Rapid modelling of the 2026 Andes virus outbreak predicts limited transmissibility and low mainland outbreak risk

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Abstract

Background
In May 2026, an outbreak of Andes virus (ANDV) infection was reported among passengers and crew of the cruise ship MV Hondius. As of 27 May, 13 linked cases and three deaths had been reported, with ongoing concern about onward transmission after disembarkation.

Methods
We conducted a responsive analysis of the ongoing outbreak using publicly available data published by international public health bodies. We reconstructed plausible transmission chains and fitted a stochastic agent-based model of onboard transmission to estimate the probability of transmission per close contact. We then extrapolated the inferred per-contact transmissibility to mainland UK contact rates and simulated potential mainland outbreaks using a stochastic hybrid agent-compartment model.

Findings
The model identified a pattern of early transmission heterogeneity consistent with superspreading aboard the ship. After accounting for this heterogeneity, estimated per-contact transmissibility was low, with a median value of 0.006 (95% interval: 0.001–0.019). This corresponded to an onboard R_0, defined as the expected number of infections caused by an average infected person aboard the ship, of 0.36 (95% interval: 0.11–1.24). Extrapolating to mainland UK contact rates gave a mainland R_0 of 0.19 (95% interval: 0.06–0.67), below the (R=1) threshold required for sustained transmission.

Interpretation
Continued control measures remain appropriate given the severity of ANDV infection, and our results do not exclude onward viral transmission if containment measures fail. However, the inferred transmissibility of ANDV in this outbreak suggests that the risk of a sustained or sizeable mainland outbreak is low.

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Introduction

Andes virus (ANDV) is a New World hantavirus that causes hantavirus cardiopulmonary syndrome (HPS), a severe respiratory disease with high case fatality rate[1]. Human infections usually occur through exposure to infected rodents, but ANDV differs from other hantaviruses as person-to-person transmission has been documented, particularly after close, prolonged contact[1,2]. In May 2026, an outbreak of ANDV was detected among passengers and crew of the expedition cruise ship MV Hondius, prompting an international response involving medical evacuations, quarantine, and monitoring of those onboard[3]. As of 29 May 2026, ECDC reported 13 linked cases, including 11 confirmed and two probable cases, and three deaths[4]. The possibility of onward transmission after disembarkation has received substantial media attention[5–7], reflecting uncertainty over whether ANDV could sustain outbreaks outside the shipboard setting.

Cruise ships impose unique conditions on virus transmission: passengers and crew share enclosed spaces, dining areas, cabins, corridors, and organised activities, and the same individuals may have repeated close contacts over multiple days[8]. By contrast, mainland contact data indicate substantially lower rates of close contact between individuals, with mean daily contact rates ~2-fold lower than those inferred for cruise ship settings[9]. The basic reproduction number, R_0, describing the expected number of secondary infections caused by one infectious individual in a fully susceptible population, is determined by the per-contact probability of transmission, the contact rate between individuals, and the duration of infectiousness[10]. A shipboard outbreak can therefore have a higher R_0 than would be expected on the mainland, even if the underlying transmissibility of a virus is unchanged. Mathematical modelling can estimate transmissibility by fitting an epidemiological model to outbreak data, even under conditions of limited data availability[11], provided sufficient information is available on the infectious period and outbreak contact rates. The virus's inferred transmissibility may then be extrapolated to a different setting, providing a quantitative estimate of outbreak risk under different conditions.

A previous study used data from the 2026 MV Hondius outbreak to evaluate hantavirus risk in rural Argentina[12]. Here, we use publicly available data alongside a stochastic agent-based simulation of onboard transmission to estimate ANDV transmissibility and onboard R_0. We then extrapolate the inferred transmissibility to a mainland setting to infer the risk and size of outbreaks that might occur should an infectious case be transmitted out of quarantine. Our analysis indicates ANDV has limited human-to-human transmissibility and a low probability of sustained mainland transmission, supporting the need for continued isolation and monitoring while suggesting that the risk of widespread community transmission is low.

Methods

Disease Progression Model

ANDV infection was assumed to progress through susceptible, exposed (i.e., incubating), prodromal (i.e. infectious, mildly symptomatic), HPS, and recovered states. The start of the prodromal state was assumed to correspond to the date of any non-specific symptoms (e.g., fever, fatigue, chills, myalgia, headache, dizziness, or gastrointestinal symptoms) and ended with severe symptom onset. Within the prodromal state, transmission was assumed to occur at a uniform rate. For simplicity, we assumed that individuals in the HPS state do not contribute to onward transmission, reflecting an expected sharp reduction in contacts due to immobility, cabin confinement, or ICU isolation. Recovered individuals were assumed immune for life,

consistent with evidence that hantavirus infection induces long-lived humoral immunity and the lack of evidence for reinfection[13,14].

Epidemiological Parameters

The R package MASS[15] was used to fit wait-time distributions to data on the incubation and prodromal phases of viral infection from a previous publication[16]. Conditional on survival from severe disease, the wait-time distribution of the HPS period was inferred from the reported median hospital stay in[17] of 16 days (IQR: 13.0–27.0 days). Mortality following progression to HPS was modelled as a case-fatality probability. CFR estimates for Andes virus infection vary from 20% to 40%[3,14,18]. In the current outbreak, three deaths occurred among thirteen ANDV infections, for a CFR of 23%.

Case Data

Publicly available data were used to describe each confirmed and presumptive case in the MV Hondius outbreak (Supplementary Table 1). Case 01 was treated as the primary case, and the above fitted distributions was used to assess the probability of Cases 02-13 representing secondary or tertiary transmissions. For each candidate infector-recipient pair, we calculated a timing likelihood across days when the infector was prodromal and the recipient was asymptomatic, using the wait-time distributions to estimate the probability that infection on that day would produce the recipient's observed symptom onset date. Timing likelihoods were then normalised for each recipient case, providing a probability of transmission from each possible infector.

MV Hondius Occupancy

Publicly available data were used to reconstruct the manifest of the MV Hondius (Supplementary Table 2). We recorded the numbers of passengers and crew embarking, disembarking, and dead/medically evacuated from 1 April 2026 to final passenger disembarkation in Granadilla, Tenerife on 11 May 2026. Passenger cabin numbers and berth sizes (twin, triple, quadruple) were taken from public ship descriptions. These descriptions list 38 crew cabins, three of which are single berth (captain, ship doctor, expedition leader), with the remainder assumed to be twin berths. Individual-level cabin occupancy data were unavailable, and passengers and crew were therefore assigned cabins at random with the following constraints: Case 01 is deterministically assigned to a twin passenger cabin with a second occupant; and all single berth crew cabins are occupied before assigning twin berth crew cabins. Ordinary disembarkation followed the dates and numbers recorded in the manifest. Except for Case 01 and their co-occupant, the specific passengers and crew leaving the model at each disembarkation was chosen randomly. Crew disembarked as individuals, and passengers as travelling groups defined by shared cabin occupancy. Unique cabin occupancy and disembarkation schemes were produced for each model run.

MV Hondius Contact Rates

A close-contact exposure event sufficient for ANDV transmission was defined by the World Health Organisation (WHO) and US Centers for Disease Control and Prevention (CDC) as remaining within 2 metres of an infectious individual in an enclosed setting for 15 minutes[19,20] [20,21]. In the absence of detailed information about contact rates between individuals on the MV Hondius, we parameterised shipboard contact rates using the high-resolution cruise-ship contact network study[8]. This study used Bluetooth proximity devices to measure contacts

between passengers and crew across four three-day cruise sailings. It reports a median number of unique individuals contacted per day – defined as a minimum of 15 minutes spent at a distance of less than two metres – of 14.9 (95% intervals: 1.3–68.8). We modelled heterogeneity in daily unique contacts using a lognormal distribution fitted to these quantiles (Supplementary Figure 1). We found no published estimate of within-cabin close contact rates on cruise ships; in its absence, we assume $\lambda_{cabin} = 12$, equivalent to 3 hours of close contact daily between cabin mates.

On 2 May 2026, after hantavirus infection was identified in Case 03, cabin confinement and social distancing measures were implemented onboard, with unknown effects on contact rates. This effect was modelled as a fixed proportion reduction in daily contacts and estimated during model fitting.

Model Fitting

A stochastic agent-based model was parameterised using the epidemiological, ship occupancy, and contact-rate assumptions described above. Using this model, we jointly calibrated three uncertain parameters: the per-contact-event transmission probability, the daily unique contact rate of Case 01, and the effectiveness of cabin confinement and social distancing.

For each sampled parameter combination, the model simulated daily contacts and transmission between infectious and susceptible individuals. Simulations were rejected if they failed to generate enough onward infections for the observed outbreak. For accepted simulations, a pseudo-likelihood was calculated from the probability of observing the recorded symptom-onset dates given the simulated exposure dates and fitted incubation-period distribution. For simulations generating more than twelve onward infections, excess infections were incorporated by considering the probability of the cases remaining unobserved as of the model fitting cut-off date (28 May). Parameter-set likelihoods were then calculated by averaging across accepted simulations.

Mainland Outbreak Model

Symmetric age-stratified mainland contact rates were calculated from the UK POLYMOD social contact survey dataset[9] using the socialmixr R package[21], as described elsewhere[22]. Data were grouped into four age categories: preschool-aged children (0-4 years old); school-aged children (5-18 years old); adults (19-64 years old); and older adults (65+ years old). Contacts were filtered to include only face-to-face interactions lasting at least 15 minutes.

To estimate possible UK mainland outbreak size, we created a stochastic discrete-time hybrid agent–compartment model with S-E-Prodromal-HPS-R disease progression and a one-day timestep. The model was parameterised to resemble the UK population and stratified by age-group as described above. Susceptible and recovered individuals were represented as age-specific compartment counts, while infected individuals were represented explicitly as agents from exposure until recovery or death. This allowed individual infection trajectories to be sampled directly from the fitted incubation, prodromal, and HPS duration distributions, while avoiding explicit representation of the full population.

Mathematical Implementation

Full descriptions of the formulae for calculating epidemiological parameters, population parameters, pseudo-likelihoods, and modelling processes are provided in the Supplementary Methods.

Results

MV Hondius Outbreak

ANDV cases associated with the MV Hondius outbreak are shown in Figure 1A. The presumptive primary case (Case 01) was a 70-year-old male travelling with his wife (Case 02, 69-year-old female) and may have been exposed during a birdwatching trip to a landfill site in Ushuaia, Argentina, on 27 March[23]. After embarking the MV Hondius on 1 April, Case 01 developed mild non-specific symptoms on 3 April, including fever, headache, and diarrhoea. By 6 April, his symptoms included dizziness, tachycardia, and tachypnoea, and, after rapid clinical deterioration, Case 01 died aboard the vessel on 11 April.

Ten days later (21 April), a 60-year-old male developed fever and respiratory discomfort (Case 03); followed on 22 April by gastrointestinal symptoms in Case 02, and on 23 April by fever and respiratory symptoms in an 80-year-old female berthed two cabins from the primary case (Case 04). On 24 April, Case 02 was medically evacuated from the MV Hondius, and died on 26 April. On April 27, Case 03 was medically evacuated and hospitalised. By 1 May, a further four individuals had developed non-specific symptoms, including the ship's doctor (Case 05, 41-year-old male), expedition guide (Case 06, 56-year-old male), and two individuals who had disembarked prior to symptom onset (Case 07, 64-year-old male; and Case 08, 65-year-old male). On 2 May, hantavirus infection was PCR-confirmed in Case 03 and the ship introduced cabin confinement and social distancing measures to reduce onboard contacts. The same day, Case 04 died aboard the vessel. Cases 05 and 06 were medically evacuated and hospitalised four days later (6 May). All passengers and most crew disembarked the MV Hondius on 10-11 May and were subsequently repatriated. As of 27 May 2026, five further cases had been reported, all hospitalised as a precaution.

Inferring Transmission Order

Distributions fitted to data describing observed incubation and prodromal periods from previous human ANDV cases[16] showed ANDV to have a considerable incubation period, with inferred median 18.4 days (95% interval: 9.8-34.3 days, Figure 1B). The median prodromal period was 4.3 days (95% interval: 1.65-7.0 days, Figure 1C). The long incubation period, and the specific timings of observed cases associated with the MV Hondius, were highly informative of the most likely transmission source of each observed case, under a model of random mixing aboard ship (Figure 1D). In this model, cases 02, 03, 04, and 08 were inferred to be infected by Case 01 with near certainty. Cases 05 to 08 were also likely infected by Case 01, with inferred probabilities between 82 and 92%. Subsequent cases 09 to 13, who tested positive after disembarkation on 10-11 May, were likely to have been tertiary infections, with probabilities between 95% and 99% of infection by individuals other than Case 01. The data are therefore most consistent with two rounds of transmission: secondary infections from Case 01 to Cases 02-08, followed by tertiary transmission to Cases 09-13.

Observed Reproduction Number

Straightforward calculations involving the observed reproduction number R_{obs} are suggestive of a pattern of superspreading on board the ship. The observed reproduction number divides the number of transmissions by the number of infected people. Excluding within-cabin transmission, which may be atypical, Case 01 produced six outside-cabin observed secondary infections. From the five secondary cases who developed symptoms onboard, five further tertiary infections have been reported, giving an overall R_{obs} of 1.83. Assuming a Poisson distribution of transmission, this suggests that the six transmissions from Case 01 were unusual, having a probability of roughly 0.8%. Excluding Case 01 from the derivation to prevent bias gives $R_{obs} = 1$, making the six transmissions even more unusual. This suggests Case 01 may have been an atypical transmitter, although cabin confinement measures introduced on 2 May may also have contributed to differences in secondary and tertiary transmission rates.

R_{obs} is known to have a vulnerability towards upward bias relative to the true population R_0 because detected outbreaks often arise from early transmission chains involving individuals whose contact rates or infectiousness are unusually high[24]. To estimate the true population R_0 more rigorously, a model incorporating expected onboard contact heterogeneity was needed.

Estimating Transmission Probability

A stochastic agent-based model of onboard transmission fitted to case data describing observed infections, but accounting for potential unobserved infections, estimated a per-contact transmission probability of 0.006 (95% interval: 0.001, 0.019, Figure 2A). In our model a contact was defined being of 15-minute duration: Both within-cabin and between-cabin contacts were included within this definition, multiple contacts between individuals being possible within the same day. A heterogeneous contact distribution was modelled (Supplementary Figure 1).

Within the modelled contact network aboard the MV Hondius, the inferred per-contact result translated into an estimated R_0 aboard the MV Hondius of 0.36 (95% interval: 0.11, 1.24). The contact rate of Case 01 was weakly identifiable, yet suggestive of Case 01 being an above-average transmitter (Figure 2B): The 95% interval exceeded the median expected contact rate of ~15 with a posterior mean multiply in excess of that value. A statistic describing the effectiveness of control measures showed an upward likelihood trend as effectiveness increased towards 1, but was largely unidentifiable, with the 95% posterior interval spanning a large proportion of the prior range (Figure 2C).

Extrapolating the per-contact transmission probability to a counterfactual mainland contact setting, designed to represent the absence of control measures, we inferred that ANDV would have a mainland R_0 of 0.19 (95% interval: 0.06, 0.67), below the R = 1 threshold. These results suggests that ANDV has a low transmissibility and is unlikely to sustain long-term chains of mainland transmission.

Model-fitted estimates were strongly influenced by assumptions about shipboard contact rates (Supplementary Figure 2), with reductions in the contact rate resulting in compensatory increases in the estimated per-contact transmission probability. Notably, reducing median daily contacts to 9 produced an estimate of per-contact transmission probability which, when extrapolated to a mainland contact setting, produced a mainland R_0 estimate of 0.27 (95% interval: 0.09, 1.06), indicating a small probability of exceeding the $R = 1$ threshold required for sustained onward transmission. This scenario assumes contact rates aboard the MV Hondius were almost equivalent to the ~8.12 contact rate experienced on the mainland, which is unlikely

given the shipboard environment. An alternative scheme that sampled a new contact rate for each individual on each day, thus making high-contact behaviour transient rather than persistent, inferred a higher per-contact transmission probability but still led to an inferred mainland R_0 below 1: 0.34 (95% interval: 0.16, 0.89).

Mainland Outbreak Risk

A hybrid agent-compartment model (Figure 3A), parameterised to resemble the UK population, suggested that mainland outbreaks are unlikely to lead to sustained transmission, with 79.5% of simulated outbreaks producing zero onward transmission, and 96.2% concluding with fewer than four total cases. Models described contact rates between four age groups: 0-4 years old; 5-18 years old; 19-64 years old; and 65+ years old (Figure 3B). Simulations seeding a single exposed individual showed the vast majority of simulated outbreaks dying out with little impact, with outbreaks involving multiple cases being seen in occasional instances among the 10^6 simulations performed for each age group (Figure 3C). Simulations seeded with an index case in the 5-18 years old age group had a slightly increased likelihood of onward transmission due to increased within-group contact among school-age individuals. Conversely, the lowest risk of onward transmission was observed when seeding to the low-contact 65+ years old age group. With the caveats that uncertainty in the true case fatality ratio of 2026 ANDV is considerable, and that ANDV treatment is rapidly evolving[25], the most likely outcome involved zero fatalities from ANDV-induced HPS (95% range: 0 to 2). Together, these simulations suggest that in the absence of superspreading events, ANDV is unlikely to produce considerable outbreaks in a mainland setting, with a low risk of producing short stuttering transmission chains comprising a small number of infected individuals.

Discussion

In this responsive study to an ongoing outbreak, we used publicly available data and agent-based modelling of the MV Hondius to estimate ANDV transmissibility, then extrapolated this estimate to a mainland setting to assess further outbreak risk. The inferred per-contact transmission probability for ANDV was low, with superspreading inferred to drive the early shipboard outbreak. Our result suggests that, in the absence of further superspreading events, ANDV is unlikely to sustain long-term mainland transmission.

Our result is potentially unexpected given an outbreak aboard MV Hondius involving 13 people, with an observed reproduction number R_{obs} of 1.83 (excluding within-cabin transmission). R_{obs} taken from the early stages of an outbreak often upwardly biases estimates of the true population R_0[24], as detected outbreaks are more likely to arise from early transmission chains with individuals whose contact rates or infectiousness are unusually high. Our inference of a mainland ANDV R_0 is consistent with the scarcity of large ANDV outbreaks observed to date. While around 100-200 cases of ANDV are observed each year in South America[26], and serological studies in that area suggest exposure of the order 1%[27], substantial outbreaks, while not unheard of[28], are rare.

Our approach has several limitations. It relies on public outbreak data collected during an active response. Details of exposure histories, cabin allocation, contact patterns, and case detection may change as further information becomes available. We note that, at the date of model calibration (27 May), a small probability mass remains for further detection of cases directly associated with transmission aboard the MV Hondius: Detection of further cases beyond this date should have only a minor impact on parameter estimates under the pseudo-likelihoods defined here. The fitted transmission probability is also highly sensitive to assumptions about

shipboard contact rates. Given the strong influence of contact-rate assumptions on transmission estimates, and the frequency of cruise-ship infectious disease outbreaks[29,30], further studies are urgently needed to characterise close-contact patterns in these settings. The disease progression distributions used throughout this study were fitted from previous human ANDV cases, which may not fully represent the phenotypes of the 2026 outbreak strain or the evolutionary potential of ANDV. We note that the mainland model does not incorporate behavioural responses to an emerging outbreak, considering the counterfactual case of an outbreak with no such response.

Given these limitations, our results should not be interpreted as ruling out further transmission after disembarkation, or as suggesting any reduction in the continued monitoring or isolation of passengers, crew, and close contacts. Given the severity of HPS, and the potential for delayed symptom onset after exposure, preventing even a single additional case in this outbreak should remain the goal.

Ethics statement

This study used only publicly available outbreak investigation data reported prior to this study by multiple sources, including the WHO, the ECDC, and public media organisations. No individually identifiable data were collected or generated by the authors. Ethical approval was not required.

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Author contributions

Conceptualization: RI; Data curation: RI; Formal analysis: RI; Funding acquisition: CJRI; Investigation: RI; Methodology: RI, CJRI; Project administration: CJRI; Software: RI; Supervision: CJRI; Validation: RI, CJRI; Visualization: RI; Writing – original draft: RI, CJRI; Writing – review & editing: RI; CJRI

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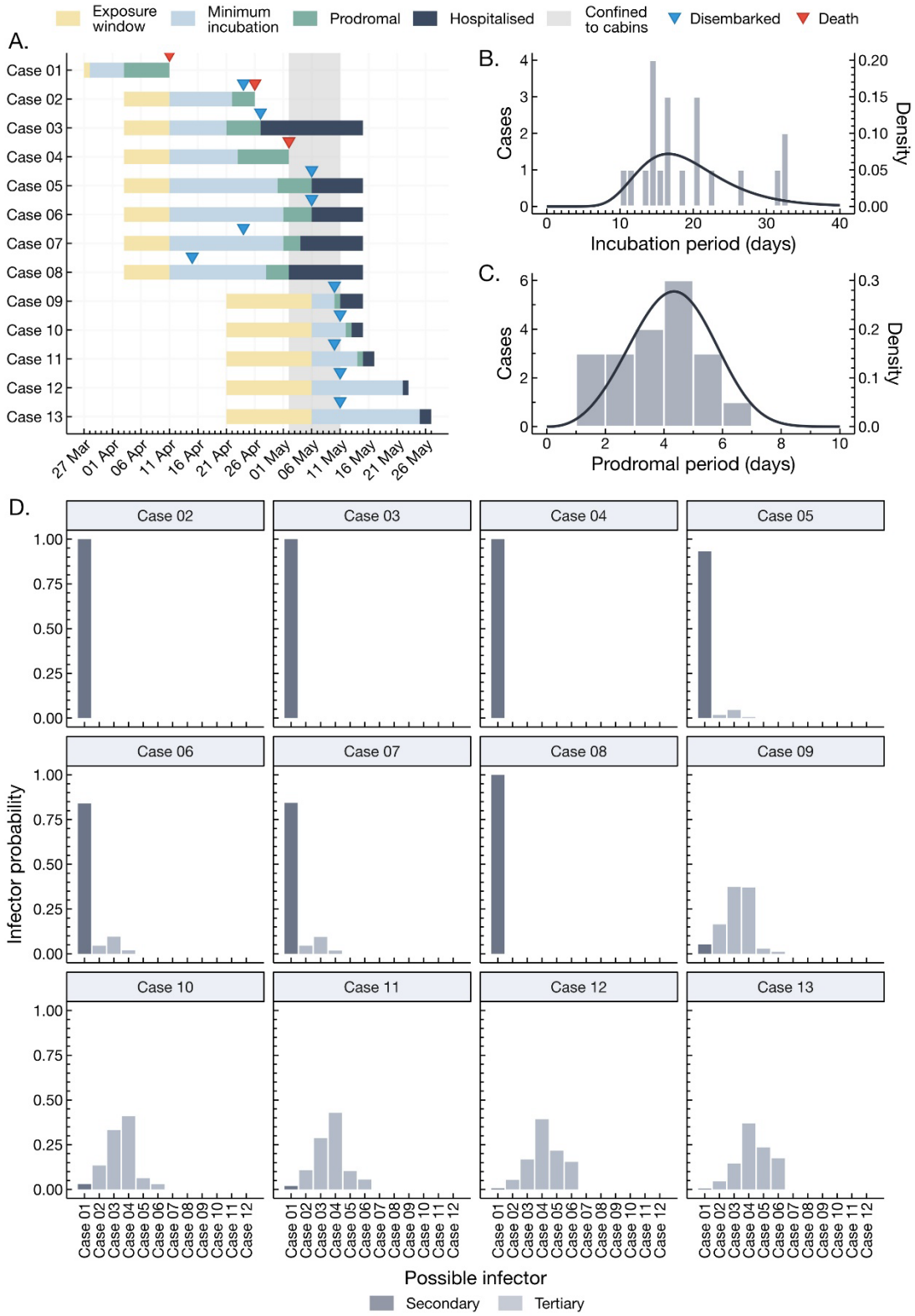

Figure 1: MV Hondius case timelines and inferred transmission. A) Clinical and exposure dates for Andes virus positive cases detected aboard the MV Hondius as of 25 May 2026. Exposure windows and minimum incubation periods are shown for the most likely inferred transmission source (secondary/tertiary) for each case. B) Incubation periods estimated from Vial et al., with the fitted lognormal distribution overlaid in blue. C) Prodromal periods estimated from Vial et al., with the fitted Weibull distribution overlaid in blue. D) Normalised probabilities of each candidate infector for Cases 02–12, classified as secondary transmission from Case 01 (dark blue) or tertiary transmission from other cases (light blue).

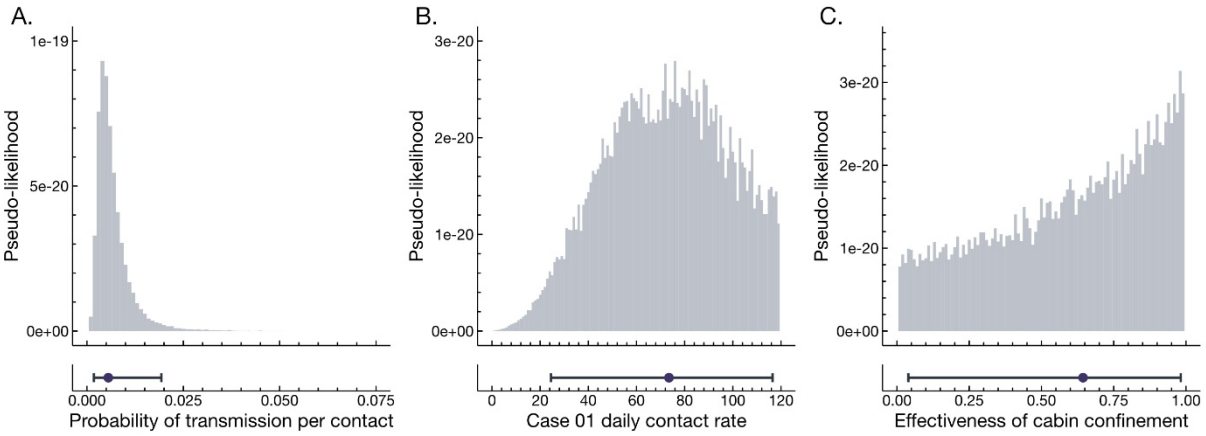

Figure 2: Parameter calibration to MV Hondius case data. Simulation-based pseudo-likelihoods for the three fitted MV Hondius transmission model parameters: A) per-contact transmission probability, $P(transmission \mid contact)$; B) daily unique contact rate of Case 01, C_{Case01}; and C) effectiveness of cabin confinement and social distancing, e_{conf}. Median (dots) and 95% intervals (horizontal whiskers) of the parameter distributions are shown below each distribution.

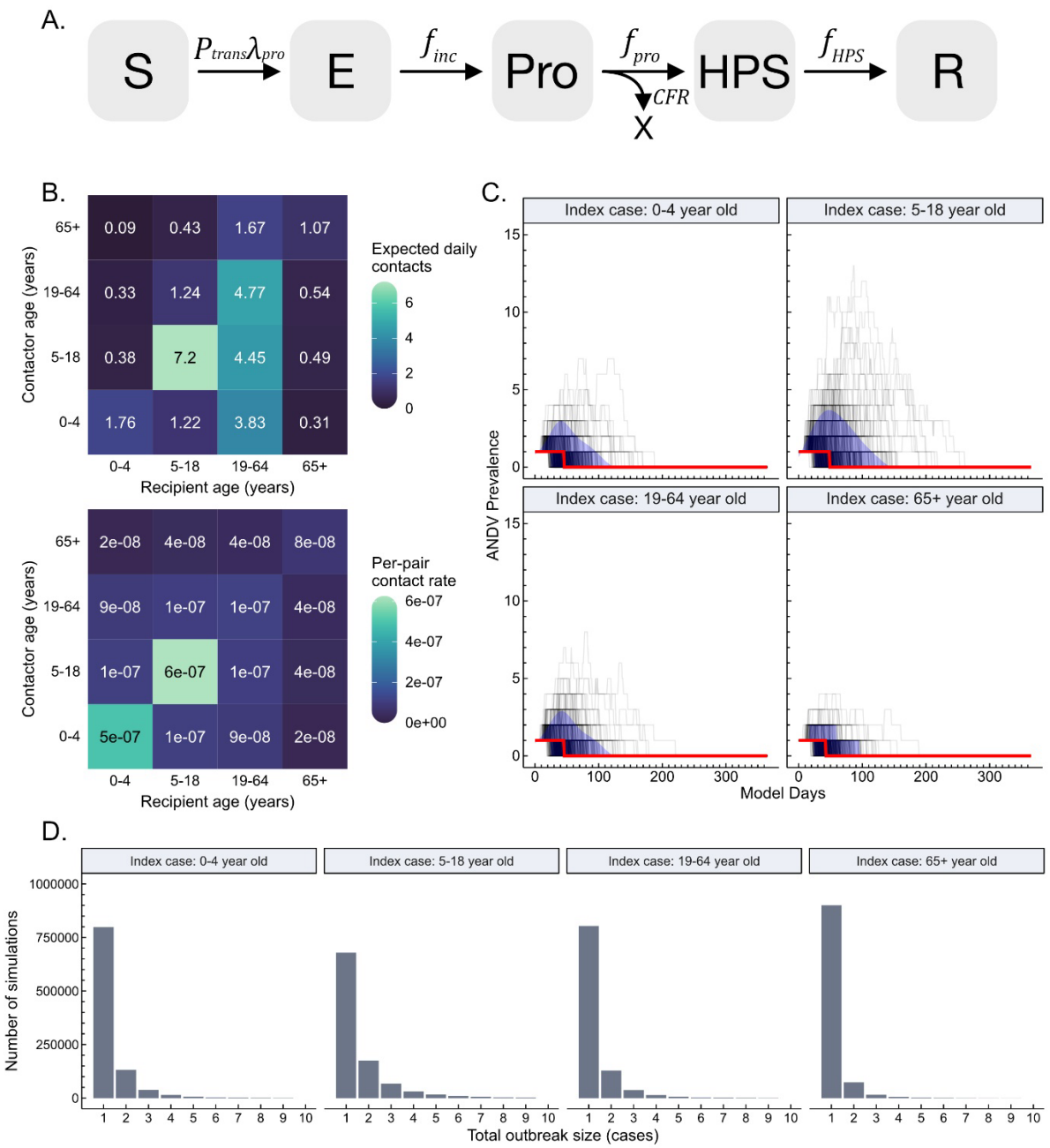

Figure 3: Simulated UK mainland outbreak trajectories by age of the mainland index case. A) Disease progression structure of the stochastic hybrid agent–compartment model used to simulate mainland transmission. B) Age-stratified expected daily contact rates (above) and corresponding per-pair contact rates after accounting for UK age-group population sizes (below) derived from UK POLYMOD data [9]. C) Simulated prevalence trajectories for mainland outbreaks following a single MV Hondius-to-mainland transmission event, stratified by the age group of the newly infected mainland individual. Grey lines show individual stochastic simulations (10,000 representative simulations shown of 1,000,000 total); red lines show the median trajectory and blue areas indicate smoothed lower and upper 95% quantiles. D) Histograms showing total ANDV outbreak sizes across 1,000,000 simulations per index case age group.