**Text S2. Calculation of the propagation threshold by the Next Generation Approach.**

The Next Generation Approach [1] is used to calculate the basic reproductive number of the disease, $R_0$. This method defines $R_0$ as the dominant eigenvalue of the Next Generation Operator. The Jacobian matrix of the variables transmitting the disease is evaluated at the disease extinction point and written as $J = M - D$, where $M$ corresponds to the events where infectious individuals appear and $D$ to the events where infectious individuals disappear ($M \geq 0$ and $D$ a diagonal matrix $> 0$). The dominant eigenvalue of the matrix $MD^{-1}$ corresponds to the number $R_0$.

The individuals which carry the disease are the infectious rats $I$ and the free infectious fleas $F$. We consider $\frac{dI}{dt} = g$ and $\frac{dF}{dt} = f$. The Jacobian matrix we study is:

$$J = \begin{pmatrix} \frac{dg}{dI} & \frac{dg}{dF} \\ \frac{df}{dI} & \frac{df}{dF} \end{pmatrix} = \begin{pmatrix} -(d+m) & \beta\frac{S}{S+I+R}(1-e^{-a(S+I+R)}) \\ N(d+m) & -d_f - (1-e^{-a(S+I+R)}) \end{pmatrix} \tag{1}$$

The Jacobian matrix evaluated in ($S^* = K$, $I^* = 0$, $R^* = 0$, $N^* = K_f$, $F^* = 0$) is:

$$J^* = \begin{pmatrix} -(d+m) & \beta(1-e^{-aK}) \\ K_f(d+m) & -d_f - (1-e^{-aK}) \end{pmatrix} \tag{2}$$

$$= \begin{pmatrix} 0 & \beta(1-e^{-aK}) \\ K_f(d+m) & 0 \end{pmatrix} - \begin{pmatrix} (d+m) & 0 \\ 0 & d_f + (1-e^{-aK}) \end{pmatrix} \tag{3}$$

$J^*$ can thus be written as (M - D).

$$MD^{-1} = \begin{pmatrix} 0 & \frac{\beta(1-e^{-aK})}{d_f+(1-e^{-aK})} \\ K_f & 0 \end{pmatrix} \tag{4}$$

The eigenvalues of $MD^{-1}$ are $\pm\sqrt{\frac{\beta K_f}{1+\frac{d_f}{1-e^{-aK}}}}$.
Therefore,

$$\rho(MD^{-1}) = R_0 = \sqrt{\frac{\beta K_f}{1+\frac{d_f}{1-e^{-aK}}}} \tag{5}$$

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## References

1. Diekmann O, Heesterbeek J (2000) Mathematical epidemiology of infectious diseases: model building, analysis and interpretation. Chichester: John Wiley.