Supplementary Materials for:

Positive feedback loops exacerbate the influence of superspreaders in disease transmission

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1. Calculating the final epidemic size using the method of Ma and Earn (2006)

The model is given by:

$$\frac{dS}{dt} = -S\beta_L(L + pH) \quad [1]$$

$$\frac{dL}{dt} = S\beta_L((1-\sigma_L)L + p(1-\sigma_H)H) - (\alpha+\gamma)L \quad [2]$$

$$\frac{dH}{dt} = S\beta_L(\sigma_L L + \sigma_H pH) - (\alpha+\gamma)H \quad [3]$$

$$\frac{dR}{dt} = \gamma(H + L) \quad [4]$$

From equation [1] dividing both sides by S and integrating both sides with respect to t

$$\log\left[\frac{S(\infty)}{S(0)}\right] = -\beta_L \int_0^\infty L\, dt - p\beta_L \int_0^\infty H\, dt \quad [5]$$

To solve equation [2] we rearrange equation [1] to get $\beta_L pSH$ in terms of S and L and substitute into [2]. Integrating both sides with respect to t and assuming that $L(\infty) = 0$ gives:

$$-L(0) = (\sigma_H - 1)[S(\infty) - S(0)] + \int_0^\infty S\beta_L L(\sigma_H - \sigma_L)\, dt - (\gamma+\alpha)\int_0^\infty L\, dt \quad [6]$$

To solve equation [3] we rearrange equation [1] to get $\beta_L SL$ in terms of S and H and substitute into [3]. Integrating both sides with respect to t and assuming that $H(\infty) = 0$ gives:

$$-H(0) = -\sigma_L[S(\infty) - S(0)] + \int_0^\infty S\beta_L pH(\sigma_H - \sigma_L)\, dt - (\gamma + \alpha)\int_0^\infty H\, dt \qquad [7]$$

The final epidemic size is the difference between the number of susceptible at $t = 0$ and $t = \infty$ i.e. $Z = S(0) - S(\infty)$. Rearranging [6] and [7] in order to get the integrals of H and L with respect to time, and substituting into [5] gives:

$$\log\left[\frac{S(\infty)}{S(0)}\right] = -\frac{\beta_L}{\alpha + \gamma}\left(L(0) + pH(0) - (1 - \sigma_H + p\sigma_L)Z + (\sigma_H - \sigma_L)\beta_L \int_0^\infty SL + p^2 SH\, dt\right)$$

When $\sigma_H = \sigma_L$ this gives the same solution as in Ma and Earn (2006), and for a fixed population size of 1 and in the limit $I(0) \to 0, S(0) \to 1$ the final epidemic size, Z, for all of the models they considered, is given by $Z = 1 - e^{-R_0 Z}$ (Ma & Earn, 2006). However, in a model where there is a positive feedback loop, with superspreaders generating more superspreaders, there is an extra positive term which makes the exponent of the exponential term larger and still negative and so makes the final epidemic size bigger; the larger the difference between σ_H and σ_L, the larger the impact on the final epidemic size.

2. Calculating the basic reproductive number, R_0, using the method of Diekmann et al. (2010)

We calculated R_0 following the next generation approach of Diekmann et al. (2010), where R_0 is the dominant eigenvalue of the matrix K_L, obtained from the transmission matrix T and the

inverse of the transition matrix Σ (K_L = -$T\Sigma^{-1}$), derived from the equations of the system presented in the main paper (and above):

$$T = \begin{pmatrix} N\beta_L(1-\sigma_L) & pN\beta_L(1-\sigma_H) \\ N\beta_L\sigma_L & pN\beta_L\sigma_H \end{pmatrix}$$

$$\Sigma = \begin{pmatrix} -(\alpha+\gamma) & 0 \\ 0 & -(\alpha+\gamma) \end{pmatrix}$$

and so

$$K_L = \begin{pmatrix} \frac{N\beta_L(1-\sigma_L)}{(\alpha+\gamma)} & \frac{pN\beta_L(1-\sigma_H)}{(\alpha+\gamma)} \\ \frac{N\beta_L\sigma_L}{(\alpha+\gamma)} & \frac{pN\beta_L\sigma_H}{(\alpha+\gamma)} \end{pmatrix}$$

The dominant eigenvalue (R_0) of K_L is, as presented in the main paper:

$$R_0 = \frac{N\beta_L\left(1+p\sigma_H-\sigma_L+\sqrt{(\sigma_L-1-p\sigma_H)^2-4p(\sigma_H-\sigma_L)}\right)}{2(\alpha+\gamma)}.$$

We also note that in the absence of superspreading ($p = \sigma_H = \sigma_L = 0$), the basic reproductive number for a pathogen purely transmitting via low-titre, non-superspreaders, is:

$$R_0^L = \frac{N\beta_L}{\alpha+\gamma}.$$

3. Threshold superspreading rates for an epidemic

From the above expression for R_0 we can calculate analytical expressions for key threshold values of p (the relative transmission advantage of superspreading) for an epidemic to take off ($R_0 \geq 1$):

i) how strong does superspreading need to be to allow an epidemic, when transmission from superspreaders always generates new superspreaders (i.e., when $\sigma_H = 1$)?

Setting $\sigma_H = 1$ in the above expression for R_0, setting that expression equal to 1 (the threshold for an epidemic to occur), and solving for p gives:

$$p_1 = \frac{(\alpha + \gamma)}{N\beta_L} = \frac{1}{R_o^L}.$$

For the baseline parameter values used to generate Fig. 2, $p_1 = 1.25$.

Hence, even if superspreaders always generate new superspreaders ($\sigma_H = 1$), if $R_o^L < 1$ (such that non-superspreaders alone are not able to cause an epidemic) there is a lower limit of p that is greater than 1, that must be exceeded in order for an epidemic to occur. In other words, even 100% transmission of superspreading is not necessarily sufficient to drive an epidemic of a pathogen with only mild levels of superspreading.

ii) how strong does superspreading need to be to drive an epidemic, when there is no positive feedback loop between superspreaders (i.e., when $\sigma_H = \sigma_L$)?

Setting $\sigma_H = \sigma_L$ in the above expression for R_0, setting that expression equal to 1 and solving for p gives:

$$p_2 = \frac{\alpha + \gamma - N\beta_L(1-\sigma_L)}{N\beta_L\sigma_L} = \frac{{}^{1}/_{R_o^L} - (1-\sigma_L)}{\sigma_L} = \frac{p_1 - (1-\sigma_L)}{\sigma_L}.$$

Hence in the absence of a positive feedback loop in superspreader transmission, the rate of superspreader advantage (p) needs to exceed a threshold value determined by the baseline R_0 in the absence of superspreading (R_o^L) and the rate at which non-superspreaders spontaneously generate superspreaders (σ_L), in order for an epidemic to occur. This threshold is shown in Fig. 2 of the main paper by the value of p along the x-axis (when $\sigma_H = \sigma_L$), at the boundary where $R_0 = 1$. For the baseline parameter values used to generate Fig. 2, $p_2 = 6$.

Supplementary References

Diekmann, O., Heesterbeek, J. A. P., & Roberts, M. G. (2010). The construction of next-generation matrices for compartmental epidemic models. *Journal of the Royal Society Interface*, *7*(47), 873–885. https://doi.org/10.1098/rsif.2009.0386

Ma, J., & Earn, D. J. D. (2006). Generality of the final size formula for an epidemic of a newly invading infectious disease. *Bulletin of Mathematical Biology*, *68*(3), 679–702. https://doi.org/10.1007/s11538-005-9047-7