Full Title

Potential impact of sexual transmission of Ebola virus on the epidemic in West Africa

Short Title

Modeling sexual transmission of Ebola virus

Authors

Jessica L. Abbate[1,2,3 * ♭]

Carmen Lia Murall[4 *]

Heinz Richner[1]

Christian L. Althaus[5]

[*]These authors contributed equally to this article.

[♭] Address correspondence to: jessica.abbate@ird.fr

Affiliations

1. Institute for Ecology and Evolution, University of Bern, Bern, Switzerland

2. UMR MIVEGEC (UMR CNRS 5290, IRD 224, UM), Institute for Research of

Development (IRD), Montpellier, France

3. UMR UMMISCO (UMI 209 IRD-UPMC), Bondy, France

4. Max-Planck Institute for Dynamics and Self-Organization, Gottingen, Germany

5. Institute of Social and Preventive Medicine (ISPM), University of Bern, Bern,

Switzerland

Abstract

Sexual transmission of Ebola virus disease (EVD) 6 months after onset of symptoms has

been recently documented, and Ebola virus RNA has been detected in semen of survivors

up to 9 months after onset of symptoms. As countries affected by the 2013-2015

epidemic in West Africa, by far the largest to date, are declared free of Ebola virus

disease (EVD), it remains unclear what threat is posed by rare sexual transmission events

that could arise from survivors. We devised a novel mathematical model that includes

sexual transmission from convalescent survivors: a SEICR (susceptible-exposed-

infectious-convalescent-recovered) transmission model. We fitted the model to weekly

incidence of EVD cases from the 2014-2015 epidemic in Sierra Leone. Sensitivity

analyses and Monte Carlo simulations showed that a 0.1% per sex act transmission

probability and a 3-month convalescent period (the two key unknown parameters of

sexual transmission) create very few additional cases, but would extend the epidemic by

83 days [95% CI: 68-98 days] (p < 0.0001) on average. Strikingly, a 6-month

convalescent period extended the average epidemic by 540 days (95% CI: 508–572

days), doubling the current length, despite an insignificant rise in the number of new

cases generated. Our results show that current recommendations for abstinence and

condom use should reduce the number of sporadic sexual transmission events, but will

not reduce the length of time the public health community must stay vigilant. While the

number of infectious survivors is expected to greatly decline over the coming months, our

results show that transmission events may still be expected for quite some time as each

event results in a new potential cluster of non-sexual transmission. Precise measurement

of the convalescent period is thus important for planning ongoing surveillance efforts.

Key Words: Ebola virus; epidemiology; emerging infectious disease; sexually

transmitted infection; mathematical modeling; basic reproductive number

Introduction

Recent reports suggesting the potential for sexual transmission of Ebola virus from convalescent survivors have raised a number of important questions regarding its impact on the final phase of the epidemic in West Africa [1,2]. Even once the worst hit countries of Guinea, Liberia, and Sierra Leone are declared free of Ebola virus disease (EVD), rare cases may still arise from the large number of remaining survivors. Importantly, sexual transmission is dependent on the frequency of infections rather than the density of available hosts, allowing chains of transmission to persist at low susceptible densities where non-sexual transmission would typically fail to occur [3]. Perhaps the most crucial element for bringing the epidemic to an end is maintaining vigilance in the community and preventing – or quickly responding to – new chains of transmission. Thus, it is important to investigate the potential impact of convalescent sexual transmission on the transmission dynamics in general, and on the tail of the epidemic in particular, to understand how long that vigilance might remain critical.

Follow-up studies on survivors of the 1995 outbreak in the Democratic Republic of Congo [4] and the 2000 [5] and 2007 [6] outbreaks in Uganda have raised awareness of what is now being termed "post-Ebola syndrome" (post-Ebola sequelae) – debilitating illnesses from myalgia to uveitis – which can persist for at least 21 months after the onset of symptoms. Though the virus is no longer detected in the blood after acute EVD symptoms disappear, active (replicating) virus has been documented in ocular fluid, rectal fluids, vaginal fluids, and semen [1,4,7,8]. Transmission to sexual partners was never confirmed in earlier outbreaks, but was suspected to have occurred in at least one instance

[4]. Similarly, cases of sexual transmission of other hemorrhagic fever infections, notably

by the closely related Marburg virus, have been suspected in the past [9,10]. Studies from

the West African outbreak, showing viremia in semen 4-6 months after onset of

symptoms in 65% of men tested (7-9 months in 26%) [1] and presenting molecular

evidence of sexual transmission from a survivor 179 days after onset of symptoms [2],

suggest that sexual transmission from convalescent men can and does occur.

Sexual transmission of Ebola virus from convalescent survivors is likely a rare event, but

researchers have warned that it should be considered in epidemiological models that are

used to predict the trajectory of an outbreak [11]. To this end, we devised a novel

mathematical model for EVD transmission: SEICR (susceptible-exposed-infectious-

convalescent-recovered), which includes a component for convalescent sexual

transmission from convalescent survivors who maintain active Ebola virus replication..

We illustrated the model by fitting it to weekly EVD incidence from Sierra Leone, the

largest population of recovering survivors from the current West Africa epidemic. We

performed sensitivity analysis to understand the influence of key unknown parameters,

such as the duration of the convalescent period and the transmission probability per

sexual contact. We also performed Monte Carlo simulations to explore the impact of

sexual transmission on the epidemic tail in Sierra Leone.

Methods

Transmission model. We extended a SEIR (susceptible-exposed-infected-recovered)

modeling framework, which has been extensively used to describe EVD transmission

[12–14], by adding a component for sexual transmission from convalescent survivors

who maintain active Ebola virus replication (Fig. 1). The resulting SEICR model has five

states: susceptible, *S*, exposed, *E*, symptomatic and infectious, *I*, convalescent, *C*, fully

recovered and immune, *R*, and dead, *D*. The model is represented by the following set of

ordinary differential equations (ODEs):

102
$$\frac{dS}{dt} = -\beta(t)SI - \beta_S \, pC \frac{S}{N}$$
$$\frac{dE}{dt} = \beta(t)SI + \beta_S \, pC \frac{S}{N} - \sigma E$$
$$\frac{dI}{dt} = \sigma E - \gamma I$$
$$\frac{dC}{dt} = (1-f)\gamma I - \alpha C \qquad (1)$$
$$\frac{dR}{dt} = \alpha C$$
$$\frac{dD}{dt} = f\gamma I$$

where $N = S + E + I + C + R$ denotes the total population size. We assumed the non-

sexual transmission rate, $\beta(t)$, to be initially constant (β_0) before it starts to decay

exponentially due to the effect of control interventions and behavior change after time τ :

$\beta(t) = \beta_1 + (\beta_0 - \beta_1)e^{-k(t-\tau)}$ [12]. The sexual transmission parameter, β_s, can be described as

the product of two parameters ($\beta_s = \eta q$) that we will consider separately: η is the per sex

act transmission probability of Ebola virus from convalescent men, and q is the daily rate

at which they engage in sexual intercourse. The number of convalescent individuals are

scaled by p, which is the proportion of convalescent survivors who are sexually active

men. $1/\sigma$ and $1/\gamma$ represent the average durations of incubation and symptomatic

infection, respectively. f is the case fatality rate. The average duration after which

convalescent patients recover completely and shed no further replicating Ebola virus from

their body is given by $1/\alpha$. We assumed that sexual transmission is frequency-dependent

[3,15,16], i.e., the probability that the sexual partner of a convalescent man is susceptible

is given by S/N.

Figure 1. Schematic illustration of EVD transmission model including sexual transmission from convalescent patients. The elements in black form the base model without sexual transmission [12–14]. The red elements (convalescent individuals and additional transmission term) were added to account for sexual transmission.

120   The basic reproductive number, R_0, for the SEICR model can be calculated using the

121   next-generation matrix method [17,18] and is given by

122
$$R_0 = \frac{\beta S_0}{\gamma} + \frac{(1-f)\, p\, \beta_s}{\alpha},$$

123   where S_0 is the initial number of susceptible individuals (see *Supplementary Material*

124   *Appendix S1*). When α goes to infinity or either $\beta_s = 0$ or $p = 0$, the equation reduces to

125   the basic reproductive number in absence of sexual transmission: $R_{0,N} = \frac{\beta S_0}{\gamma}$. Thus, the

126   second term represents the contribution of sexual transmission from convalescent patients

127   to the overall R_0: $R_{0,C} = \frac{(1-f)\, p\, \beta_s}{\alpha}$.

Model parameters. We fitted the deterministic EVD transmission model to weekly incidence of confirmed and probable cases in Sierra Leone as reported in the WHO patient database [19] (*Supplementary Material* Fig. S1). The data set was extended with weekly incidence from the situation report for the most recent weeks when no data was available in the patient database. In order to account for variability in the accuracy of reporting, we assumed that the number of reported cases follows a negative binomial distribution with mean as predicted by the model and dispersion parameter ϕ [20]. We derived maximum likelihood estimates (MLE) of the following model parameters [14,21]: the baseline transmission rate β_0, the time τ at which transmission starts to drop, the rate k at which transmission decays, and the dispersion parameter ϕ. For the fitting procedure, we assumed that there were no sexual transmission events, i.e., we set β_S to zero. The basic reproductive number in absence of sexual transmission is $R_{0,N} = \beta_0 N_0 / \gamma$, and the reproductive number in presence of partially effective control interventions is $R_{1,N} = \beta_1 N_0 / \gamma$, with N_0 being the population size of Sierra Leone. We explored value ranges for sexual transmission parameters (Table 1) based on information from the current epidemic [22] and studies of human immunodeficiency virus [23,24]. Remaining parameters were based on published values from the literature (Table 1).

Table 1: Model parameters describing EVD transmission in Sierra Leone. The indicated parameter ranges are used for the sensitivity analysis (partial rank correlation coefficients, PRCC) only.

Parameter		Value (Range)	Comments and References
Basic reproductive number without sexual transmission	$R_{0,N}$	2.13 (1.26 - 2.53)	Estimated - Range explores estimates from [13,25]
Basic reproductive number in presence of control interventions	$R_{1,N}$	0.67	Estimated
Date of onset of symptoms in index case		April 23, 2014	[13,25,26]
Rate at which transmission rate decays	k	0.011 d^{-1}	Estimated
Time at which transmission rate starts to decay	τ	51.0 d	Estimated
Incubation period	$1/\sigma$	11.4 d	[22]
Infectious period	$1/\gamma$	3.9 d	Together with the incubation period results in a generation time of 15.3 d [22]
Dispersion parameter	ϕ	0.050	Estimated
Initial population size	N_0	6.316×10^6	Based on 2014 estimate [27]
Sexual transmission probability (per coital act)	η	0.001 (0.0005 − 0.002)	Roughly based on sexual transmission probability of HIV per coital act from infected men [24]
Case fatality rate	f	0.69	[22]
Frequency of sex acts	q	0.272 d^{-1} (0.136 − 0.544)	8.27 coital acts per month [23]
Proportion of convalescent survivors who are infectious and sexually active	p	0.347 (0.1725-0.694)	Of 47.4% male survivors, 73.1% are aged 15-45 [22]
Rate at which convalescent survivors recover completely	α	1/87.35 d^{-1} (1/174.7 − 1/43.7)	3 months after onset of symptoms [4,28] and assuming an infectious period of 3.9 days

Deterministic model and sensitivity analysis. We solved the system of ODEs

numerically using the function *ode* from the *deSolve* package in the R software

environment for statistical computing [29]. We compared the following response

variables of the model: the epidemic peak number of exposed, *E*, acute, *I*, and

convalescents, *C*, cases; the cumulative number of EVD cases, deaths, and recoveries; the

date at the epidemic peak; the daily and cumulative incidence of sexual transmission; and

the date at which the last symptomatic case either died or entered into convalescence

("day of last case"). We defined the day of last case as the time when the number of

symptomatic and infectious individuals, *I*, dropped below 0.5. We considered the

following parameters for the sensitivity analysis: the per sex act transmission probability

of Ebola virus from convalescent men (η), the proportion of convalescent survivors who

are sexually active men (*p*), the rate at which they engage in sexual intercourse (*q*), and

the rate at which convalescent patients recover completely and shed no further replicating

Ebola virus from their body (α). The sensitivity of the response variables to changes in R_0

was explored simultaneously as a comparison. We generated 1000 parameter

combinations from the uniform ranges, log-transformed [0.5x − 2x] for the parameter

values for η, *p*, *q*, and α, given in Table 1 via Latin hypercube sampling using the

Huntington and Lyrintzis correlation correction method (function *lhs* from R package

pse) [30]. We then calculated partial rank correlation coefficients (PRCCs) using 50

bootstrap replicates [31].

Monte Carlo simulations. We performed stochastic simulations of the SEICR model

with and without sexual transmission using Gillespie's algorithm [32]. We specifically

investigated the following response variables from the simulations: the cumulative

number of EVD cases, the size and date of the epidemic's peak incidence (daily number

of new symptomatic infections), and the date of last case (last day that symptomatic

infections, I, fell below 1). Summary statistics were based on the results of 1000

simulation runs for each transmission scenario. We calculated the average of the peak and

total cumulative number of EVD cases by including all simulations runs, i.e., also the

simulations that rapidly go extinct. In contrast, the average dates of the epidemic peak

and last case were based on the simulated epidemic trajectories over which 50 or more

cases were accumulated.

Results

Contribution of sexual transmission to overall R_0. Assuming a conservative baseline

scenario ($\eta = 0.001$ and $1/\alpha = 3$ months; Table 1), the reproductive number of a

convalescent infection, $R_{0,C}$, is 0.0024. This corresponds to only 0.12% of the overall R_0

of 2.0224. Increasing the convalescent period from 3 to 6 months, the contribution of $R_{0,C}$

(0.0051) to the overall R_0 rises to 0.25%. The equation for $R_{0,C}$ (see *Methods*) illustrates

that doubling the per sex act transmission probability has the same impact as doubling the

convalescent period. It is important to note that the relative contribution of sexual

transmission to the overall reproductive number rises as the effective reproductive

number drops during the epidemic due to the effects of control interventions and

decreasing density of susceptible hosts (see *Supplementary Material* Fig. S2).

Effect of sexual transmission parameters on epidemic dynamics. The two key unknown

parameters of sexual transmission are the per sex act transmission probability, η, and the

rate at which convalescent survivors fully recover, α. Both parameters were found to have

very small effects on the peak number of infected or exposed patients (Fig. 2A; Fig. 3A;

Figs. 4A, 4B, 4C; Fig. S2; Fig. S3). The duration of the convalescent period has a large

impact on the peak number of convalescent individuals, while η does not (compare Fig.

2A and Fig. 3A). The total number of recovered individuals is reached more slowly the

longer the convalescent period (Fig. 2B), which is not an effect caused by η (Fig. 3b).

While the convalescent periods ($1/\alpha = [3 - 9$ months]) and the values of η ($\eta = [0.0005 - $

$0.002]$) we explored create very few extra cases (Fig. 2B and Fig. 3B), sensitivity

analyses revealed that a higher per sex act transmission probability, η, a higher proportion

of sexually active convalescent individuals, p, or a higher frequency of sex acts, q, have

larger impacts on the total number of cases than would proportional increases in the

convalescent period (see *Supplementary Material*, Fig. S3A). Sensitivity analyses also

revealed that these sexual transmission parameters could produce a small delay in the

epidemic peak, more so than would changes in the convalescent period (see

Supplementary Material, Fig. S3B).

Figure 2. Effect of convalescent period on EVD epidemics. The average duration of the convalescent period (1/α) is varied between 3 and 9 months. (A, B): Epidemic trajectories in presence (broken lines) and absence of sexual transmission (solid lines). Vertical lines mark the day of last symptomatic case. (C) Daily incidence of sexual transmission. (D) Cumulative number of sexual transmission events. Note that the vertical axes vary across panels.

Figure 3. Effect of per sex act transmission probability on EVD epidemics. The per sex act transmission probability (η) is varied between 0.05% and 0.2%. (A, B): Epidemic trajectories in presence (broken lines) and absence of sexual transmission (solid lines). Vertical lines mark the day of last symptomatic case. (C) Daily incidence of sexual transmission. (D) Cumulative number of sexual transmission events. Note that the vertical axes vary across panels.

The number of sexual transmission events expected from the baseline scenario (η = 0.001

and 1/ α = 3 months) is 31.2, the majority of which will occur around the peak of the

epidemic (Fig. 2C and Fig. 3D) and thus likely go undetected. Doubling either η or 1/ α

results in nearly equal increases in the incidence and cumulative number of sexual

transmission events (Fig. 2C, 2D and Fig. 3C, 3D), with either leading to roughly double

the number of sexually transmitted cases over the course of the whole epidemic (> 60

cases). It should be noted that the total number of cases increases more than by simply the

number of sexual transmission events, because each sexual transmission event results in a

new potential cluster of non-sexual transmission. The day of last case is affected more by

the convalescent period than the per sex act transmission probability (represented by

vertical lines in Fig. 2A and Fig. 3A), a result confirmed by the sensitivity analysis (see

Supplementary Material, Fig. S3A). The tail of the epidemic will depend on a small

number of events that are likely to be affected by stochastic processes, thus we used

Monte Carlo simulations to explore this behaviour.

Impact of sexual transmission on the epidemic tail. We performed stochastic

simulations of the EVD transmission model to investigate the epidemic dynamics when

the number of new cases becomes small, i.e, during the tail of the epidemic. Comparing

model simulations while assuming a convalescent period of 3 months to those without

sexual transmission confirmed the deterministic results that sexual transmission from

convalescent survivors does not lead to a significant increase in the cumulative number of

infected cases (non-STI: 11,092 +/- 627 cases; STI: 10,944 +/- 642 cases; Wilcox rank

sum test: $W = 491990$, $p = 0.53$), nor the size (non-STI: 77 +/- 4.1 new cases per day;

STI: 75 +/- 4.2 new cases per day; $W = 493710$, $p = 0.62$) or timing (non-STI: day 187

+/- 0.9; STI: day 187 +/- 0.9; $t = 0.19$, df = 1017.4, $p = 0.85$) of the epidemic peak

incidence (Fig. 4A, 4B, 4C). This conservative period of potential sexual transmission,

which has recently been shown to extend well beyond 3 months in at least 65% of

patients [1], lengthened the average date on which the last active case could be detected

by nearly three months (non-STI: 548 +/- 4.0 days; STI: 630 +/- 6.6 days; difference: 83

days [95% CI: 68-98 days], $t = -10.8$, df = 867.97, $p < 0.0001$; Fig. 4D, 4E, 4G, 4H). The

width of the tail (s.d. = 151 days) was such that 23.4% of the 529 simulated epidemics

that accumulated at least 50 cases still experienced symptomatic individuals 730 days

(two years) after the start of the epidemic (Fig. 4H). Strikingly, when the convalescent

period was extended from 3 months to 6 months, the projected length of the epidemic

increased to a mean of 1088 days (+/- 15.5), with 84.0% of the 538 sustained epidemics

taking over two years to end (Fig. 4F, 4I). However, the average number of new cases

produced remained small (11,869 +/- 663 days; W = 482790, p = 0.18). Importantly,

there is greater variance in the tail of the epidemic when sexual transmission is

considered, and this uncertainty grows with the length of the convalescent period (Fig.

4G, 4H, 4I).

Figure 4. Impact of convalescent period on the tail of the EVD epidemic. Monte Carlo simulations of the weekly incidence of new cases (A, B, C) and the sporadic occurrence of sexual transmission events at the epidemic tail (D, E, F), assuming no sexual transmission (A, D), and sexual transmission with a 3 (B, E) and 6 months (C, F) convalescent period. Light red lines show the result of 200 simulated trajectories, with corresponding mean (thick purple line) and standard errors (thin purple lines). Black dots denote incident cases in Sierra Leone as reported by the WHO [19]. The dark red lines in (D), (E), and (F) highlight a single representative trajectory, and the blue dots along the horizontal axis indicate a sexual transmission event. Histograms of the day of the last EVD case from 1,000 simulated epidemics in absence of sexual transmission (G) and for a convalescent period of 3 (H) and 6 (I) months.

Discussion

Our study shows that the length of the convalescent period will determine whether or not sexual transmission of Ebola virus from recovering patients will have a profound effect on the length of time it will take for the epidemic to completely fade. For Sierra Leone, we found that an average convalescent period of 3 months, and a per sex act transmission probability of 0.1%, could extend the EVD epidemic in Sierra Leone by an average of 83 days (95% CI: 68–98 days). Such a scenario would be consistent with the occurrence of a small number of sexual transmission events during the end-phase of the epidemic. However, assuming an average convalescent period of 6 months led to simulated epidemics whose tails were much more variable, and much longer, despite a lack of significant increase in the total number of cases. So far, the reported cases of sexual

transmission of EVD remain rare [1,2]. Hence, the per sex act transmission probability of

Ebola virus from male convalescent survivors is unlikely to be higher than 0.1%, and

might well be below this value. Our sensitivity analysis indicates that the duration of the

EVD epidemic is heavily influenced by the period during which convalescent men can

transmit sexually, calling for a better understanding of the persistence and duration of

infectivity of Ebola virus RNA in convalescent patients.

We extended an accepted modeling framework that has been widely used to describe the

epidemic trajectories of EVD outbreaks and epidemics [12–14]. To our knowledge, this is

the first study using mathematical modeling to assess the potential impact of sexual

transmission of Ebola virus on the epidemic in West Africa. In addition, given the

generality of the model, this is also the first model that investigates the impact of

including a secondary transmission route from convalescent individuals. This model,

then, may also have implications for other pathogens with this kind of secondary

transmission route (e.g. some adenoviruses [33]; see [34] for examples across mammal

species) including other neglected tropical diseases, such as African sleeping sickness

[35], and other hemorrhagic fevers that display pathologies similar to EVD [9,10].

In the absence of a better understanding of sexual transmission of EVD, mathematical

modeling currently remains the only tool to explore its potential impact on the epidemic

trajectory. There are several extensions to this work that could be considered, including

transmission by other fluids (e.g., vaginal secretions [4,7]) and asymptomatic infection

[36,37], considering spatial aspects of sexual transmission [38], and heterogeneity in

sexual behavior [3,39]. We assumed the duration of convalescence to be exponentially

distributed. Eggo *et al*. [40] fitted a series of unimodal distributions to the data on Ebola

virus RNA detection in semen recently reported by Deen *et al*. [1] and found that the

convalescence period could be best described by a gamma distribution. Furthermore,

Deen *et al*. [1] found that the cycle-threshold values decreased over time, indicating that

the Ebola virus load in semen and the viral infectivity might also decrease during the

convalescence period. Uncertainty in the data is not limited to sexual transmission; we

fitted our model to weekly incidence of confirmed and probable cases in Sierra Leone,

but did not take into account potential underreporting as others have done recently [36].

In addition, EVD is known to exhibit superspreading characteristics [41,42], and

superspreading events could lead to explosive regrowth of the epidemic after the

occurrence of a new case through sexual transmission [41]. Finally, like other negative-

sense single-stranded RNA ((-)ssRNA) viruses [43], the species currently circulating in

West Africa has been estimated to have high substitution rates [26,44,45]. This rapid

evolution detected throughout the current outbreak zone suggests that within- or between-

host adaptation of the virus leading to pro-longed persistence in the seminal fluids is

possible. However, evolution of sexual transmission becoming the primary route of

spread is highly unlikely.

Awareness of the potential for sexual transmission has led to WHO issuing

recommendations that ask convalescent men to abstain from sexual activity as much as

possible and to use condoms for up to 6 months after the onset of symptoms [28].

Condom use and social awareness of the risks of sexual transmission during

convalescence should have an impact on the per sex act transmission probability (η) and

the frequency of sex acts (q), respectively. Our results show that condom use should

reduce the number of sporadic sexual transmission events during the tail of the epidemic

and after discharge of all remaining symptomatic individuals. However, the time during

which the public health community must stay vigilant is not reduced because these

interventions will not affect the time during which convalescent survivors can shed

infectious virus ($1/\alpha$). This is especially poignant since adherence to these

recommendations will never be 100%. Thus, our results suggest that the current

requirement for declaring a region free from EVD (42 days following either death or a

second negative RT-PCR test of the blood from the last known patient), officially

declared in Sierra Leone on 7 November 2015 [46], may be premature.

As more data about the convalescent survivors of EVD becomes available, this and future

mathematical modeling studies will help to better understand the potential

epidemiological consequences of sexual transmission on the EVD epidemic in West

Africa. Precise estimates are important for providing convalescent survivors with sound

advice that balances protection of the community with the harm that could come from

unnecessary stigmatization [47–49].

Acknowledgements

We thank Benjamin Roche for helpful suggestions on simulation results.

References

1. Deen GF, Knust B, Broutet N, Sesay FR, Formenty P, Ross C, et al. Ebola RNA

Persistence in Semen of Ebola Virus Disease Survivors — Preliminary Report. N

Engl J Med. 2015; doi:10.1056/NEJMoa1511410

2. Mate SE, Kugelman JR, Nyenswah TG, Ladner JT, Wiley MR, Cordier-Lassalle T,

et al. Molecular Evidence of Sexual Transmission of Ebola Virus. N Engl J Med.

2015; doi:10.1056/NEJMoa1509773

3. Anderson RM, May RM. Infectious Diseases of Humans: Dynamics and Control.

Oxford: Oxford Univeristy Press; 1991.

4. Rowe AK, Bertolli J, Khan AS, Mukunu R, Muyembe-Tamfum JJ, Bressler D, et

al. Clinical , Virologic , and Immunologic Follow-Up of Convalescent Ebola

Hemorrhagic Fever Patients and Their Household Contacts , Kikwit , Democratic

Republic of the Congo. J Infect Dis. 1999;179 Suppl: 28–35.

5. Clark D V, Kibuuka H, Millard M, Wakabi S, Lukwago L, Taylor A, et al. Long-

term sequelae after Ebola virus disease in Bundibugyo, Uganda: a retrospective

cohort study. Lancet Infect Dis. Elsevier Ltd; 2015;3099: 1–8. doi:10.1016/S1473-

3099(15)70152-0

6. Bausch DG, Towner JS, Dowell SF, Kaducu F, Lukwiya M, Sanchez A, et al.

Assessment of the risk of Ebola virus transmission from bodily fluids and fomites.

J Infect Dis. 2007;196 Suppl : S142–S147. doi:10.1086/520545

7. Rodriguez LL, De Roo A, Guimard Y, Trappier SG, Sanchez A, Bressler D, et al.

Persistence and genetic stability of Ebola virus during the outbreak in Kikwit,

362  Democratic Republic of the Congo, 1995. J Infect Dis. 1999;179 Suppl : S170–6.

363  doi:10.1086/514291

364 8. Varkey JB, Shantha JG, Crozier I, Kraft CS, Lyon GM, Mehta AK, et al.

365  Persistence of Ebola Virus in Ocular Fluid during Convalescence. N Engl J Med.

366  2015;372: 2423–2427. doi:10.1056/NEJMoa1500306

367 9. Ergonul O, Battal I. Potential sexual transmission of Crimean-Congo hemorrhagic

368  fever infection. Jpn J Infect Dis. 2014;67: 137–8.

369 10. Slenczka W, Klenk HD. Forty Years of Marburg Virus. J Infect Dis. 2007;196:

370  S131–135. doi:10.1086/520551

371 11. Rogstad KE, Tunbridge A. Ebola virus as a sexually transmitted infection. Curr

372  Opin Infect Dis. 2015;28: 83–85. doi:10.1097/QCO.0000000000000135

373 12. Chowell G, Hengartner NW, Castillo-Chavez C, Fenimore PW, Hyman JM. The

374  basic reproductive number of Ebola and the effects of public health measures: the

375  cases of Congo and Uganda. J Theor Biol. 2004;229: 119–126.

376  doi:10.1016/j.jtbi.2004.03.006

377 13. Althaus CL. Estimating the Reproduction Number of Ebola Virus (EBOV) During

378  the 2014 Outbreak in West Africa. PLOS Curr Outbreaks. 2014; 1–9.

379  doi:10.1371/currents.outbreaks.91afb5e0f279e7f29e7056095255b288

380 14. Althaus CL, Low N, Musa EO, Shuaib F, Gsteiger S. Ebola virus disease outbreak

381  in Nigeria: Transmission dynamics and rapid control. Epidemics. Elsevier B.V.;

382  2015;11: 80–84. doi:10.1016/j.epidem.2015.03.001

383 15. Thrall PH, Antonovics J. Polymorphism in sexual versus non-sexual disease

384  transmission. Proc R Soc B Biol Sci. 1997;264: 581–587.

385 16. Garnett GP. An introduction to mathematical models in sexually transmitted

386   disease epidemiology. Sex Transm Infect. 2002;78: 7–12. doi:10.1136/sti.78.1.7

387 17. Diekmann O, Heesterbeek JAP. Mathematical Epidemiology of Infectious

388   Diseases. Chichester: John Wiley and Sons; 2000.

389 18. Diekmann O, Heesterbeek J a, Metz J a. On the definition and the computation of

390   the basic reproduction ratio R0 in models for infectious diseases in heterogeneous

391   populations. J Math Biol. 1990;28: 365–382. doi:10.1007/BF00178324

392 19. World Health Organization. Ebola data and statistics: Data on new cases per epi

393   week for Sierra Leone [Internet]. 2015 [cited 18 Nov 2015]. Available:

394   http://apps.who.int/gho/data/node.ebola-sitrep.ebola-country-SLE-

395   20151118?lang=en

396 20. Kucharski AJ, Camacho A, Flasche S, Glover RE, Edmunds WJ, Funk S.

397   Measuring the impact of Ebola control measures in Sierra Leone. Proc Natl Acad

398   Sci. 2015;112: 201508814. doi:10.1073/pnas.1508814112

399 21. Althaus CL. Rapid drop in the reproduction number during the Ebola outbreak in

400   the Democratic Republic of Congo PrePrints. PeerJ Prepr. 2015;3: e1418.

401   doi:10.7717/peerj.1418

402 22. WHO Ebola Response Team. Ebola Virus Disease in West Africa — The First 9

403   Months of the Epidemic and Forward Projections. Engl New J Med. 2014;371:

404   1481–1495. doi:10.1056/NEJMoa1411100

405 23. Gray RH, Wawer MJ, Brookmeyer R, Sewankambo NK, Serwadda D, Wabwire-

406   Mangen F, et al. Probability of HIV-1 transmission per coital act in monogamous,

heterosexual, HIV-1-discordant couples in Rakai, Uganda. Lancet. 2001;357:

1149–1153. doi:10.1016/S0140-6736(00)04331-2

24.   Wawer MJ, Gray RH, Sewankambo NK, Serwadda D, Li X, Laeyendecker O, et

al. Rates of HIV-1 transmission per coital act, by stage of HIV-1 infection, in

Rakai, Uganda. J Infect Dis. 2005;191: 1403–1409. doi:10.1086/429411

25.   Alizon S, Lion S, Murall CL, Abbate JL. Quantifying the epidemic spread of Ebola

virus (EBOV) in Sierra Leone using phylodynamics. Virulence. 2015;5: 825–827.

doi:10.4161/21505594.2014.976514

26.   Gire SK, Goba A, Andersen KG, Sealfon RSG, J PD, Kanneh L, et al. Genomic

surveillance elucidates Ebola virus origin and transmission during the 2014

outbreak. Science (80-). 2014;345: 1369–1372. doi:10.1126/science.1259657

27.   The World Bank. Sierra Leone country at a glance [Internet]. 2015. Available:

http://www.worldbank.org/en/country/sierraleone

28.   World Health Organization. WHO website [Internet]. Available:

http://www.who.int/reproductivehealth/topics/rtis/ebola-virus-semen/en/

29.   R Core Team. R: A Language and Environment for Statistical Computing. Vienna,

Austria: R Foundation for Statistical Computing; 2014.

30.   Chalom A, Prado PIKL. pse: Parameter space exploration with Latin Hypercubes.

2014.

31.   Blower SM, Dowlatabadi H. Sensitivity and Uncertainty Analysis of Complex

Models of Disease Transmission: An HIV Model, as an Example. Int Stat Rev.

1994;62: 229–243. doi:10.2307/1403510

32.   Gillespie DT. Exact Stochastic Simulation of couple chemical reactions. J Phys

Chem. 1977;81: 2340–2361. doi:10.1021/j100540a008

33.   Swenson PD, Lowens MS, Celum CL, Hierholzer JC. Adenovirus types 2, 8, and

37 associated with genital infections in patients attending a sexually transmitted

disease clinic. J Clin Microbiol. 1995;33: 2728–2731.

34.   Dejucq N, Jégou B. Viruses in the Mammalian Male Genital Tract and Their

Effects on the Reproductive System Viruses in the Mammalian Male Genital Tract

and Their Effects on the Reproductive System. 2001;65: 208–231.

doi:10.1128/MMBR.65.2.208

35.   Rocha G, Martins a., Gama G, Brandão F, Atouguia J. Possible cases of sexual and

congenital transmission of sleeping sickness [5]. Lancet. 2004;363: 247.

doi:10.1016/S0140-6736(03)15345-7

36.   Leroy EM, Baize S, Volchkov VE, Capron M, Debré P, Mccormick JB, et al.

Human asymptomatic Ebola infection and strong inflammatory response. Lancet.

2000;355: 2210 – 2215.

37.   Bellan SE, Pulliam JRC, Dushoff J, Meyers LA. Ebola control: effect of

asymptomatic infection and acquired immunity. Lancet. Elsevier Ltd; 2014;384:

1499–1500. doi:10.1016/S0140-6736(14)61839-0

38.   Merler S, Ajelli M, Fumanelli L, Gomes MFC, Piontti APY, Rossi L, et al.

Spatiotemporal spread of the 2014 outbreak of Ebola virus disease in Liberia

and the effectiveness of non-pharmaceutical interventions: a computational

modelling analysis. Lancet Infect Dis. Elsevier Ltd; 2015;3099: 1–8.

doi:10.1016/S1473-3099(14)71074-6

39.   Smith J, Nyamukapa C, Gregson S, Lewis J, Magutshwa S, Schumacher C, et al.

453   The Distribution of Sex Acts and Condom Use within Partnerships in a Rural Sub-

454   Saharan African Population. PLoS One. 2014;9: e88378.

455   doi:10.1371/journal.pone.0088378

456   40.   Eggo RM, Watson CH, Camacho A, Kucharski AJ, Funk S, Edmunds WJ.

457   Duration of Ebola virus RNA persistence in semen of survivors: population level

458   estimates and projections. Eurosurveillance. 2015;20: pii=30083.

459   doi:http://dx.doi.org/10.2807/1560-7917.ES.2015.20.48.30083

460   41.   Althaus CL. Ebola superspreading. Lancet Infect Dis. 2015;15: 507–508.

461   doi:10.1016/S1473-3099(15)70135-0

462   42.   Toth DJ a, Gundlapalli A V, Khader K, Pettey WBP, Rubin M a, Adler FR, et al.

463   Estimates of Outbreak Risk from New Introductions of Ebola with Immediate and

464   Delayed Transmission Control. Emerg Infect Dis J. 2015;21: 1402.

465   doi:10.3201/eid2108.150170

466   43.   Duffy S, Shackelton L a., Holmes EC. Rates of evolutionary change in viruses:

467   patterns and determinants. Nat Rev Genet. 2008;9: 267–276. doi:10.1038/nrg2323

468   44.   Park DJ, Dudas G, Wohl S, Goba A, Whitmer SLM, Andersen KG, et al. Ebola

469   Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra

470   Leone. Cell. 2015;161: 1516–1526. doi:10.1016/j.cell.2015.06.007

471   45.   Tong Y-G, Shi W-F, Liu D, Qian J, Liang L, Bo X-C, et al. Genetic diversity and

472   evolutionary dynamics of Ebola virus in Sierra Leone. Nature. 2015;524: 93–96.

473   doi:10.1038/nature14490

46.   World Health Organization. WHO Ebola Situation Report (11 November 2015).

[Internet]. 2015. Available:

http://apps.who.int/iris/bitstream/10665/194050/1/ebolasitrep_11Nov2015_eng.pdf

?ua=1&ua=1

47.   Davtyan M, Brown B, Folayan MO. Addressing Ebola-related Stigma: Lessons

Learned from HIV/AIDS. Glob Health Action. 2014;7: 1–4.

doi:10.3402/gha.v7.26058

48.   Obilade TT. Ebola Virus Disease Stigmatization; The Role of Societal Attributes.

Int Arch Med. 2015;8: 1–19. doi:10.3823/1613

49.   Sprecher A. Handle Survivors with Care. N Engl J Med. 2015;

doi:10.1056/NEJMe1512928

485