Appendix

S1. The deterministic SIRS model

The deterministic SIRS model is defined by the following system of differential equations:

\[
\begin{align*}
\frac{dS}{dt} &= -\beta SI + \alpha R \quad (1) \\
\frac{dI}{dt} &= \beta SI - \gamma I \quad (2) \\
\frac{dR}{dt} &= \gamma I - \alpha R. \quad (3)
\end{align*}
\]

Here, \(S\), \(I\), and \(R\) represent the fractions of the species assemblage that are susceptible, infectious, or recovered, respectively. Therefore, \(S + I + R = 1\). \(\beta\) is the transmission rate, \(\gamma\) the recovery rate, and \(\alpha\) the immunity loss rate. The initial conditions are \(S(0) > 0\), \(I(0) > 0\), and \(R(0) = 0\).

This system cannot be solved analytically due to the nonlinear term \(\beta SI\) in equations 1 and 2. However, we may approach its behavior qualitatively. If every species is initially susceptible, then a newly introduced Wolbachia-infected species is expected to infect others at the rate \(\beta\) during the expected infectious period \(1/\gamma\). Therefore, this infectious species is expected to infect on average \(\beta/\gamma\) species. This quantity is called the basic reproduction number (or basic reproductive ratio) and is denoted by \(R_0\):

\[
R_0 = \frac{\beta}{\gamma}. \quad (4)
\]

Verbally, \(R_0\) is defined as the average number of secondary infections that occur when one infective is introduced into a completely susceptible host population. An infection can invade and persist in a new host assemblage if and only if \(R_0 > 1\); otherwise, the infection should die out. Any infection that, on average, is not transmitted to more than one new host is not going to spread (Keeling and Rohani, 2008).

In order to analyze the long-term behavior of the epidemic, we consider the equilibrium states of the system, with \(\frac{dS}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0\). The disease-free equilibrium can be expressed as \((S_{det}^*, I_{det}^*, R_{det}^*) = (1, 0, 0)\). With regard to the (positive) endemic equilibrium, we are mainly interested in the proportion of infected species at equilibrium, \(I_{det}^*\). The endemic equilibrium for the proportion of infecteds is given by

\[
I_{det}^* = \frac{1 - \gamma/\beta}{1 + \gamma/\alpha} = \frac{1 - 1/R_0}{1 + \gamma/\alpha}. \quad (5)
\]

Obviously, the endemic equilibrium is only feasible if \(R_0 > 1\); otherwise, it would be less than or equal to zero. This agrees with the condition for an infection to be able to spread initially.

S2. The Gillespie algorithm

We make use of the direct method of the Gillespie algorithm which is a procedure for generating time-evolution trajectories of finite populations in continuous time (Gillespie, 1977). Here, we follow the approach by Keeling and Rohani (2008). We consider a network (species assemblage) of size \(N\). Every node in the network is represented by its current infection state. The state vector \(s(t) = (s_1(t), \ldots, s_N(t))\) assigns to every node \(i = 1, \ldots, N\) its infection state at time \(t\), with

\[
s_i(t) = \begin{cases} 
1 & \text{if node } i \text{ is susceptible at time } t \\
2 & \text{if node } i \text{ is infectious at time } t \\
0 & \text{if node } i \text{ is recovered at time } t.
\end{cases} \quad (6)
\]
Given an initial time $t_0$ and assuming that node $i = 1$ is the only infectious one, the initial state is given by $s_1(t_0) = 2$ and $s_i(t_0) = 1$, where $l = 2, \ldots, N$. The transition probability of every node $i$ at time $t$ is captured by the rate vector $r(t) = (r_1(t), \ldots, r_N(t))$, with

$$r_i(t) = \begin{cases} \beta \sum_{j=1}^{n_i} H_{c_j^i} & \text{if } s_i(t) = 1 \\ \gamma & \text{if } s_i(t) = 2 \\ \alpha & \text{if } s_i(t) = 0. \end{cases} \quad (7)$$

Again, $\beta$ is the transmission rate, $\gamma$ the recovery rate, and $\alpha$ the immunity loss rate. $H_j$ is equal to one if node $j$ is infectious; otherwise, $H_j$ is zero. $c_1^i, c_2^i, \ldots, c_{n_i}^i$ are the $n_i$ contacts of node $i$. Therefore, $\sum_{j=1}^{n_i} H_{c_j^i}$ is the number of infectious contacts by which node $i$ can become infected. Considering the initial state of $r(t)$, we have one single infectious node which is node $i = 1$; therefore, $r_1(t_0) = \gamma$. All other nodes are susceptible. Every susceptible node that is connected to node 1 is assigned $r(t_0) = \beta$, all other susceptible nodes have $r(t_0) = 0$.

With $s(t_0)$ and $r(t_0)$ at hand, we start the update of $s(t)$ to see how the fractions of susceptible, infectious, and recovered nodes change over time. According to the Gillespie algorithm, we determine 1) when the next transition occurs, and 2) which node $m$ is the next one performing this transition and thus changing its state $s_m(t)$. Let $p_1, p_2$ be two random numbers drawn from the uniform distribution in the unit interval, and $r_0 = \sum_i r_i(t)$. The time step to the next transition $\tau$ is an exponentially distributed random number scaled by the sum of all transition rates, $r_0$:

$$\tau = \frac{1}{r_0} \ln \left( \frac{1}{p_1} \right). \quad (8)$$

The index of the next node that changes its state is

$$m = \text{the smallest integer satisfying } \sum_{i=1}^{m} r_i(t) > p_2 r_0. \quad (9)$$

This procedure ensures that the next node at which a transition occurs is drawn randomly, but proportional to $r_i(t)$. The time is advanced by $\tau$, and $s(t)$ is updated according to

$$s_m(t+\tau) = \begin{cases} 1 & \text{if } s_m(t) = 0 \\ 2 & \text{if } s_m(t) = 1 \\ 0 & \text{if } s_m(t) = 2. \end{cases} \quad (10)$$

As for the update of $r(t)$, we have to distinguish three cases:

1. The changing node $m$ has just lost its immunity and is again susceptible: $s_m(t+\tau) = 1$. Therefore,

$$r_m(t+\tau) = \beta \times \text{number of infectious contacts} = \beta \sum_{j=1}^{n_i} H_{c_j^i}. \quad (11)$$

2. The changing node $m$ has just become infected: $s_m(t+\tau) = 2$. Therefore,

$$r_m(t+\tau) = \gamma \quad (12)$$

$$r_v(t+\tau) = r_v(t) + \beta, \quad (13)$$

where the index $v$ represents all susceptible nodes that are connected to the node $m$.

3. The changing node $m$ has just recovered: $s_m(t+\tau) = 0$. Therefore,

$$r_m(t+\tau) = \alpha \quad (14)$$

$$r_v(t+\tau) = r_v(t) - \beta. \quad (15)$$

After the update of both $s(t)$ and $r(t)$, the process is iterated as long as $I(t) > 0$ and $t < t_{\text{max}}$. 

2
References


Additional figures

Figure S1. For high $\alpha$ values, $I^*$ does not change with further increasing $\alpha$. Shown are results for three $\beta/\gamma$ values: $\beta/\gamma = 10$ (a), $\beta/\gamma = 1$ (b), and $\beta/\gamma = 0.5$ (c). Note that, compared to Figure 3c, the value range on the x-axis is shifted to the right by two orders of magnitude, and $t_{\text{max}}$ is increased fivefold. Each $I^*$ value was calculated independently with 500 simulation runs per value. Bold dots and lines indicate means and medians, respectively; boxes show lower and upper quartiles; error bars encompass data within 1.5 times the interquartile range. $N = 100$ and $t_{\text{max}} = 5 \times 10^6$ years in all panels; $\beta = 10^{-4}$, $\gamma = 10^{-5}$ (a), $\beta = \gamma = 10^{-5}$ (b), and $\beta = 10^{-5}$, $\gamma = 2 \times 10^{-5}$ (c). All rates are given per year.
Figure S2. A constant ratio between $\beta$, $\gamma$ and $\alpha$ does not affect $I^*$. Shown are results for three $\beta: \gamma: \alpha$ ratios: $\beta: \gamma: \alpha = 10:1:100$ (a), $\beta: \gamma: \alpha = 1:1:100$ (b), and $\beta: \gamma: \alpha = 1:2:100$ (c). Each $I^*$ value was calculated independently with 500 simulation runs per value. Bold dots and lines indicate means and medians, respectively; boxes show lower and upper quartiles; error bars encompass data within 1.5 times the interquartile range. $N = 100$ in all panels; $\beta$ values range (from left to right) from $1.11 \times 10^{-2}$ to $1.11 \times 10^{-5}$ (a), from $2.01 \times 10^{-3}$ to $2.01 \times 10^{-6}$ (b), and from $1.51 \times 10^{-3}$ to $1.51 \times 10^{-6}$ (c). All rates are given per year. $\gamma$ and $\alpha$ values can be computed for each $\beta: \gamma: \alpha$ ratio according to $T \approx \frac{1}{\beta} + \frac{1}{\gamma} + \frac{1}{\alpha}$. $t_{max}$ values were chosen sufficiently large to obtain equilibrium results, but never larger than $10^7$ years.
Figure S3. The influence of long-range connections on incidence $I^*$ for network size $N = 100$. Shown are results as a function of available time $t_{\text{max}}$ for open-ring (without long-range connections) and small-world network (with long-range connections; inset), with (a) $\beta/\gamma = 2$ and (b) $\beta/\gamma = 0.6$. Each $I^*$ value was calculated independently with 500 simulation runs per value. Bold dots and lines indicate means and medians, respectively; boxes show lower and upper quartiles; error bars encompass data within 1.5 times the interquartile range. (a) $\beta = 2 \times 10^{-5}$, $\gamma = 10^{-5}$, $\alpha = 10^{-3}$; (b) $\beta = 10^{-5}$, $\gamma = 1.67 \times 10^{-5}$, $\alpha = 10^{-3}$. All rates are given per year.