RVFV-infected livestock abortions by RNAeasy Mini Kit (Qiagen) and also shipped from Moshi to the US CDC (Figure 1) [14].

RNA from human samples was extracted using MagMax Pathogen RNA/DNA kit (Thermo Fisher Scientific). RVFV RNA in both human and cattle samples was detected by utilizing assays targeting the L segment (details are given in the Supplementary Materials) [21]. A target against human β−2 microglobulin was used to assess human specimen integrity. A bovine GAPDH assay designed to target glyceraldehyde 3-phosphate dehydrogenase mRNA was utilized to assess cattle specimen integrity [22]. Human and cattle samples with cycle threshold values <32 were considered positive for RVFV and are referred to as “cases” hereafter.

While the primary objective of shipping samples to the US CDC was to perform RVFV RT-qPCR and serology, a secondary objective was to test for CCHF virus (CCHFV) RT-qPCR and serology. CCHFV RT-qPCR testing used an assay targeting the NP gene in the S segment (details are given in the Supplementary Materials) [21].

Whole-Genome Sequencing and Phylogenetic Analysis of RVFV-Positive Samples

Human samples positive by RT-qPCR for RVFV underwent RNA sequencing. Libraries were constructed using the NEB Ultra II RNA Library Prep kit and sequenced on an Illumina MiSeq (Illumina) or ISEQ100. Geneious Prime version 2022.0.2 was used to map the reads to the RefSeq RVF genome. Cattle samples positive for RVFV were sequenced by amplicon-based sequencing using the Oxford Nanopore MinION instrument (Oxford Nanopore Technologies). Amplicons were trimmed at the 5′ and 3′ end before mapping to the RefSeq RVF strain [23].

Phylogenetic analysis was performed on complete RVFV genomes detected from humans and cattle. Alignments were made using Geneious Prime, trimmed to remove ambiguous bases from both ends of all sequences, normalized such that all sequences had the same

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final length, and exported as phylip alignment files. The trees were generated by submitting phylip alignments to the IQTree web server to generate maximum-likelihood trees with 1000 bootstrap iterations [24]. Tree figures were generated using the FigTree software version 1.4.4. Node labels represent a bootstrap percentage, and the scale bar shows branch length per unit of 0.01 substitutions per site. Viral lineages were designated as described by Bird et al [25].

Serology for RVFV and CCHFV

Testing for RVFV and CCHFV immunoglobulin G (IgG) was performed using enzyme-linked immunosorbent assays (ELISA) to detect human RVFV and CCHFV virus IgG in serum specimens as originally described for detection of Ebola antibodies by Ksiazek et al and adapted to CCHFV by Bryan et al and RVFV by Shoemaker et al [26–28]. All serologic testing was performed on samples collected at enrollment.

Additional Laboratory Investigations

Participants enrolled antemortem underwent molecular detection for blood pathogens by the TaqMan Array Card (TAC) multiplex for febrile illness [21]. The TAC panel was performed at the Kilimanjaro Christian Research Institute Biotechnology Laboratory and was specified in the original study protocol before the cattle outbreak was detected. The TAC panel is a real-time PCR-based microfluidic system customized for the current study to detect 20 bacteria, 2 fungi, 3 protozoa, and 19 viruses, including RVFV and CCHFV. Nucleic acid extraction was performed on 800 μL of archived human whole blood samples using the High Pure Viral Nucleic Acid Large Volume Kit (Roche) and eluted in 150 μL with 75 μL subjected to the TAC panel. A sample was considered positive if a reaction yielded cycle threshold values of <35 or <40 if confirmable by plate-based PCR using cognate assays. The confirmatory PCR used the same primer and probe oligonucleotide targets as the targets in the TAC panel design.

Whole-blood samples from decedents were sent to Duke-National University of Singapore Medical School for next-generation sequencing analysis as part of the original study protocol. RNA was extracted from whole-blood samples using the Quick-RNA Viral Kit (Zymo Research). RNA was eluted in 15 μL of RNase-free water and used to prepare libraries for next-generation sequencing. Library construction and enrichment were performed using the Twist Comprehensive Virus Research Panel (Twist Bioscience) according to the manufacturer's instructions. The enriched libraries were sent for next-generation sequencing to NovogeneAIT Genomics (NovogeneAIT Genomics Singapore Pte Ltd, Singapore) (details are given in the Supplementary Materials).

Statistical Analysis

Descriptive analyses were performed using STATA version 16.1 (StataCorp) and R Statistical Software version 4.3.2 (R Core Team 2023; RStudio, Inc). Continuous variables were expressed using means and ranges. Categorical variables were expressed as frequencies.

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Research Ethics

This study was performed in accordance with the ethical standards of the Helsinki Declaration. Written consent was obtained from all human participants or their next of kin. Ethical approval was obtained from the Research Ethics Committee of Kilimanjaro Christian Medical University College (295); the National Health Research Ethics Review Committee of the National Institute for Medical Research in Tanzania (NIMR/HQ/R.8c/Vol.IX/1000); the University of Otago Ethics Committee (H17/069); the University of Glasgow Medical, Veterinary, and Life Sciences Ethics Committee (200140152 and 20017006); and an Institutional Review Board of Duke University (Pro00016134).

RESULTS

Sociodemographic Characteristics of the Cohort

From 7 September 2016 through 31 May 2019, we enrolled 1351 human participants; sufficient samples were available to perform RVFV RT-qPCR in 656 (48.6%) (Figure 1). Of participants who underwent RT-qPCR, 537 (81.9%) were enrolled antemortem and 119 (18.1%) postmortem. Among all participants, mean age was 30 years (range, 1–96 years), 302 (46.2%) were female, and 170 (26.2%) reported contact with cattle (Table 1).

RT-qPCR for RVFV and CCHFV

RVFV was detected by RT-qPCR in serum, plasma, or whole blood from 4 (0.6%) participants, of which 3 (75.0%) were enrolled antemortem and 1 (25.0%) enrolled postmortem. All RVFV RT-qPCR–positive participants enrolled antemortem were also positive for RVFV by the TAC pathogen panel and RVFV was likewise detected by next-generation sequencing in the decedent with RVFV detection by RT-qPCR. CCHFV was not detected by RT-qPCR, TAC pathogen panel, or next-generation sequencing among participants who underwent testing.

Of RVFV-infected persons, the mean age was 41 years (range, 23–57 years), 2 (50.0%) were female, and 3 (75.0%) reported contact with cattle. The dates of enrollment for the 4 human cases were from 29 June through 23 August 2018, and those of the cattle outbreak were from 16 May through 11 August 2018 (Figure 2). Three of the human cases resided in villages of wards within the Kilimanjaro Region. These were the urban wards of Hai Mjini and Pasua and the periurban ward of Kilema Kusini. One human case was from the Manyara Region and resided in the periurban ward of Msitu wa Tembo (Figure 3).

A complete diagnostic autopsy was performed on the decedent with RVF and the virus was detected by RT-qPCR in brain, heart, and liver tissue. Detailed review of the medical chart revealed that the decedent suffered a spontaneous abortion within the month before hospitalization and laboratory studies revealed hepatic and renal dysfunction. Gross pathology revealed evidence of hemorrhagic complications with blood visualized in the peritoneal space as well as the small and large intestines. Notable microscopic findings were acute tubular necrosis in the kidneys and fulminant hepatocyte necrosis of the liver.

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Serological Testing for RVFV and CCHFV

Of 656 participants who underwent serological testing, 8 (1.2%) were positive for anti-RVFV IgG antibodies. Among seropositive participants, mean age was 45 years (range, 14–68 years), 2 (25.0%) were female, and 5 (62.5%) reported contact with cattle. Enrollment for 4 seropositive participants occurred in 2017 and the remaining 4 were enrolled from June to July 2018. Of the 4 seropositive participants enrolled from June to July 2018, 2 were RT-qPCR positive for RVFV (Table 2).

Anti-CCHFV IgG was detected in 5 (0.8%) participants of the 656 who underwent serologic testing. Among seropositive participants, mean age was 45 years (range, 22–75 years), 2 (40.0%) were female, and 2 (40.0%) reported cattle contact. No participant was positive for both anti-RVFV IgG and anti-CCHFV IgG.

Phylogenetic Analysis of Human and Cattle RVF Cases

Complete RVFV genomes were available for 2 (50.0%) human and 11 (78.6%) cattle infections (Figure 1). Phylogenetic analysis revealed that 10 cattle and the 2 human strains clustered to lineage B. One cattle strain belonged to lineage E and was distinct from the Smithburn livestock vaccine strain (Figure 4).

DISCUSSION

We provide evidence that an interepizootic period RVF outbreak identified among dairy cattle in northern Tanzania was associated with contemporaneous severe and fatal infections among humans, undetected by routine RVF surveillance. Phylogenetic analysis revealed that the majority of RVFV strains belonged to a lineage detected in prior epizootics across East Africa. As previously reported and confirmed here, this outbreak is notable for the presence of 2 circulating viral lineages, and the detection of cases within or near urban areas [14].

Phylogenetic analysis revealed that while most strains in this outbreak belonged to RVFV lineage B and were closely related to those from the 2006–2007 outbreak in East Africa, 1 livestock abortion sequence clustered to RVFV lineage E [14, 29]. A large RVFV lineage B outbreak was identified in Kenya in 2006–2007 and subsequently involved central and northern Tanzania [30]. Given the absence of a major recognized epizootic in East Africa since 2007, our findings suggest long-term persistence of lineage B RVFV. Indeed, previous studies examining the ancestry of viruses associated with the 2006–2007 outbreak found a direct evolutionary relationship with those identified in the 1997–1998 outbreak in East Africa [29].

The livestock abortion strain that clustered to lineage E was distinct from the attenuated RVFV Smithburn vaccine strain and was most closely related to a sequence imported into China from Angola [14, 31]. We are aware of no specific epidemiologic link between Angola and the study location in northern Tanzania. However, movement or importation of infected livestock is generally hypothesized to be a major mechanism for RVFV emergence in new geographic areas [32]. Detection of multiple circulating viral lineages has been previously described [29]. The finding suggests not only that diverse RVFV lineages circulate during the interepizootic period but also pose a risk for RVFV genomic

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reassortment that has been documented under both natural and experimental conditions [29, 33]. One particular concern is the emergence of reassortants with altered pathogenicity, transmissibility, vector range, or host range.

An epidemiologic feature of this outbreak that requires further discussion was the detection of cases within or near urban areas. Major epizootics have mainly occurred in remote and rural areas, and much of the knowledge learned about interepizootic transmission is the result of studies conducted in such settings [2]. Recent evidence suggests that urbanization of RVF in sub-Saharan Africa is a concern, especially in rapid and unplanned settlements that produce environmental conditions suitable for mosquitoes and mosquito-borne infections [34, 35]. Our results indicate that human RVFV infections occur in periurban and urban environments in northern Tanzania; this finding parallels the recent findings of cattle infection in periurban environments in the same catchment [14]. Such settings may enable new patterns of RVFV transmission that must be understood to develop effective control and prevention strategies.

It is notable that we identified no wards with both RVFV-infected cattle and humans; 1 human case also reported no cattle contact. While this may reflect the incomplete coverage of our livestock abortion surveillance and the hospital-based design of our febrile illness research, these findings may suggest that some human infections are acquired through modes of transmission that do not involve direct contact with infected animals. As 1 example, studies suggest that the consumption and handling of raw milk may be a relevant exposure for RVFV transmission [36]. During the previously described cattle outbreak, we documented evidence of RVFV nucleic acids in the milk of infected dams [14]. These findings highlight the importance of understanding if animal-source foods may serve as vehicles for RVFV transmission because food value chains originating in rural and periurban areas extend widely beyond these communities and into large urban centers.

While testing of whole blood and serum samples by real-time PCR did not detect any acute cases of CCHF, our serologic results identified evidence of past CCHFV infection among 5 participants. CCHF is increasingly recognized as a globally important disease that is associated with case fatality risk of approximately 30–40% among hospitalized patients and high risk for transmission in health care settings. Substantial knowledge gaps remain concerning the burden and epidemiology of CCHF in sub-Saharan Africa and further research is needed [37].

Our study has several limitations that warrant further discussion. First, the scale of the outbreak in humans is uncertain because patients with less severe manifestations of RVF may not have presented for hospital care. Thus, interepizootic RVFV transmission may have occurred over a wider spatial scale than reported here due to the limited geographic scope of our surveillance. Second, while our case report form did record contact with cattle, it did not contain more detailed questions on livestock management activities or milk consumption practices that may expose individuals to RVFV. Thus, we were limited in our ability to infer possible modes of transmission to humans. Finally, cases described here occurred following a rainy season in East Africa that was characterized by above-average rainfall [38]. The

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extent to which the interepizootic/epidemic disease activity described here occurs during periods of low to average rainfall warrants further investigation.

In summary, we identified human RVF illnesses, including an autopsy-confirmed RVF death, concurrent with an apparently localized RVF livestock outbreak in the Kilimanjaro Region. These findings suggest there is likely substantial undetected transmission of RVFV during IEPs, and of particular concern is the transmission near and within urban areas. While most RVFV strains belonged to lineage B, the detection of 2 viral strains in an outbreak—lineage B, as well as a lineage E strain highly related to RVFV described in Angola—suggests complex transmission patterns during the IEP. Our findings indicate that enhanced surveillance and further molecular epidemiologic characterization of RVFV are needed to improve our understanding of RVFV transmission dynamics during the IEP and to inform strategies to prevent RVF epizootics and epidemics. Finally, we found serologic evidence of past CCHFV infection among some participants highlighting the need for further research to define the epidemiology of CCHF in northern Tanzania.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Data sharing.

Data collected for the study include individual participant data and a data dictionary defining each field in the set. These will be made available in the form of deidentified data upon a reasonable request made to the corresponding author. Access will be subject to Tanzanian regulations and institutional review board approvals.

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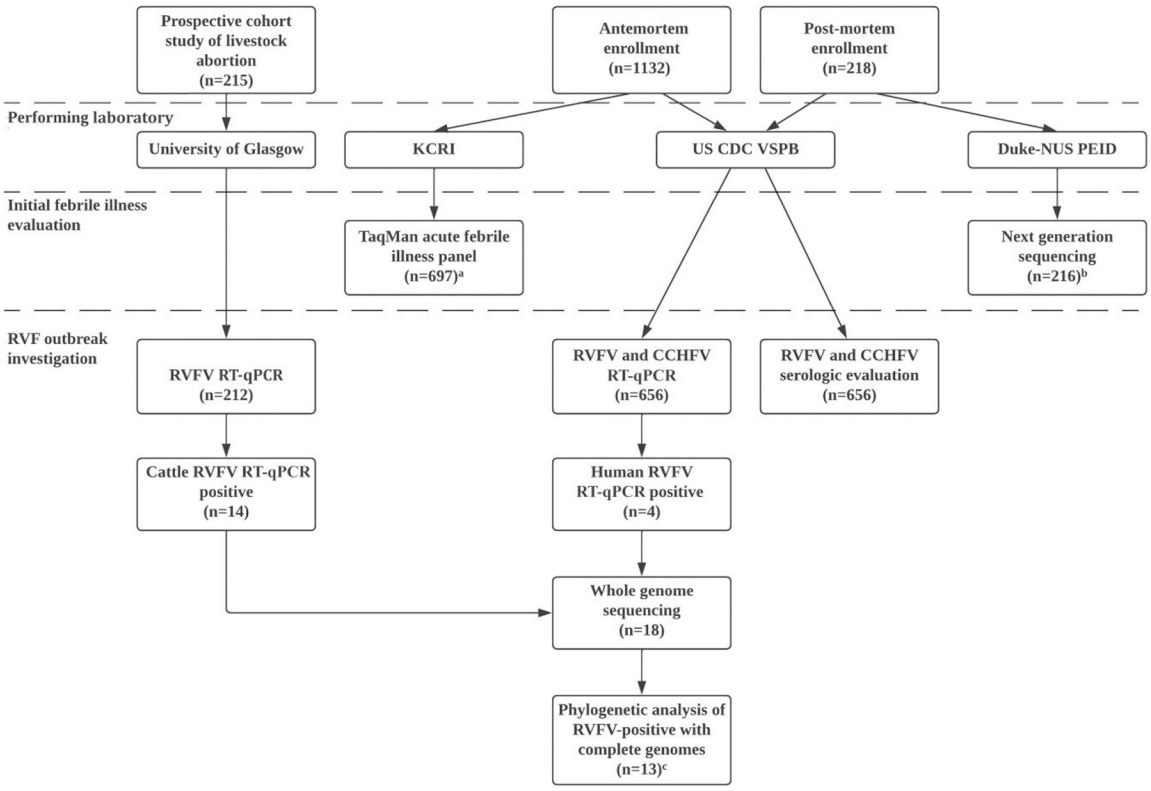


Figure 1.

Flow chart of participant enrollment and testing for Rift Valley fever virus and Crimean-Congo hemorrhagic fever virus in a prospective cohort study evaluating the etiology of severe and fatal febrile illness, Northern Tanzania, 2016–2019. [a]TaqMan acute febrile illness panel detected RVFV in 3 participants enrolled antemortem. [b]Next-generation sequencing detected RVFV in 1 participant enrolled postmortem. [c]Complete genomes available for 11 cattle and 2 human samples. Abbreviations: CCHFV, Crimean-Congo hemorrhagic fever virus; Duke-NUS PEID, Duke-National University of Singapore Program in Emerging Infectious Diseases; KCRI, University of Virginia/Kilimanjaro Clinical Research Institute; RT-qPCR, reverse transcription quantitative polymerase chain reaction; RVFV, Rift Valley fever virus; US CDC VSPD, United States Centers for Disease Control and Prevention Viral Special Pathogen Branch.

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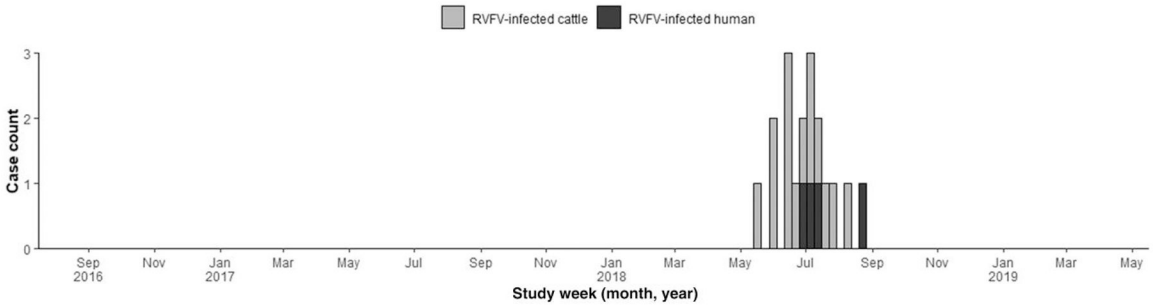


Figure 2.

Epidemic curve illustrating human and cattle Rift Valley fever virus infections detected by RT-qPCR in 2018, Kilimanjaro Region, northern Tanzania, 2016–2019. Abbreviations: RT-qPCR, reverse transcription quantitative polymerase chain reaction; RVFV, Rift Valley fever virus.

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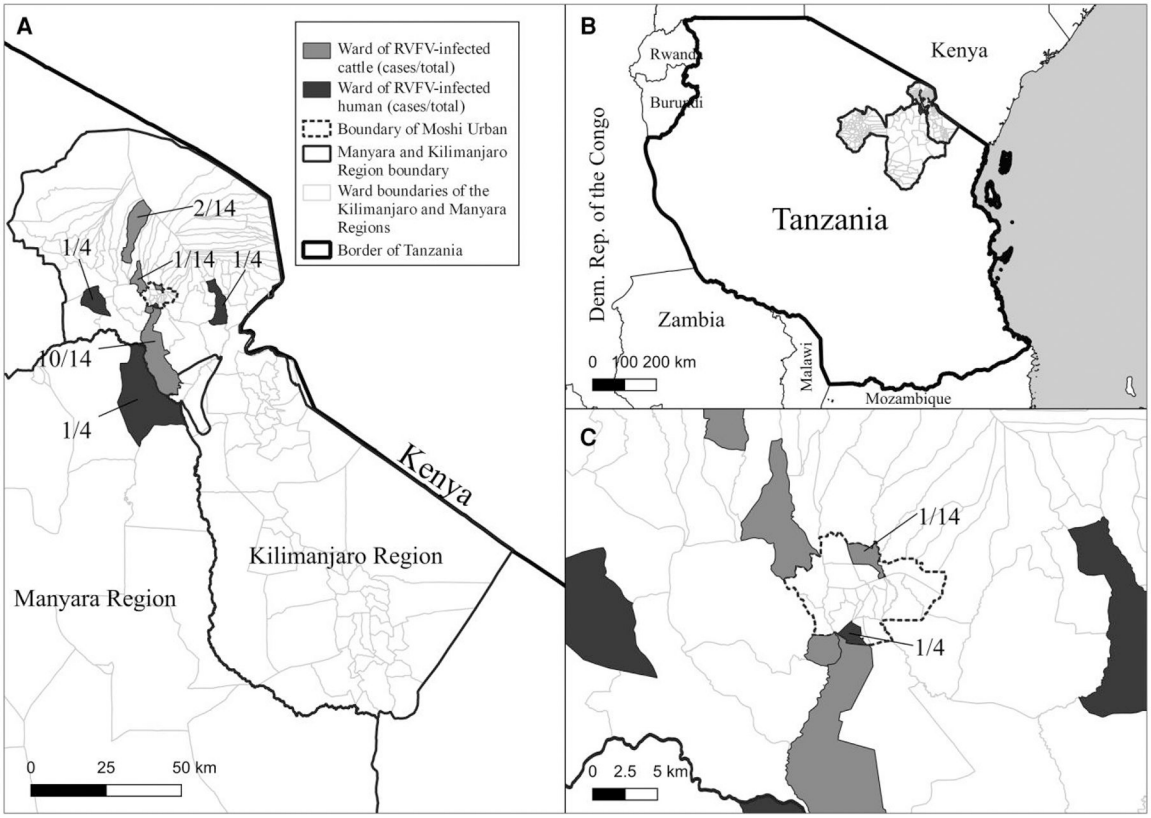


Figure 3.

Location of 4 human and 14 cattle Rift Valley fever virus infections in northern Tanzania: (*A*) ward location of cases is gray shaded, (*B*) Tanzania with the Kilimanjaro and Manyara Regions outlined, and (*C*) Moshi Urban is outlined.

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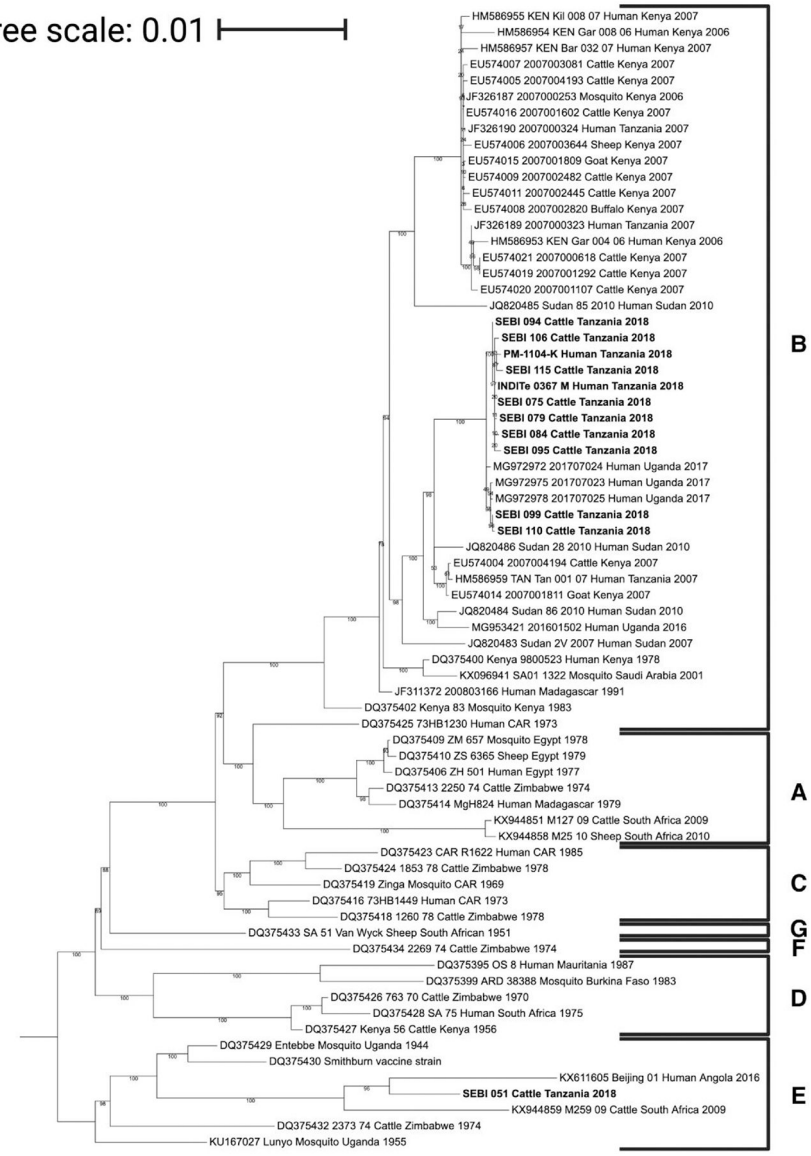


Figure 4.

Phylogenetic analysis of complete L segment of Rift Valley fever virus strains obtained from infected humans and cattle in northern Tanzania, 2018. The scale bar shows branch length per unit of 0.01 substitutions per site. Sequences are labeled with GenBank accession number and designated strain names with country and year of origin. Sequences from this study and the previous cattle outbreak study are highlighted in bold with unique study identifiers and species of origin. Lineages of viral lineages are labeled according to Bird et al [25].

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Table 1.

Sociodemographic and Clinical Characteristics of Hospitalized Participants Enrolled in a Prospective Cohort Study Evaluating the Etiology of Severe and Fatal Febrile Illness and Tested for RVFV and CCHFV, Northern Tanzania, 2016–2019

Variables	Entire Cohort (n = 656)	Antemortem Enrollment (n = 537)	Postmortem Enrollment (n = 119)
Sociodemographics			
Age, y, mean (range)	30 (1–96)	27 (1–92)	43 (1–96)
Female, n (%)	302 (46.2)	254 (47.5)	48 (40.3)
Cattle contact, n (%)	170 (26.2)	118 (22.1)	52 (46.0)
RVFV laboratory findings			
RVFV IgG positive, n (%)	8 (1.2)	8 (1.5)	0 (0)
RVFV RT-qPCR positive, n (%)	4 (0.6)	3 (0.6)	1 (0.8)
CCHFV laboratory findings			
CCHFV IgG positive, n (%)	5 (0.8)	5 (0.9)	0 (0)
CCHFV RT-qPCR positive, n (%)	0 (0)	0 (0)	0 (0)
Vital outcome			
In-hospital mortality, n (%)	119 (18.2)	0.0 (0)	119.0 (100.0)

Abbreviations: CCHFV, Crimean-Congo hemorrhagic fever virus; IgG, immunoglobulin G; RT-qPCR, reverse transcription quantitative polymerase chain reaction; RVFV, Rift Valley fever virus.

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Table 2.

Demographic, Clinical, and Laboratory Characteristics of 4 RVFV RT-qPCR–Positive Human Participants Enrolled in a Prospective Cohort Study Evaluating the Etiologies of Febrile Illness in the Kilimanjaro Region, Northern Tanzania, 2018

Enrollment	Age, y	Sex	Cattle Contact	TAC AFI PCR	RVFV-IgG	NGS
Antemortem	55	Male	+	+	+	NA[a]
Antemortem	28	Male	+	+	+	NA[a]
Antemortem	57	Female	−	+	−	NA[a]
Postmortem	23	Female	+	NA[a]	−	+

+, present or detected; −, not present or not detected.

Abbreviations: IgG, immunoglobulin G; NA, not available; NGS, next-generation sequencing; RT-qPCR, reverse transcription quantitative polymerase chain reaction; RVFV, Rift Valley fever virus; TAC AFI PCR, TaqMan array card acute febrile illness PCR panel.

[a]TAC AFI were not performed on postmortem enrollments, and NGS was not performed on antemortem enrollments.