Supporting Information

Potential impact of sexual transmission on Ebola virus epidemiology: Sierra Leone as a case study

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S1 Appendix. Calculating $R_0$

At the beginning of the epidemic when the population is entirely susceptible ($S/N = 1$), the SEICR model from the main text can be written as:

$$
\begin{align*}
\frac{dS}{dt} &= -\beta SI - \beta S pC, \\
\frac{dE}{dt} &= \beta SI + \beta S pC - \sigma E, \\
\frac{dI}{dt} &= \sigma E - \gamma I, \\
\frac{dC}{dt} &= (1 - f)\gamma I - \alpha C, \\
\frac{dR}{dt} &= \alpha C, \\
\frac{dD}{dt} &= f\gamma I.
\end{align*}
$$

The model has three disease stages, exposed, $E$, infected, $I$, and convalescent, $C$, and thus, a vector representing these disease stages can be defined as $x(t) = \begin{pmatrix} E \\ I \end{pmatrix}$. Let $F$ be the infection matrix and $V$ be the transition matrix. Since both $I$ and $C$ can transmit the virus, the matrices $F$ and $V$ become

$$
F = \begin{pmatrix}
0 & \beta S_0 & \beta S p \\
0 & 0 & 0 \\
0 & 0 & 0
\end{pmatrix} \quad \text{and} \quad V = \begin{pmatrix}
\sigma & 0 & 0 \\
-\sigma & \gamma & 0 \\
0 & -(1 - f)\gamma & \alpha
\end{pmatrix}.
$$
The progression through disease stages can be found from \( x' = Fx(t) - Vx(t) \), and thus the expected number of secondary infections is

\[
\int_0^\infty Fx(t)dx = Kx(0),
\]

where the next generation matrix is \( K = F V^{-1} \) and its positive real eigenvalue is the basic reproductive number:

\[
R_0 = \frac{\beta s_0}{\gamma} + \frac{(1-f)\beta s p}{\alpha}.
\]

Note that when \( \alpha \) goes to infinity or either \( \beta_s = 0 \) or \( p = 0 \), the equation reduces to \( R_0 = \frac{\beta s_0}{\gamma} \), which is the basic reproductive number in absence of sexual transmission. Therefore, the contribution of sexual transmission to the overall \( R_0 \) is simply

\[
R_{0,C} = \frac{(1-f)\beta s p}{\alpha}.
\]