PROCEEDINGS B

royalsocietypublishing.org/journal/rspb

Research

Cite this article: Rostal MK *et al*. 2025 Localized Rift Valley fever virus persistence explains epidemic and interepidemic dynamics and guides control strategies. *Proc. R. Soc. B* **292**: 20250453.
https://doi.org/10.1098/rspb.2025.0453

Received: 14 February 2025
Accepted: 9 June 2025

Subject Category:
Ecology

Subject Areas:
health and disease and epidemiology, ecology

Keywords:
Rift Valley fever, transovarial transmission, vector dynamics, vaccination, Rift Valley fever virus

Authors for correspondence:
Melinda K. Rostal
e-mail: rostal@onehealthresearch.net
Louise Matthews
e-mail: louise.matthews@glasgow.ac.uk

Electronic supplementary material is available online at https://doi.org/10.6084/m9.figshare.c.7920926.

THE ROYAL SOCIETY PUBLISHING

Localized Rift Valley fever virus persistence explains epidemic and interepidemic dynamics and guides control strategies

Melinda K. Rostal[1,2,3], Jamie C. Prentice[2,4], Noam Ross[5], Alan Kemp[6], Peter N. Thompson[3], Assaf Anyamba[7,8,9], Sarah Cleaveland[2], Claudia Cordel[10], Veerle Msimang[6], Petrus Jansen van Vuren[6,11], Daniel T. Haydon[2], William B. Karesh[12], Janusz T. Paweska[6] and Louise Matthews[2]

[1]One Health Research Consulting, Glen Rock, NJ, USA
[2]School of Biodiversity, One Health and Veterinary Medicine, University of Glasgow, Glasgow, UK
[3]Faculty of Veterinary Science, Epidemiology Section, Department of Production Animal Studies, University of Pretoria, Onderstepoort, Gauteng, South Africa
[4]The Roslin Institute, The University of Edinburgh, Roslin, Midlothian, UK
[5]rOpenSci, New York, NY, USA
[6]Centre for Emerging Zoonotic and Parasitic Diseases, National Institute for Communicable Diseases, Johannesburg, South Africa
[7]University of Maryland, Baltimore County, Baltimore, MD, USA
[8]Earth Science Division, NASA Goddard Space Flight Center, Greenbelt, MD, USA
[9]Universities Space Research Association, Columbia, MD, USA
[10]ExecuVet PTY LTD, Bloemfontein, Free State, South Africa
[11]CSIRO-Health and Biosecurity, CSIRO Australian Centre for Disease Preparedness Business Unit, East Geelong, Victoria, Australia
[12]One Health Concepts, Easton, CT, USA

MKR, 0000-0002-6563-5280; SC, 0000-0002-0456-0959; DTH, 0000-0002-1240-1886; LM, 0000-0003-4420-8367

Rift Valley fever (RVF) is an emerging disease with devastating impacts on livestock health and livelihoods. The risk of RVF virus (RVFV) emergence in new regions and the effectiveness of a strategy for preventing establishment are impacted by how infection persists at local scales. Multiple mechanisms have been proposed for its persistence in regions prone to epidemics, including maintenance via transovarial transmission (TOT) but whether and how TOT can support local persistence is not well understood. Through the development of host- and multi-vector climate-driven simulation models to recreate observed patterns of prevalence and outbreak frequency, we show that TOT has the potential to play an important role in local persistence through seasonal cold or dry periods. Local persistence required annual low-level transmission of RVFV concurrently with substantial TOT, whereas the infrequent large outbreaks hampered long-term persistence in our simulations. We show that under this mode of local persistence, large outbreaks can be prevented with low-level vaccination, but that the long-term local persistence can only be interrupted with many years of sustained vaccination. Determining the role of TOT in persistence is critical for designing countermeasures to prevent establishment after emergence.

1. Introduction

Arboviruses have emerged and re-emerged with increasing frequency globally during the past 50 years [1], including chikungunya, West Nile and Zika viruses [1,2]. A better understanding of viral ecology (e.g. overwintering mechanisms [3]) could have allowed faster detection and response during the

initial epidemics, reducing the magnitude of the outbreaks and the risk of the viruses establishing endemicity. Rift Valley fever virus (RVFV) is present across Africa and has emerged in new regions outside of Africa. Important gaps in understanding RVFV persistence and maintenance mechanisms limit our ability to predict and target mitigation efforts against outbreaks and expansion.

First reported in Kenya in 1931 [4], RVFV was detected in South Africa in 1950 [5], and subsequent outbreaks indicate endemicity throughout Africa [6]. Specifically, South Africa reported widespread outbreaks in 1950–1951, 1974–1975 and 2010–2011 and multiple, isolated outbreaks during intervening years [7]. In 1990, RVFV emerged in Madagascar, the first report outside continental Africa [8], with further emergence in Saudi Arabia/Yemen in 2000 [9] and the Comoros in 2007 [10]. This pattern of emergence suggests there is a high risk of global RVFV spread. However, the underlying mechanisms of RVFV persistence have not been identified, despite a significant body of work focused on RVFV ecology.

Widespread and severe outbreaks of Rift Valley fever (RVF) manifest as abortion storms and high neonatal mortality in ruminant livestock resulting in significant economic losses [11]. Clinical disease in people ranges from mild fever and myalgia to rare haemorrhagic fever cases [12]. Outbreak periods are interspersed with interepidemic periods lasting 2–25 years [13]. The mean seroprevalence estimate from interepidemic ruminant studies conducted across Africa was 15% (2.5–97.5 percentile interval: 1–40%) [13]. During interepidemic periods, there is evidence of RVFV circulation in livestock at a sufficiently low frequency that cases often remain undetected [14,15]. Wildlife can also be infected, and seroconversions during interepidemic periods suggest that some species may also support low-level RVFV interepidemic circulation, similar to the role livestock play [16].

After RVFV was detected in larval and unfed *Aedes mcintoshi*, these floodwater mosquitoes were proposed to be a primary reservoir of RVFV and to maintain it via transovarial (and horizontal) transmission (TOT) [17]. Due to difficulties in establishing floodwater *Aedes* breeding colonies, laboratory estimation of RVFV TOT fraction (the proportion of infected eggs laid by an infected female mosquito) has yet to be measured in African mosquitoes [18]. However, a recent study provided the first experimental evidence of RVFV TOT, identifying TOT in 2–10% of progeny of infected females of the North American mosquito, *Culex tarsalis* [19]. To date, there is no field evidence that *Culex* spp. can transmit RVFV transovarially, though they can transmit RVFV horizontally. Despite the limited field evidence, TOT has long been proposed as an 'overwintering mechanism' to maintain RVFV during the prolonged dry (or cold) periods between outbreaks [20]. The possible overwintering mechanisms for RVFV include (i) TOT, (ii) no overwintering mechanism is necessary and vectors can maintain transmission throughout the dry period with the survival of infected vectors, (iii) dormant adult mosquitoes (previously reported for other pathogens [3]), or (iv) animal movement (metapopulation dynamics). Yet no mechanistic model has demonstrated the feasibility of the TOT persistence mechanism at a localized scale (e.g. a small, seasonal wetland, with no outlet, also known as a 'pan') while producing realistic host infection dynamics.

We examine the mechanisms of decadal, localized RVFV persistence that reflects historical climatic and epidemic conditions of a regional epicentre for widespread RVF outbreaks, the Free State Province, South Africa. We developed a model of sheep and two vectors: *Culex* (horizontal transmission only) and floodwater *Aedes* (horizontal and TOT and with a univoltine life cycle—the eggs hatch during one period per year). Specifically, we examine whether interepidemic persistence is possible at this local scale, examine the role of TOT in persistence, identify other key parameters in the maintenance of RVFV, estimate the reproduction number (R_0) and examine implications for vaccination strategies.

2. Material and methods

We developed a deterministic, ordinary differential equation (ODE)-based compartmental model with a single livestock host (sheep) and two mosquito vectors, forced by climatic parameters (electronic supplementary material, figure S1 and tables S1–S4 for full methods and model description). Specifically, we used a susceptible (S), infected (I) and recovered (R) system (SIR) to simulate the numbers of sheep and lambs (including compartments for passive immunity and vaccination) and a susceptible, exposed (E) and infected system (SEI) for the *Aedes* and *Culex* mosquitoes (electronic supplementary material, equations S1–S30). Our closed system included TOT and horizontal transmission by *Aedes* and amplification through horizontal transmission by *Culex* which continue to hatch throughout the season, maintaining the natural succession between these vector species [17,21,22]. The study system we are simulating requires an overwintering mechanism as the cold and dry temperatures in the Free State substantially limit the population abundance of mosquitoes during this season. In our model, overwintering may be achieved by TOT or overwintering infected adult *Culex* mosquitoes. The demographic state variables (electronic supplementary material, table S1) include the host that is represented by lambs (L; 6.5 months or less) and adult sheep (S). Lambs are born into the system (as limited by the carrying capacity; NLmax). Lambs born to infected or recovered sheep have maternal antibodies (AL) that persist approximately for four months. The host mortality rate, percent of hosts sold, and flock size were estimated from our unpublished data in the Free State, South Africa and the rate of sale of adult sheep was set to maintain the sheep at a constant population. The parameters for vaccination rate (vax, vax.prop) are set to zero in all simulations, except those that are explicitly examining the impacts of vaccination. The life stages of the vectors are modelled equivalently: eggs (E) are laid, the aquatic stage is modelled as one compartment (larvae and pupae, ALP), then they emerge as 'young' adults that do not immediately take a blood meal (AY). Once they take their first blood meal (A), they continue to lay eggs according to their gonotrophic cycles. The eggs of floodwater *Aedes* spp. require a desiccation period, and therefore they have an additional compartment, newAE. These eggs transfer to the *Aedes* egg (AE) compartment as appropriate for their infection status after 30 days. We use temperature and precipitation to drive hatching (electronic supplementary material) and estimate daily larval development and mortality rates (electronic supplementary material, table S2). The simulations are localized to the sheep and

vectors within a single pan. A pan (similar to a playa or dambo), is a temporary wetland that floods in the rainy season and the water remains until it evaporates as there is no outlet [23]. These are the primary breeding sites of many floodwater *Aedes* and have long been associated with RVF outbreaks [24].

To simulate the typical interepidemic RVFV conditions associated with successive below-average rainfall seasons, we assumed a univoltine life cycle in the transovarially transmitting vector. We used 34 years (1983–2017) of rainfall data from Bultfontein (latitude: −28.40, longitude: 26.26) extracted from African Rainfall Climatology (ARC) data records [25,26] and temperature data from the nearest South African Weather Service stations (latitude: −28.95, longitude: 26.33) in Free State, South Africa (electronic supplementary material, figure S2). The climate data were used to drive vector hatching and development and mortality rates [24,27] (electronic supplementary material, tables S2 and S3, equations S31–S33). The parameter values (electronic supplementary material, table S4) were taken from the literature, where available, estimated from published and unpublished questionnaire data we collected in South Africa (Ngoshe et al. [28], see electronic supplementary material). Voluntary written consent was obtained from all participants included in the studies from which the data came. For four parameter groups (vector carrying capacities and bite rates, TOT fraction and AE mortality rate) that could have a substantial impact on RVFV dynamics, we used a Latin hypercube to vary these parameters in 80 000 simulations. We evaluated simulations to identify plausible sets of parameters to meet our explanatory, rather than predictive, modelling goals. Each simulation was assessed using six criteria that conform with broadly observed patterns of RVFV epidemiology in this system—outbreaks resulting in high seroprevalence, following interepidemic periods with low-level RVFV transmission and declining seroprevalence until the next outbreak (electronic supplementary material). Within simulations that met these criteria, we used visual comparisons to historical data to identify an exemplar simulation, which best reproduced the general patterns of outbreaks reported in the Free State of South Africa. The parameter values from this exemplar simulation were used for the figures and as the baseline for other comparison simulations (electronic supplementary material, table S4). We used a conservative measure of persistence, sustaining at least one infection in the host population per season (September–August) for each of the 34 years of the simulation.

We conducted a sensitivity analysis of selected parameters (electronic supplementary material, table S5) using 4000 draws from a Latin hypercube [29,30] (electronic supplementary material). Each parameter was evaluated based on its effect on six outcomes: persistence, mean annual seroprevalence, the proportion of infected AE at the end of the simulation, mean outbreak length, mean outbreak size and maximum outbreak size. Annual estimates were summarized over the mosquito growth season in South Africa (September–August). The results were analysed using a partial correlation coefficient (PCC) analysis [29].

R_0 was numerically estimated at the mean and peak vector and host population sizes using a next generation matrix approach [31] (electronic supplementary material, equations S34–S36). The effective reproduction number (R_e) was estimated using the susceptible host and vector populations at each timestep. We also conducted a sensitivity analysis of R_0 to varying parameters. To compare within-year RVFV dynamics (e.g. persistence throughout an outbreak) and RVFV dynamics between years (persistence from one year to the next), we defined an additional quantity—the seasonal R_0. In this system, TOT is the parameter that allows infection to spread from one year to the next. Therefore, R_0 calculated with the TOT set equal to zero ($q = 0$) captures only the within-year transmission. We refer to this quantity as the seasonal R_0.

We identified the proportion of the flock that would need to be vaccinated throughout the simulation period to eventually drive RVFV to extinction via simulation.

3. Results

(a) Decadal, localized persistence is possible

Our simulations indicated that RVFV can persist for over 30 years within a localized area or pan, producing realistic outbreak and infection patterns (figure 1) over a narrow range of parameters (figure 2, orange and black striped region). The exemplar simulation generated small annual RVF outbreaks with three large outbreaks (infecting >25% of the flock) occurring in 1987, 1999 and 2009 (figure 1*a*) that were associated with a higher ratio of infected *Culex* to infected *Aedes* (figure 1*b*; electronic supplementary material , S3). Two of these large outbreaks aligned well with reported outbreaks in South Africa during the time frame, the largest of which was in 2010–2011 (figure 1*a*). The population of infected AEs remained stable throughout the simulation (figure 1*c*) and the mean proportion of infected AEs was 0.003 (electronic supplementary material, table S6). The exemplar simulation had a low mean annual proportion of infected adult vectors, ranging from 0 to 0.04 (electronic supplementary material, table S6), and the mean annual seroprevalence was 22.8% (median: 16.2%; range 10.4–58.6%; electronic supplementary material, table S6). Excluding the three large outbreaks, the average incidence was 7 per 100 hosts per year. The calculated R_0 was 1.01 at the mean population sizes of *Aedes* and *Culex*, increasing up to 1.8 at the mean of the annual peak population sizes for the exemplar simulation. R_0 was most sensitive to the *Aedes* and *Culex* bite and mortality rates (electronic supplementary material, figures S4 and S5).

(b) Transovarial transmission, a plausible mechanism for localized Rift Valley fever virus persistence

In the absence of TOT, the virus became locally extinct after one year of simulation (electronic supplementary material, figure S6A,B). In a system with no horizontal transmission (i.e. no viral expansion in the host or *Culex* populations), RVFV became extinct in the host population after seven years, but infected *Aedes* adults were present for up to a decade (electronic

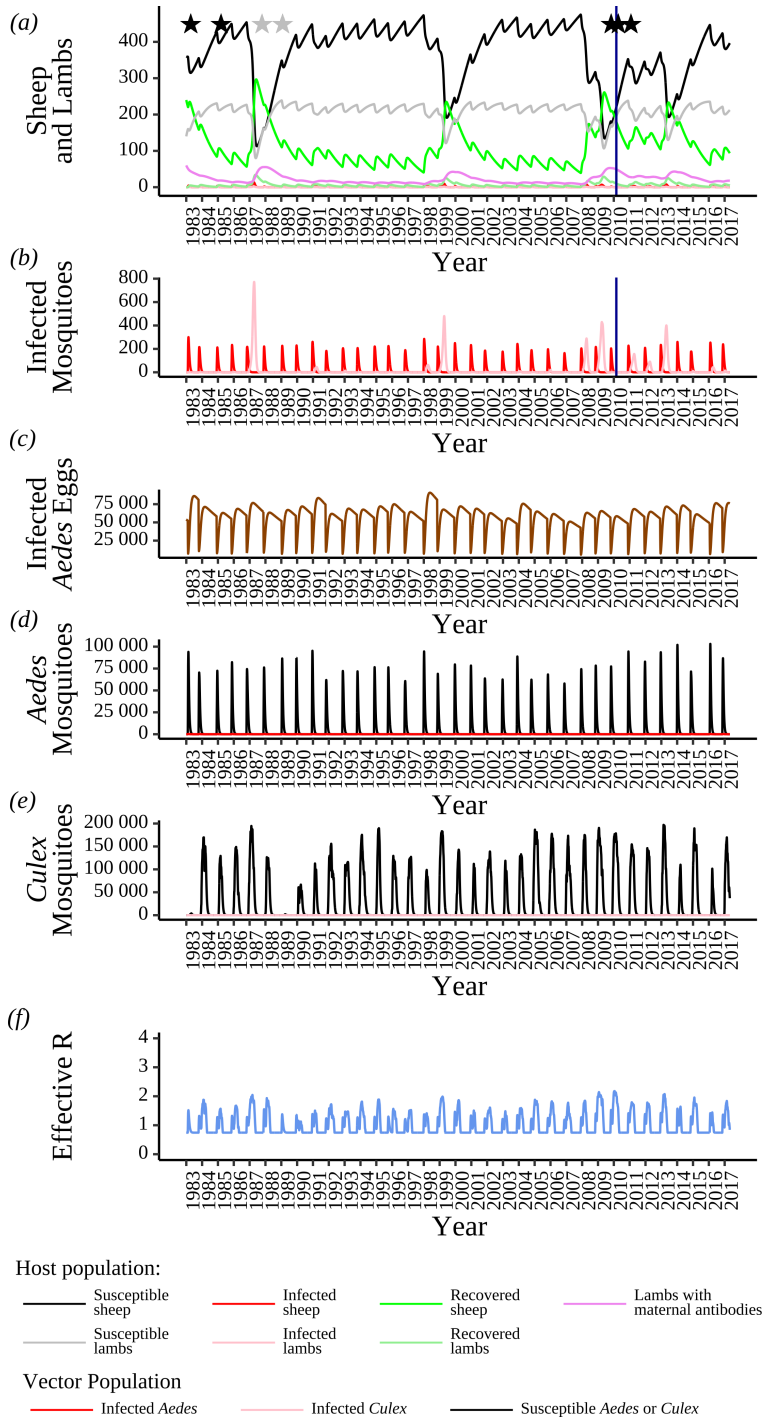

Figure 1. The full simulation of RVFV infection dynamics with two vectors (*Aedes* and *Culex*) in a single host system run for 34 years. Annual circulation is evident with several small outbreaks over the years and three very large outbreaks (one of which occurred in 2009). (*a*) The simulated populations of susceptible (black/grey), infected (red/pink) and recovered (green/light green) sheep/lambs. The dark blue line indicates the approximate time of the 2010 outbreak. The black stars indicate the year where there was a recorded RVF outbreak in the Central Plateau portions of the Free State and/or Northern Cape. The grey stars indicate a year in which an RVF outbreak was recorded but it is unknown where in South Africa the outbreak occurred [7]. (*b*) The populations of infected *Aedes* (red) and *Culex* (pink) mosquitoes are shown and the 2010 outbreak is marked by the dark blue line. (*c*) The number of infected *Aedes* eggs in the environment is indicated in brown over time. (*d*) The total populations of susceptible (black) and infected (red) *Aedes* mosquitoes are shown over time. (*e*) The total populations of susceptible (black) and infected (pink) *Culex* mosquitoes are shown over time. (*f*) Changes in the effective reproduction number as the simulation proceeds.

supplementary material, figure S6C,D). Viral persistence increased gradually as TOT fraction increased up to 0.6 (commensurate with up to nine years of persistence), beyond which the system rapidly changed to support persistence for the entire 34 year period (electronic supplementary material, figure S7B). In our model, when considering persistence for at least 3 years, TOT fractions between 0.46 and 0.80 supported mean seroprevalence levels of 1–40% (electronic supplementary material, figure S7A).

In our sensitivity analysis, all six outcome factors (RVFV persistence, mean annual seroprevalence, mean outbreak size, mean outbreak length and maximum outbreak size) were sensitive to TOT fraction (figure 3). Viral persistence and the mean seroprevalence in the 34 year system were very sensitive to small changes in the *Aedes* transmission parameters, bite rate and the external incubation rate (electronic supplementary material, figure S7). As we varied key parameter(s), we saw rapid switching of behaviours from systems with low seroprevalence and short-term persistence to systems with high seroprevalence and

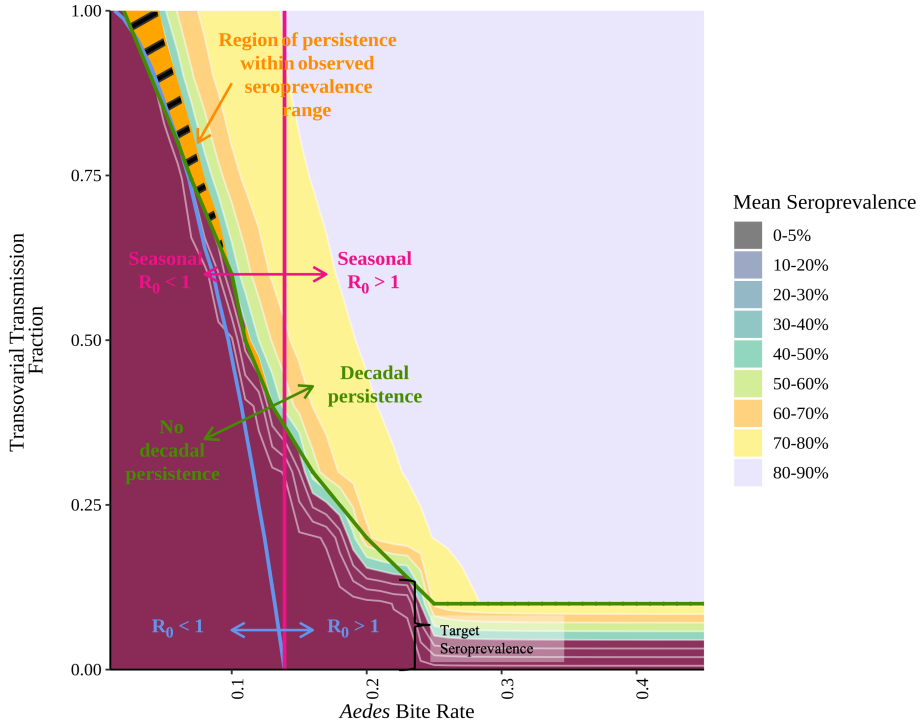

Figure 2. Contours of mean seroprevalence as TOT fraction and *Aedes* bite rate are varied. The target seroprevalence range (1–40%) is shown in red. For each TOT fraction simulated (intervals of 0.1), the lowest *Aedes* bite rate that supported decadal (34 year) persistence is shown (green line) such that parameter value combinations in the space above the green line support decadal persistence. We included the lines for $R_0 = 1$ (in blue) and the seasonal $R_0 = 1$ (in pink). The seasonal R_0 is equal to the R_0 when it is calculated with zero transovarial transmission. When seasonal $R_0 > 1$, the outcome is either short-term persistence or seroprevalences much higher than the target range. The orange and black region represents the parameter space that supported decadal persistence within the target seroprevalence. This falls within the region where seasonal $R_0 < 1$ (left of pink line) and $R_0 > 1$, corresponding to a regime with limited expansion of infected vectors during outbreaks, and sufficient TOT for $R_0 > 1$, which can allow long-term persistence.

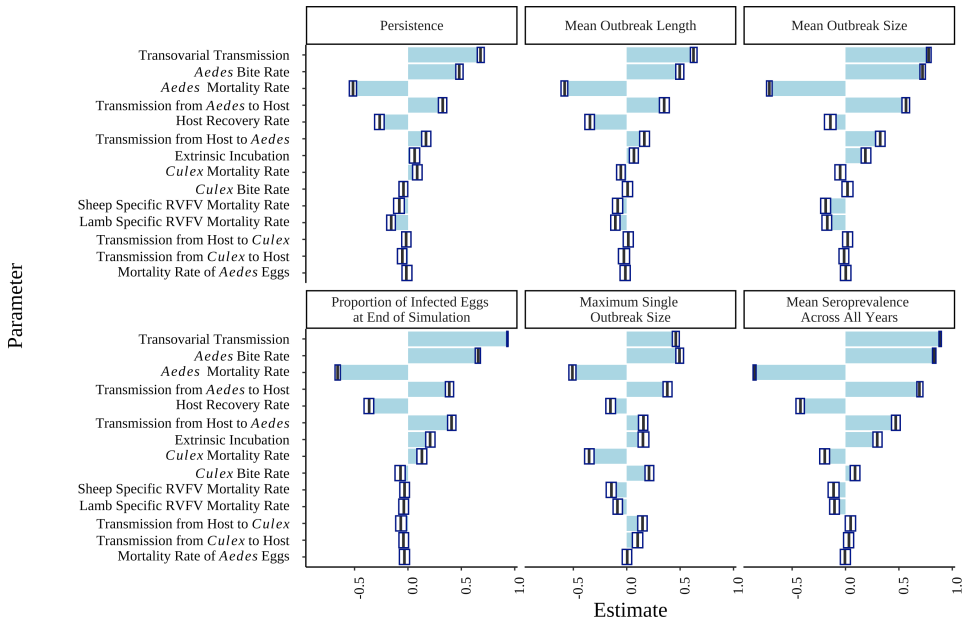

Figure 3. Tornado plot of the partial correlation coefficient (PCC) estimates and 99% confidence interval of the 4000 runs of the Latin hypercube sensitivity analysis. The PCC estimates indicate the sensitivity of each outcome factor of interest to the selected parameters in the model. The box plot shows the 99% confidence interval, and the blue bar shows the coefficient estimate. The larger the absolute value of the estimate, the more sensitive that outcome factor is to a specific parameter.

long-term persistence (electronic supplementary material, figures S7 and S8). Among the 4000 runs in the sensitivity analysis, 53% resulted in RVFV extinction and 36% resulted in unrealistically high seroprevalences.

Decadal persistence at target (1–40%) seroprevalence ranges (figure 2, orange hatched region) required R_0>1 and seasonal R_0<1 (where seasonal R_0 is calculated as R_0 without TOT to capture the within-year dynamics; figure 2 and electronic supplementary material, S8). When requiring target seroprevalence and RVFV persistence, R_0 was only consistently above unity at a high TOT fraction (>0.6), though persistence was possible for occasional simulations with a TOT of 0.4–0.5 (figure 2). Seasonal

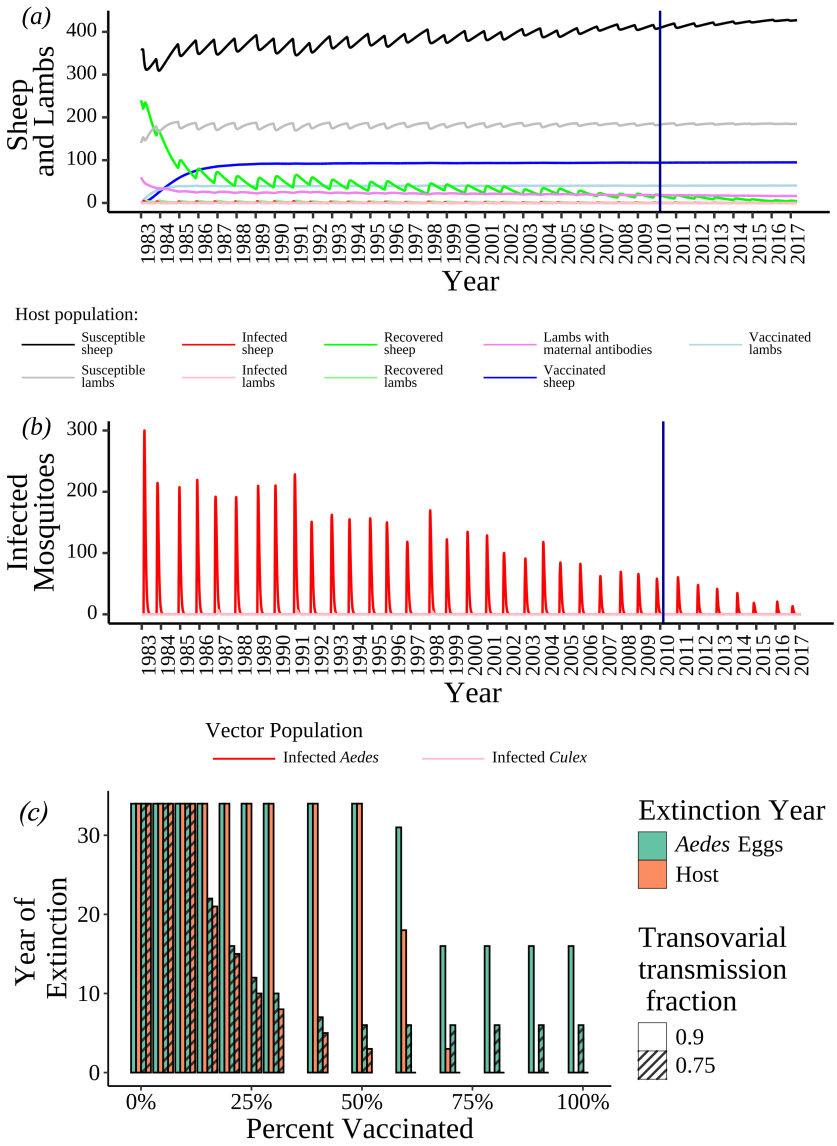

Figure 4. Simulation of the RVFV dynamics when 18% of susceptible lambs are vaccinated for (*a*) the sheep and lamb populations and (*b*) the infected *Aedes* egg population. (*c*) The vaccination coverage the flock is maintained at versus the number of years until extinction in the host and *Aedes* egg populations at relatively low (0.75) and high (0.9) transovarial transmission fractions.

R_0<1 indicates relatively little expansion of the infected vector population during outbreaks. Simulations where the seasonal R_0 was above unity and within the target seroprevalence resulted in multiple large outbreaks (R_0>1 during outbreak years), which drove RVFV extinct.

(c) Seasonal R_0 and vector dynamics drive outbreaks

The system was resilient to a single large outbreak resulting in high host immunity (figure 4*d*), multiple large outbreaks (resultant of RVFV expansion in the *Culex* vector), eventually led to RVFV extinction in the host population (electronic supplementary material, figure S9A, left) and a reduction in the number of infected AEs over time (electronic supplementary material, figure S9C, left). Similarly, the sensitivity analysis outcome that was most affected by the *Culex* parameters was the maximum single outbreak size (figure 3). These dynamics are exemplified by simulations with a 25% lower *Culex* mortality rate that resulted in RVFV extinction (electronic supplementary material, figure S9, left).

In a system where no amplifying (*Culex*) vectors can transmit RVFV horizontally, we see long-term persistence with no outbreaks and a potential, eventual transition from low-level transmission (<11% of sheep infected per year) to a moderate level of transmission with 11–18% of sheep infected annually (electronic supplementary material, S10). In our simulations, small numbers of susceptible *Culex* survived most winters, though no infected *Culex* survived a season. Large outbreaks (seasonal R_0 > 1) occurred when there was RVFV expansion within the *Culex* population (figure 1*b*; electronic supplementary material, figures S3 and S9).

(d) Implications for vaccination as a mitigation tool

Under vaccination of the host population, infection in the vector population was maintained after extinction in the host population, with a greater difference in extinction times for higher TOT (figure 4*c*). To drive RVFV to extinction required vaccination coverage of at least 18% to be maintained in the host for 29 years (figure 4*a*). Vaccination coverage of <18% may prevent large outbreaks, while maintaining RVFV persistence (electronic supplementary material, figure S11). At vaccination coverage of 50% and TOT of 0.75 extinction in the host could be achieved in 3 years, but sufficient infection remained in the vector population to initiate outbreaks for nearly 6 years if vaccination were stopped. At higher TOT (0.9), infection would persist long-term in the host and vector populations (figure 4*c*).

4. Discussion

As RVFV spreads beyond Africa, it is critical to understand the mechanisms of transmission to prevent RVFV establishment in new regions. We simulated local persistence of RVFV, which reproduced historical outbreak patterns and resulted in a realistic seroprevalence pattern. In our simulations, decadal persistence in this closed system under temperate environmental conditions depended on TOT and limited expansion in the vector populations, though it was very sensitive to multiple key parameters. Multiple large outbreaks resulting in rapid expansion of RVFV in the host population and driven by *Culex* led to a high seasonal R_0 and reduced persistence by driving RVFV extinct within the AE population. Long-term, low-level vaccination prevented large outbreaks, though it supported low-level circulation of RVFV. To prevent long-term persistence, our model indicates that a consistent and annual vaccination regimen is necessary.

(a) Long-term, localized persistence is possible

Our simulations suggest that RVFV can persist locally for decades. While explanatory rather than predictive, our model produced a realistic pattern of outbreaks with two of the three large outbreaks occurring close to times when outbreaks were reported by the Free State or an unspecified location in South Africa [7]. The simulated outbreak in 1987 was larger than expected from the literature [7], this may be the result of initial conditions (in 1983). The large, simulated outbreak in 2009 fits reasonably well to the timing of the large 2010–2011 outbreaks in the Free State. This suggests that the model represents a plausible mechanism for localized RVFV persistence. We used the historical outbreak data only to confirm that our model simulated realistic RVF outbreak patterns. Given the uncertainty of environmental parameters (e.g. soil saturation and vegetation) and the dearth of hydrological data available to develop precise vector hatching thresholds for the South African pans, the model was not expected to replicate the years in which RVF outbreaks occurred.

The mean annual seroprevalence simulated was 22.8% (range 10.4–58.6%), which is within the range of reported ruminant seroprevalence estimates across Africa [13]. The range overlaps with the confidence interval of a recent seroprevalence estimate in unvaccinated ruminants in the Free State [28]. It is important to evaluate whether the model can reproduce the observed pattern of low interepidemic transmission interspersed with large outbreaks. Most other simulation models either simulated a high proportion of immune/recovered animals over time [32,33] or only presented the infectious host dynamics to demonstrate RVFV infection periodicity without presenting the recovered or susceptible host dynamics [34,35]. The few studies that do simulate interepidemic periods, with low seroprevalence, are at a regional scale (seee path B in [36]; see also [37,38]), and/or incorporate movement using a metapopulation structure [37,39]. A metapopulation system may be able to support RVFV maintenance as ruminant movement along livestock trading routes has been implicated in the RVFV spread [40–42] and maintenance. However, isolated RVF outbreaks have been observed [7] and probably contribute to observed spatially patchy patterns of seroprevalence [43], which suggests that local persistence occurs.

(b) Transovarial transmission, a plausible mechanism for localized Rift Valley fever virus persistence

Our analysis suggests that TOT is likely a key contributor to long-term RVFV persistence in a system where temperature and/or rainfall patterns make the survival of overwintering, RVFV-infected adult mosquitoes unlikely. TOT is an important contributor towards R_0 surpassing unity (discussed below) and provides a mechanism for overwintering in our simulations. Other models have also suggested that TOT is critical in ecosystems with a prolonged dry period [20,32]. However, simulation of RVFV dynamics in more favourable climatic conditions may not require TOT for RVFV persistence [20,36,37]). Lo Iacono *et al.*'s [36] path A model suggested that TOT of RVFV was not required, although this simulation resulted in extremely high interepidemic seroprevalence (approximately 80–90%). On the regional scale (based on the water surface area available in Kenya), they were able to simulate large RVFV outbreaks interspersed with interepidemic periods with a low seroprevalence (path B) when environmental conditions (mean annual temperatures 18–22°C and mean water surface area 3000–4000 m^2) resulted in 'unstable persistence' of RVFV, including environmental transitions between systems that did and did not require an overwintering mechanism and resembled chaotic behaviour. Regions in both Kenya (e.g. Ijara) and South Africa have prolonged dry seasons, which in South Africa is coupled with a temperate ecosystem. Our simulation suggests that TOT is a plausible mechanism to support RVFV persistence under these conditions.

Our model was highly sensitive to multiple parameters, including *Aedes* and *Culex* bite rates and RVFV transmission parameters. Small changes to these parameters led either to extinction or to a persistent, unrealistically high, host seroprevalence. Our model's sensitivity suggests that while RVFV may persist in some pans, RVFV extinction is possible in other pans depending on how these traits/rates vary with host and vector population sizes and composition. The relatively high proportion of sensitivity analysis simulations in which RVFV went extinct supports conditional and heterogeneous persistence. Future investigation with a stochastic model could estimate the local extinction rate, though it would likely result in a smaller parameter space in which observed dynamics would arise. Favier *et al.* [44] suggested that, although RVFV may become extinct at local scales, it could be maintained within a network of local pans by the movement of livestock between seasonally inundated pans. Sumaye *et al.* [39] also used movement to simulate RVFV dynamics with a low interepidemic seroprevalence. Future extensions of our current model to the metapopulation level could examine persistence more thoroughly. Additionally, further examination with multiple species (possibly embedded within a metapopulation) would further explore the importance of ruminant size, etc., in driving RVFV dynamics, as these were not evaluated in our model.

A high TOT fraction (generally >0.6) was required to support persistence in our simulations. Sumaye *et al.* [39] also used a high TOT fraction (0.5) to simulate RVFV persistence with a comparable seroprevalence. These results challenge the common unsupported perception that the RVFV TOT fraction is low [18]. This perception may have developed because of the relatively low detection rate of RVFV in adult mosquito populations (e.g. 0.001 reported on farms following RVF outbreaks in 1974–1975 [45]). However, our simulations suggest that even with a high TOT fraction, the mean proportion of infected adults remains relatively low (0–0.04). A high TOT fraction for mosquito viruses is biologically plausible, as Culex flavivirus is solely maintained by a TOT fraction of 0.97 [46]. The only study to experimentally demonstrate RVFV TOT estimated it to be 0.02–0.10 in a species of *Culex* that has never been exposed to RVFV in nature [19]. RVFV has likely evolved a higher TOT fraction in the natural vectors. Future establishment of floodwater *Aedes* spp. breeding colonies to assess TOT fraction is needed.

Our sensitivity analysis indicated that TOT had a large effect on all outcome factors. Though R_0 had little sensitivity to changes in TOT fraction, we found that TOT made an important contribution to R_0 reaching unity in simulations with long-term persistence and were within the target seroprevalence range. This finding held even when varying parameters to which R_0 is very sensitive, e.g. *Aedes* bite rate. We saw consistent long-term persistence within the target seroprevalence range when TOT was above 0.6. In these scenarios, the seasonal R_0 was less than one, indicating the important contribution of TOT. When the target seroprevalence was achieved and the seasonal R_0 (calculated with zero TOT fraction) exceeded one, there were large RVF outbreaks without long-term persistence. Thus, achieving long-term persistence and observed seroprevalences appears to require limited seasonal RVFV spread and an overwintering mechanism such as a high TOT to boost R_0 above unity. Previous analyses have not simultaneously examined R_0 with multi-year persistence, which may explain why many have not found R_0 to be sensitive to TOT [32,34]. Given that American *Culex* spp. are capable of TOT, if American *Aedes* spp. have a higher TOT fraction, TOT could be an overwintering mechanism to sustain RVFV maintenance upon introduction to the Americas [19].

(c) Seasonal R_0 and vector dynamics drive outbreaks

The interactions between the *Aedes* and *Culex* mosquitoes were important drivers of our simulated RVFV outbreak dynamics. Though our sensitivity analysis indicated that decadal persistence and the infection dynamics were primarily driven by *Aedes* traits, with little sensitivity to *Culex* traits, we found that *Culex* bite and mortality rates were important drivers of outbreak size (contributing to seasonal R_0). R_0 was similarly sensitive to *Culex* traits, especially high *Culex* bite rates, in other simulation studies [32,47–49].

Low-level interepidemic transmission of RVFV likely requires limited expansion of RVFV in the vector and host populations. In the absence of an amplifying vector, *Aedes* mosquitoes maintained a very low-level incidence (<11% of animals infected each year) for nearly two decades in our simulations, supporting the idea that RVFV expansion in hosts is limited. Towards the end of the 34 year simulation period, there was a shift in dynamics, allowing an increase in expansion in the host and a shift towards a hyperendemic system (higher annual RVFV incidence without RVF outbreaks) as was detected in KwaZulu-Natal, South Africa [50]. The large RVF outbreaks we simulated were driven by *Culex* and resulted in rapid expansion within the host population (seasonal R_0> 1), while still remaining limited within the much larger population of adult *Aedes* and *Culex* mosquitoes (maximum proportion of infected vectors was approx. 4% within each population), which is in line with the low detection rate reported in mosquitoes during RVF outbreaks [45]. Larger outbreaks counterintuitively led to declines in the infected AE population due to the induction of high rates of host immunity. The population size of infected AEs at the start of the season is likely important for a system where persistence is unstable.

Trait variation within the community of vectors and whether overwintering is required may explain the variation in interepidemic period duration among regions [13]. Cavalerie *et al.* [20] estimated the horizontal vector transmission fraction based on the observed relative abundance of different mosquito species in Mayotte and their laboratory-determined transmission fractions. Thus, the potential for widely variable *Culex* population sizes and transmission, bite and demographic rates based on local vector communities may determine whether RVFV can persist via a given TOT fraction. Our model did not support the continued growth of the *Culex* populations during most winters, though small populations of susceptible adult *Culex* survived. No overwintering *Culex* were infected with RVFV. Our simulations suggest that in systems that rely on TOT, RVFV persistence is enhanced in the absence of large outbreaks. This could explain why some interepidemic periods last for decades.

(d) Implications for vaccination as a mitigation tool

The effect of TOT on RVFV persistence has implications for vaccination strategies. Our simulations suggest that a low vaccination coverage (18%) could drive RVFV to extinction; however, a high TOT fraction requires maintenance of this vaccination coverage for decades before extinction in this closed system. Low-coverage vaccination programmes may prevent large RVF outbreaks without driving RVFV to local extinction. This could provide a cost-effective option for resource-limited countries to minimize the losses associated with epidemic RVFV by reducing the severe clinical outcomes of mass abortion and infection amplification, potentially decreasing the risk of spillover into people (which is usually associated with contact with infected animals) and substantially moderating the economic cost of RVF outbreaks.

Higher annual vaccination coverage drove RVFV extinct more rapidly. Given the importance of TOT, persistence of RVFV was only partially dependent on expansion in the host population and it could be maintained solely by TOT for several years before being driven to extinction. Higher vaccination coverage would be necessary if wildlife or metapopulation dynamics contribute to RVFV maintenance.

In the case of a new emergence in a temperate region, we recommend maintaining local vaccination programmes (preferably with one of the many vaccines in development that support differentiating infection from vaccinated animals, aka 'DIVA') for several years, even if no cases are observed in the years after the outbreak. This strategy has the potential to reduce or eliminate the population of infected AEs within a local pan used exclusively by livestock. Though not evaluated here, mosquito control in a pan may additionally reduce the population of infected AEs, larvae and hatching of adults, especially when used in conjunction with vaccination after an outbreak or any cause of reduced AE populations (e.g. drought). This could reduce or possibly eliminate undiagnosed, interepidemic infections and prevent endemic RVF outbreaks at that pan even in the presence of abnormally high precipitation and flooding. Assuming there is a large ruminant outbreak associated with RVFV emergence and that is detected within the first season, it may be possible to eliminate RVFV before it is fully established.

(e) Study limitations and future directions

This study represents one of the first modelling studies to investigate local persistence while maintaining the flock mean seroprevalence within the range that is seen in natural systems. Our model assumptions result in several limitations and highlight where additional field research is needed to clarify RVFV ecology.

Our simulations only included a single host, sheep, as these are the most economically valuable and abundant domestic ruminant species in areas representative of our study area in central South Africa. Cattle typically have higher seroprevalence levels than sheep [13], which may be attributed to their high biomass attracting more mosquito bites or to their longer life span and slower population turnover. Ultimately, the epidemiological dynamics will hinge on the interaction between the capacity for transmission between host and vector, the rate of decay of the population's seroprevalence and frequency of climatically forced hatching. A full understanding of a cattle-dominated system would require further investigation. Similarly, we excluded wildlife, which may impact the disease dynamics if their life history traits shift the model parameters and/or their movements require the inclusion of metapopulation dynamics. We did not examine these dynamics in detail in order to retain focus on the persistence mechanisms in our study site, where sheep are predominant. However, our findings indicate that in a cattle-dominated system with greater transmission of infection, we would expect more amplification of infection in the vectors and consequently reduced dependence on TOT to sustain infection from year to year. For example, our simulations show that for a system with an expected mean seroprevalence of 60%, local, long-term persistence would require a higher *Aedes* bite rate on the individuals with higher biomass and a TOT fraction that likely exceeds 0.2.

There are four hypotheses of RVFV maintenance [51]: (1) RVFV is maintained (overwintered) via TOT resulting in localized, low-level, annual transmission to vertebrate hosts that is not routinely detected; (2) low-level transmission of RVFV is maintained between horizontally transmitting mosquitoes and the host population without needing an overwintering mechanism; (3) RVFV may overwinter in dormant adult mosquitoes capable of supporting an arboviral infection for extended periods (e.g. overwintering *Culex* spp.); and (4) RVFV is maintained briefly via TOT and/or dormant adults before local extinction and is reintroduced by host movement.

Our primary goal was to examine whether TOT can support local persistence of infection in a region where overwintering was required (hypothesis 1). In central South Africa, where our study system is located, winter conditions have low temperatures and little precipitation, which precludes the survival of large populations of vectors, so hypothesis 2 is not supported. Our simulations predicted extremely low numbers of overwintering *Culex*, with no infected *Culex* surviving. This suggests that hypothesis 3 is not supported. However, if our modelled relationship between temperature and *Culex* larval development and mortality underestimates the winter survival of *Culex*, this could provide an alternative mechanism. As this study focuses on the possibility of local persistence, we did not address the role of metapopulation dynamics (hypothesis 4), but reintroductions of infection from outside could act to reduce the dependence on TOT. Further simulation and field studies are needed to examine when and how other maintenance systems prevail (e.g. in systems that do not require overwintering [20], where the virus can be maintained in a metapopulation system [44] or in overwintering *Culex*).

Further model validation would require estimates of longitudinal seroprevalences from either repeated cross-sectional or longitudinal studies in individual animals. In the absence of longitudinal studies that cover 30 years, we used a broad target seroprevalence range (1–40%) [13] taken from cross-sectional studies across Africa. Unfortunately, cross-sectional data lack the temporal context in which the data were collected, such as when the most recent outbreak was and how the seroprevalence

changes over time. This demonstrates the value of and the need to provide metadata with serological surveys. However, our simulation results are robust across a wide range of seroprevalences. We found that the annual mean seroprevalence varied across much of the target range during the years between outbreaks (approx. 10–48%) as the seroprevalence level decreased following outbreaks.

We used climate data to drive the mosquito dynamics, including precipitation and temperature thresholds that allow mosquito hatching. The thresholds for rainfall that are required to flood a pan will vary by soil type (clay versus sand), vegetation presence, soil saturation level, etc. We are not aware of published hydrological models for pans in South Africa and therefore did not have a reference for these parameters. The precipitation parameters were estimated based on preliminary simulations that resulted in the expected population pattern of *Aedes* and *Culex*. We consider this a very rough estimation of the hatching trigger points. We recommend further field studies to reduce the uncertainty around the hatching triggers, how this varies with geography and how it may change with climate change.

We did not include any climate sensitivity of the virus itself. Data are limited on how RVFV parameters might change (e.g. decreased extrinsic incubation period associated with increased temperature). This will also be important to understand in the face of a changing climate.

Despite the above limitations, our model and simulation suggest that TOT is a viable overwintering mechanism for long-term RVFV persistence localized to a pan. While it may not be the only persistence mechanism, TOT is likely to be important in ecosystems where mosquitoes cannot easily survive the winter/dry season.

Ethics. Ethical approval was provided by the following: US Hummingbird Institutional Review Board (no. 2014-25 24/11/2014), US DTRA Research Oversight Board (CT-2014-33 27/01/2015), SA Witwatersrand and Pretoria Universities Human Ethics Committee (M140306 30/04/2014; 140/2018 11/06/2018) and SA Provincial Departments of Health Free State and Northern Cape (NC2015/001 09/02/2015; 04/04/2015).

Data accessibility. The data and code for this project are currently archived on Zenodo [52].

Electronic supplementary material is available online [53].

Declaration of AI use. We have not used AI-assisted technologies in creating this article.

Authors' contributions. M.K.R.: conceptualization, data curation, formal analysis, funding acquisition, investigation, methodology, project administration, resources, software, validation, visualization, writing—original draft, writing—review and editing; J.C.P.: formal analysis, methodology, resources, software, supervision, validation, visualization, writing—original draft, writing—review and editing; N.R.: conceptualization, formal analysis, investigation, methodology, software, supervision, validation, visualization, writing—original draft, writing—review and editing; A.K.: funding acquisition, supervision, writing—review and editing; P.N.T.: validation, writing—review and editing; A.A.: validation, writing—review and editing; S.C.: supervision, validation, writing—review and editing; C.C.: validation, writing—review and editing; V.M.: validation, writing—review and editing; P.J.v.V.: validation, writing—review and editing; D.T.H.: conceptualization, investigation, methodology, supervision, writing—review and editing; W.B.K.: funding acquisition, validation, writing—review and editing; J.T.P.: funding acquisition, validation, writing—review and editing; L.M.: conceptualization, formal analysis, investigation, methodology, software, supervision, validation, visualization, writing—original draft, writing—review and editing.

All authors gave final approval for publication and agreed to be held accountable for the work performed therein.

Conflict of interest declaration. We declare we have no competing interests.

Funding. We would like to acknowledge the support provided by the US Department of Defense, Defense Threat Reduction Agency who supported the underlying research these models are based on: Understanding Rift Valley Fever in the Republic of South Africa (HDTRA1-14-1-0029; 2014–2019) and Reducing the Threat of Rift Valley Fever through Ecology, Epidemiology and Socio-Economics (HDTRA1-19-0033; 2019–2024). The project depicted is sponsored by the US Department of Defense, Defense Threat Reduction Agency. The content of the information does not necessarily reflect the position or the policy of the federal government, and no official endorsement should be inferred. We would also like to acknowledge the support from BBSRC: BB/M003949/1.

Acknowledgements. We want to acknowledge the data provided by the South African Weather Service, which provided the temperature data that were used to drive the model.

References

1. Wilder-Smith A, Gubler DJ, Weaver SC, Monath TP, Heymann DL, Scott TW. 2017 Epidemic arboviral diseases: priorities for research and public health. *Lancet Infect. Dis*. **17**, e101–e106. (doi:10.1016/s1473-3099(16)30518-7)
2. Calvet GA, Santos FB dos, Sequeira PC. 2016 Zika virus infection: epidemiology, clinical manifestations and diagnosis. *Curr. Opin. Infect. Dis*. **29**, 459–466. (doi:10.1097/qco.0000000000000301)
3. Koenraadt CJM, Möhlmann TWR, Verhulst NO, Spitzen J, Vogels CBF. 2019 Effect of overwintering on survival and vector competence of the West Nile virus vector *Culex pipiens*. *Parasites Vectors* **12**, 147. (doi:10.1186/s13071-019-3400-4)
4. Daubney R, Hudson JR, Garnham PC. 1931 Enzootic hepatitis or Rift Valley fever: an undescribed virus disease of sheep, cattle and man from East Africa. *J. Pathol. Bacteriol*. **34**, 545–579.
5. Gear J, Meillon B, Measroch V, Davis D. 1951 Rift Valley fever in South Africa. 2. The occurrence of human cases in the Orange Free State, the North-Western Cape Province, the Western and Southern Transvaal B. *Field Lab. Investig. Afr. J. Health Prof. Educ*. **25**, 908–912.
6. Nanyingi MO, Munyua P, Kiama SG, Muchemi GM, Thumbi SM, Bitek AO, Bett B, Muriithi RM, Njenga MK. 2015 A systematic review of Rift Valley fever epidemiology 1931–2014. *Infect. Ecol. Epidemiol*. **5**, 28024. (doi:10.3402/iee.v5.28024)
7. Pienaar NJ, Thompson PN. 2013 Temporal and spatial history of Rift Valley fever in South Africa: 1950 to 2011. *Onderstepoort J. Vet. Res.* **80**, 1–13. (doi:10.4102/ojvr.v80i1.384)
8. Morvan J, Saluzzo JF, Fontenille D, Rollin PE, Coulanges P. 1991 Rift Valley fever on the east coast of Madagascar. *Res. Virol*. **142**, 475–482. (doi:10.1016/0923-2516(91)90070-j)
9. Al-Hazmi M *et al*. 2003 Epidemic Rift Valley fever in Saudi Arabia: a clinical study of severe illness in humans. *Clin. Infect. Dis*. **36**, 245–252. (doi:10.1086/345671)
10. Sissoko D, Giry C, Gabrie P, Tarantola A, Pettinelli F, Collet L, D'Ortenzio E, Renault P, Pierre V. 2009 Rift Valley fever, Mayotte, 2007–2008. *Emerg. Infect. Dis*. **15**, 568–570. (doi:10.3201/eid1504.081045)

11. Mdlulwa Z, Ngwane CB. 2017 Evaluating the impact of 2010 Rift Valley fever outbreaks on sheep numbers in three provinces of South Africa. *Afr. J. Agric. Res*. **12**, 979–986. (doi:10.5897/ajar2016.11130)
12. McMillen CM, Hartman AL. 2018 Rift Valley fever in animals and humans: current perspectives. *Antivir. Res*. **156**, 29–37. (doi:10.1016/j.antiviral.2018.05.009)
13. Clark MHA, Warimwe GM, Di Nardo A, Lyons NA, Gubbins S. 2018 Systematic literature review of Rift Valley fever virus seroprevalence in livestock, wildlife and humans in Africa from 1968 to 2016. *PLoS Neglected Trop. Dis*. **12**, e0006627. (doi:10.1371/journal.pntd.0006627)
14. Rostal MK *et al*. 2010 Identification of potential vectors of and detection of antibodies against Rift Valley fever virus in livestock during interepizootic periods. *Am. J. Vet. Res*. **71**, 522–526. (doi:10.2460/ajvr.71.5.522)
15. Kariuki Njenga M, Bett B. 2019 Rift Valley fever virus—how and where virus is maintained during inter-epidemic periods. *Curr. Clin. Microbiol. Rep*. **6**, 18–24. (doi:10.1007/s40588-018-0110-1)
16. Rostal MK, Liang JE, Zimmermann D, Bengis R, Paweska J, Karesh WB. 2017 Rift Valley fever: does wildlife play a role? *ILAR J*. **58**, 359–370. (doi:10.1093/ilar/ilx023)
17. Linthicum KJ, Davies FG, Kairo A, Bailey CL. 1985 Rift Valley fever virus (family Bunyaviridae, genus *Phlebovirus*). Isolations from Diptera collected during an inter-epizootic period in Kenya. *J. Hyg*. **95**, 197–209. (doi:10.1017/s0022172400062434)
18. Lumley S, Horton DL, Hernandez-Triana LLM, Johnson N, Fooks AR, Hewson R. 2017 Rift Valley fever virus: strategies for maintenance, survival and vertical transmission in mosquitoes. *J. Gen. Virol*. **98**, 875–887. (doi:10.1099/jgv.0.000765)
19. Bergren NA, Borland EM, Hartman DA, Kading RC. 2021 Laboratory demonstration of the vertical transmission of Rift Valley fever virus by *Culex tarsalis* mosquitoes. *PLoS Neglected Trop. Dis*. **15**, e0009273. (doi:10.1371/journal.pntd.0009273)
20. Cavalerie L, Charron MVP, Ezanno P, Dommergues L, Zumbo B, Cardinale E. 2015 A stochastic model to study Rift Valley fever persistence with different seasonal patterns of vector abundance: new insights on the endemicity in the tropical island of Mayotte. *PLoS One* **10**, e0130838. (doi:10.1371/journal.pone.0130838)
21. Logan TM, Linthicum KJ, Thande PC, Wagateh JN, Nelson GO, Roberts CR. 1991 Egg hatching of *Aedes* mosquitoes during successive floodings in a Rift Valley fever endemic area in Kenya. *J. Am. Mosq. Control Assoc*. **7**, 109–112.
22. Linthicum KJ, Bailey CL, Davies FG, Kairo A. 1985 Observations on the dispersal and survival of a population of *Aedes lineatopennis* (Ludlow) (Diptera: Culicidae) in Kenya. *Bull. Entomol. Res*. **75**, 661–670. (doi:10.1017/s0007485300015923)
23. Tooth S, McCarthy TS. 2007 Wetlands in drylands: geomorphological and sedimentological characteristics, with emphasis on examples from southern Africa. *Prog. Phys. Geogr.* **31**, 3–41. (doi:10.1177/0309133307073879)
24. Linthicum KJ, Davies FG, Bailey CL, Kairo A. 1984 Mosquito species encountered in a flooded grassland dambo in Kenya. *Mosq. News* **44**, 228–232.
25. Love TB, Kumar V, Xie P, Thiaw W. 2004 A 20-year daily Africa precipitation climatology using satellite and gauge data. In *14th Conference on Applied Climatology*. https://www.cpc.ncep.noaa.gov/products/fews/AFR_CLIM/appl_clim.pdf.
26. Novella NS, Thiaw WM. 2016 A seasonal rainfall performance probability tool for famine early warning systems. *J. Appl. Meteorol. Climatol*. **55**, 2575–2586. (doi:10.1175/jamc-d-16-0111.1)
27. Rueda LM, Patel KJ, Axtell RC, Stinner RE. 1990 Temperature-dependent development and survival rates of *Culex quinquefasciatus* and *Aedes aegypti* (Diptera: Culicidae). *J. Med. Entomol*. **27**, 892–898. (doi:10.1093/jmedent/27.5.892)
28. Ngoshe YB *et al*. 2020 Patterns of Rift Valley fever virus seropositivity in domestic ruminants in central South Africa four years after a large outbreak. *Sci. Rep*. **10**, 10. (doi:10.1038/s41598-020-62453-6)
29. Marino S, Hogue IB, Ray CJ, Kirschner DE. 2008 A methodology for performing global uncertainty and sensitivity analysis in systems biology. *J. Theor. Biol*. **254**, 178–196. (doi:10.1016/j.jtbi.2008.04.011)
30. Drake JM, Rohani P. 2019 *Sensitivity analysis of deterministic models through latin hypercube sampling: a model for the spread of Ebola virus disease*. See https://daphnia.ecology.uga.edu/drakelab/wp-content/uploads/2015/07/sensitivity-ebola.pdf.
31. Diekmann O, Heesterbeek JAP, Roberts MG. 2010 The construction of next-generation matrices for compartmental epidemic models. *J. R. Soc. Interface* **7**, 873–885. (doi:10.1098/rsif.2009.0386)
32. Chitnis N, Hyman JM, Manore CA. 2013 Modelling vertical transmission in vector-borne diseases with applications to Rift Valley fever. *J. Biol. Dyn*. **7**, 11–40. (doi:10.1080/17513758.2012.733427)
33. Adongo D, Fister KR, Gaff H, Hartley D. 2013 Optimal control applied to Rift Valley fever. *Nat. Resour. Model*. **26**, 385–402. (doi:10.1111/nrm.12006)
34. Gaff HD, Hartley DM, Leahy NP. 2007 An epidemiological model of Rift Valley fever. *Electron. J. Differ. Equ* **2007**, 1–12.
35. Xiao Y, Beier JC, Cantrell RS, Cosner C, DeAngelis DL, Ruan S. 2015 Modelling the effects of seasonality and socioeconomic impact on the transmission of Rift Valley fever virus. *PLoS Neglected Trop. Dis*. **9**, e3388. (doi:10.1371/journal.pntd.0003388)
36. Lo Iacono G, Cunningham AA, Bett B, Grace D, Redding DW, Wood JLN. 2018 Environmental limits of Rift Valley fever revealed using ecoepidemiological mechanistic models. *Proc. Natl Acad. Sci. USA* **115**, E7448–E7456. (doi:10.1073/pnas.1803264115)
37. Nicolas G, Chevalier V, Tantely LM, Fontenille D, Durand B. 2014 A spatially explicit metapopulation model and cattle trade analysis suggests key determinants for the recurrent circulation of Rift Valley fever virus in a pilot area of Madagascar highlands. *PLoS Neglected Trop. Dis*. **8**, e3346. (doi:10.1371/journal.pntd.0003346)
38. Yang CX, Nie LF. 2016 Modelling the use of impulsive vaccination to control Rift Valley fever virus transmission. *Adv. Differ. Equ*. **2016**, 134. (doi:10.1186/s13662-016-0835-1)
39. Sumaye R, Jansen F, Berkvens D, De Baets B, Geubels E, Thiry E, Krit M. 2019 Rift Valley fever: an open-source transmission dynamics simulation model. *PLoS One* **14**, e0209929. (doi:10.1371/journal.pone.0209929)
40. Chevalier V, Rakotondrafara T, Jourdan M, Heraud JM, Andriamanivo HR, Durand B, Ravaomanana J, Rollin PE, Rakotondravao R. 2011 An unexpected recurrent transmission of Rift Valley fever virus in cattle in a temperate and mountainous area of Madagascar. *PLoS Neglected Trop. Dis*. **5**, e1423. (doi:10.1371/journal.pntd.0001423)
41. Tennant WSD *et al*. 2021 Modelling the persistence and control of Rift Valley fever virus in a spatially heterogeneous landscape. *Nat. Commun*. **12**, 13. (doi:10.1038/s41467-021-25833-8)
42. Shoemaker T *et al*. 2002 Genetic analysis of viruses associated with emergence of Rift Valley fever in Saudi Arabia and Yemen, 2000-01. *Emerg. Infect. Dis*. **8**, 1415–1420. (doi:10.3201/eid0812.020195)
43. Thiongane Y, Gonzales JP, Fati A, Akakpo JA. 1991 Changes in Rift Valley fever neutralizing antibody prevalence among small domestic ruminants following the 1987 outbreak in the Senegal river basin. *Res. Virol*. **142**, 67–70. (doi:10.1016/0923-2516(91)90029-3)
44. Favier C, Chalvet-Monfray K, Sabatier P, Lancelot R, Fontenille D, Dubois MA. 2006 Rift Valley fever in West Africa: the role of space in endemicity. *Trop. Med. Int. Health* **11**, 1878–1888. (doi:10.1111/j.1365-3156.2006.01746.x)
45. McIntosh BM, Jupp PG, Dossantos I, Barnard BJH. 1980 Vector studies on Rift Valley fever virus in South Africa. *South Afr. Med. J*. **58**, 127–132.

46. Saiyasombat R, Bolling BG, Brault AC, Bartholomay LC, Blitvich BJ. 2011 Evidence of efficient transovarial transmission of *Culex flavivirus* by *Culex pipiens* (Diptera: Culicidae). *J. Med. Entomol*. **48**, 1031–1038. (doi:10.1603/me11043)
47. Fischer EA, Boender GJ, Nodelijk G, de Koeijer AA, van Roermund HJ. 2013 The transmission potential of Rift Valley fever virus among livestock in the Netherlands: a modelling study. *Vet. Res*. **44**, 58. (doi:10.1186/1297-9716-44-58)
48. Gachohi JM, Njenga MK, Kitala P, Bett B. 2016 Modelling vaccination strategies against Rift Valley fever in livestock in Kenya. *PLoS Neglected Trop. Dis*. **10**, e0005049. (doi:10.1371/journal.pntd.0005049)
49. Pedro SA, Tonnang HEZ, Abelman S. 2016 Uncertainty and sensitivity analysis of a Rift Valley fever model. *Appl. Math. Comput*. **279**, 170–186. (doi:10.1016/j.amc.2016.01.003)
50. van den Bergh C, Venter EH, Swanepoel R, Thompson PN. 2019 High seroconversion rate to Rift Valley fever virus in cattle and goats in far northern KwaZulu-Natal, South Africa, in the absence of reported outbreaks. *PLoS Neglected Trop. Dis*. **13**, e0007296. (doi:10.1371/journal.pntd.0007296)
51. Rostal MK *et al*. Rift Valley fever epidemiology: shifting the paradigm and rethinking research priorities. *Lancet Planet. Health* In Press.
52. Rostal MK, Matthews L, Ross N, Prentice JC. 2025 One-Health-Research-Consulting/RVF_SIR_Model: Final Model. Zenodo. (doi:10.5281/zenodo.15632526)
53. Rostal MK, Prentice J, Ross N, Kemp A, Thompson PN, Anyamba A *et al*. 2025 Supplementary material from: Localized Rift Valley fever virus persistence explains epidemic and interepidemic dynamics and guides control strategies. Figshare. (doi:10.6084/m9.figshare.c.7920926)