Supplementary materials (SM)

Contents

A Equation systems

A.1 Epidemiology

The epidemiological dynamics are governed by the following set of ODEs:

$$\frac{\mathrm{d}S}{\mathrm{d}t} = \lambda - \left(\mu + \beta_I I + \beta_D D + \beta_C \frac{C}{N}\right) S, \tag{S1a}$$

$$\frac{\mathrm{d}E}{\mathrm{d}t} = \left(\beta_I I + \beta_D D + \beta_C \frac{C}{N}\right) S - \omega E, \tag{S1b}$$

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \omega E - \gamma I, \tag{S1c}$$

$$\frac{\mathrm{d}D}{\mathrm{d}t} = \alpha\theta\gamma I - \varepsilon D, \tag{S1d}$$

$$\frac{\mathrm{d}C}{\mathrm{d}t} = (1-\alpha)\,\gamma I - \sigma C, \tag{S1e}$$

$$\frac{\mathrm{d}R}{\mathrm{d}t} = \sigma C - \mu R, \tag{S1f}$$

where $N \coloneqq S + E + I + C + R$ is the total living population size, which varies with time. Notice that since life expectancy is several orders of magnitudes greater than the latency, the symptomatic and the convalescent periods, mortality rate μ can be neglected when summed with ω, γ or σ.

A.2 Price equation

The dynamics of the populations of interest are described by $4n+1$ ODEs, for all $i \in \{1, \dots, n\}$:

$$\frac{\mathrm{d}S}{\mathrm{d}t} = \lambda - \sum_{i=1}^{n} \left(\beta_{I,i} I_i + \beta_{D,i} D_i - \mu\right) S, \tag{S2a}$$

$$\frac{\mathrm{d}E_i}{\mathrm{d}t} = \left(\beta_{I,i} I_i + \beta_{D,i} D_i\right) S - \omega_i E_i, \tag{S2b}$$

$$\frac{\mathrm{d}I_i}{\mathrm{d}t} = \omega_i E_i - \gamma_i I_i, \tag{S2c}$$

$$\frac{\mathrm{d}D_i}{\mathrm{d}t} = \alpha_i \theta \gamma_i I_i - \varepsilon_i D_i, \tag{S2d}$$

$$\frac{\mathrm{d}C_i}{\mathrm{d}t} = \left(1 - \alpha_i\right) \gamma_i I_i - \sigma_i C_i. \tag{S2e}$$

The total density of each compartment is denoted by a bullet index ($\bullet$) and its dynamics satisfy

$$\frac{\mathrm{d}S}{\mathrm{d}t} = \lambda - \left(\overline{\beta_I}^{I} I_\bullet + \overline{\beta_D}^{D} D_\bullet - \mu\right) S, \tag{S3a}$$

$$\frac{\mathrm{d}E_\bullet}{\mathrm{d}t} = \left(\overline{\beta_I}^{I} I_\bullet + \overline{\beta_D}^{D} D_\bullet\right) S - \overline{\omega}^{E} E_\bullet, \tag{S3b}$$

$$\frac{\mathrm{d}I_\bullet}{\mathrm{d}t} = \overline{\omega}^{E} E_\bullet - \overline{\gamma}^{I} I_\bullet, \tag{S3c}$$

$$\frac{\mathrm{d}D_\bullet}{\mathrm{d}t} = \theta \overline{\alpha\gamma}^{I} I_\bullet - \overline{\varepsilon}^{D} D_\bullet, \tag{S3d}$$

$$\frac{\mathrm{d}C_\bullet}{\mathrm{d}t} = \overline{\gamma}^{I} I_\bullet - \overline{\alpha\gamma}^{I} I_\bullet - \overline{\sigma}^{D} D_\bullet, \tag{S3e}$$

where the bars indicate average values and the superscripts indicate the compartment in which the trait is averaged. We can already notice that the CFR and the rate at which the infectious period ends are difficult to disentangle in this system because we have second order terms (*i.e.* an average of the product $\alpha_i \gamma_i$).

B Stationary dynamics

B.1 Endemic equilibrium

At equilibrium, all time derivatives of system (S1) cancel out. If we denote by $\widetilde{H}$ the corresponding value of density H at this equilibrium, we get $\widetilde{S} = S_0 = \frac{\lambda}{\mu}$ and $\widetilde{E} = \widetilde{I} = \widetilde{D} = \widetilde{C} = \widetilde{R} = 0$ for the disease free equilibrium (DFE).

The endemic equilibrium (EE), on the other hand, is found by assuming non zero values for all $\widetilde{H}$. We thus first get that,

$$\begin{cases} \frac{\mathrm{d}I}{\mathrm{d}t} = 0 & \iff \widetilde{I} = \frac{\omega}{\gamma}\widetilde{E}, \\ \frac{\mathrm{d}D}{\mathrm{d}t} = 0 & \iff \widetilde{D} = \frac{\alpha\theta\gamma}{\varepsilon}\widetilde{I} = \frac{\alpha\theta\omega}{\varepsilon}\widetilde{E}, \\ \frac{\mathrm{d}C}{\mathrm{d}t} = 0 & \iff \widetilde{C} = \frac{(1-\alpha)\gamma}{\sigma}\widetilde{I} = \frac{(1-\alpha)\omega}{\sigma}\widetilde{E}, \\ \frac{\mathrm{d}R}{\mathrm{d}t} = 0 & \iff \widetilde{R} = \frac{\sigma}{\mu}\widetilde{C} = \frac{(1-\alpha)\omega}{\mu}\widetilde{E}. \end{cases} \tag{S4}$$

Hence,

$$\begin{aligned} \frac{\mathrm{d}E}{\mathrm{d}t} = 0 &\iff \left(\beta_I\widetilde{I} + \beta_D\widetilde{D} + \beta_C\frac{\widetilde{C}}{\widetilde{N}}\right)\widetilde{S} - \omega\widetilde{E} = 0, \\ &\iff \left(\beta_I\frac{\omega}{\gamma}\widetilde{E} + \beta_D\frac{\alpha\theta\omega}{\varepsilon}\widetilde{E} + \beta_C\frac{(1-\alpha)\,\omega}{\sigma\widetilde{N}}\widetilde{E}\right)\widetilde{S} - \omega\widetilde{E} = 0, \\ &\iff \widetilde{S} = \left(\frac{\beta_I}{\gamma} + \frac{\alpha\theta\beta_D}{\varepsilon} + \frac{(1-\alpha)\,\beta_C}{\sigma\widetilde{N}}\right)^{-1}, \end{aligned} \tag{S5}$$

and

$$\begin{aligned}\frac{\mathrm{d}S}{\mathrm{d}t} = 0 &\iff \lambda - \left(\mu + \beta_I \widetilde{I} + \beta_D \widetilde{D} + \beta_C \frac{\widetilde{C}}{\widetilde{N}}\right) \widetilde{S} = 0, \\ &\iff \mu + \beta_I \frac{\omega}{\gamma} \widetilde{E} + \beta_D \frac{\alpha\theta\omega}{\varepsilon} \widetilde{E} + \beta_C \frac{(1-\alpha)\,\omega}{\sigma \widetilde{N}} \widetilde{E} = \frac{\lambda}{\widetilde{S}}, \\ &\iff \frac{\omega \widetilde{E}}{\widetilde{S}} = \frac{\lambda}{\widetilde{S}} - \mu, \\ &\iff \widetilde{E} = \frac{\lambda - \mu \widetilde{S}}{\omega}. \end{aligned} \tag{S6}$$

It follows that

$$\begin{aligned}\widetilde{N} \coloneqq \widetilde{S} + \widetilde{E} + \widetilde{I} + \widetilde{C} + \widetilde{R} &= \widetilde{S} + \left(1 + \frac{\omega}{\gamma} + \frac{(1-\alpha)\,\omega}{\sigma} + \frac{(1-\alpha)\,\omega}{\mu}\right) \widetilde{E}, \\ &= \widetilde{S} + \left(\frac{1}{\omega} + \frac{1}{\gamma} + \left(\frac{1}{\sigma} + \frac{1}{\mu}\right)(1-\alpha)\right) \left(\lambda - \mu \widetilde{S}\right). \end{aligned} \tag{S7}$$

By combining (S5) and (S7), we can find the exact solution for $\widetilde{N}$. This closed form is excessively large and therefore not shown here. It is however possible to find a approximation of $\widetilde{N}$ as a simple function of the model's parameters with some simplifications that are shown hereafter, with a particular treatment of the $\alpha = 1$ case.

B.2 Stationary total population size approximation for $\alpha \neq 1$

In this subsection, we assume that $\alpha < 1$ (the case where $\alpha = 1$ is treated in the next subsection).

Given that life expectancy is several orders of magnitude greater than the convalescent period, *i.e.* $\frac{1}{\mu} \gg \frac{1}{\sigma}$, we have

$$\frac{1}{\omega} + \frac{1}{\gamma} + \left(\frac{1}{\sigma} + \frac{1}{\mu}\right)(1-\alpha) \approx \left(\frac{1}{\omega} + \frac{1}{\gamma} + \frac{1}{\mu}\right) - \frac{\alpha}{\mu},$$

Furthermore, since life expectancy is also several orders of magnitude greater than the latency and symptomatic period, *i.e.* $\frac{1}{\mu} \gg \frac{1}{\omega} + \frac{1}{\gamma}$, and since $\alpha \neq 1$, we finally have

$$\begin{aligned} \widetilde{N} &\approx \widetilde{S} + (1-\alpha)\left(S_0 - \widetilde{S}\right), \\ \widetilde{N} &\approx (1-\alpha)\, S_0 + \alpha \widetilde{S}. \end{aligned} \tag{S8}$$

The virulence of EBOV is usually high and its sexual transmission low compared to the two other transmission route (Abbate et al., 2016), which is why we can approximate $\widetilde{S}$ by its value by neglecting the third term in equation (S5), which leads to

$$\widetilde{S} \approx \frac{\gamma\varepsilon}{\varepsilon\beta_I + \alpha\gamma\theta\beta_D}. \tag{S9}$$

This then results in

$$\widetilde{N} \approx (1-\alpha)\, S_0 + \frac{\alpha\gamma\varepsilon}{\varepsilon\beta_I + \alpha\gamma\theta\beta_D}. \tag{S10}$$

Numerical comparisons performed on positive and stable equilibria for realistic parameter sets show that this approximation differs from the exact value by less than 10,000 individuals, which corresponds to a relative error of less than 1%, thus validating the accuracy of this approximation.

B.3 Stationary total population size approximation for $\alpha = 1$

Here we assume that $\alpha = 1$ (notice that in this case the trade-off exponent p vanishes).

We then get back to equation (S5) that becomes such that

$$\widetilde{S} = \left(\frac{\beta_I}{\gamma} + \frac{\theta\beta_D}{\varepsilon}\right)^{-1} = \frac{\gamma\varepsilon}{\varepsilon\beta_I + \gamma\theta\beta_D},$$

which shows that the exact value of $\widetilde{S}$ coincides with its equation (S9) approximation for $\alpha = 1$.

As for equation (S7), we get

$$\widetilde{N} = \left(1 - \frac{(\gamma + \omega)\,\mu}{\gamma\omega}\right)\widetilde{S} + \frac{(\gamma + \omega)\,\lambda}{\gamma\omega},$$

it is straightforward to show numerically (using parameters from Table 1) that, since $\widetilde{S}$ and $\frac{\lambda}{\mu} = S_0$ are of the same order of magnitude and that, as already mentioned, life expectancy is several orders of magnitude greater than the latency and symptomatic period, *i.e.* $\frac{1}{\mu} \gg \frac{1}{\omega} + \frac{1}{\gamma}$, which is equivalent to $\frac{(\gamma+\omega)\mu}{\gamma\omega} \ll 1$, we have

$$\widetilde{N} \approx \widetilde{S} = \frac{\gamma\varepsilon}{\varepsilon\beta_I + \gamma\theta\beta_D}, \tag{S11}$$

which shows the consistency of equation (S10) even for $\alpha = 1$.

This approximation shows a relative error of about 10^{-3} with Table 1 parameters values.

C Reproduction number derivation

The basic reproduction number, $\mathcal{R}_0$, and the relative reproduction number, $\mathcal{R}_\mathrm{m}$, are two epidemiological quantifications of the invasion potential of an infectious agent in a fully susceptible population and in an population already infected by an alternative strain, respectively. They emerge from the stability analysis of the disease free equilibrium (DFE) and the endemic equilibrium (EE) respectively. Their threshold value is 1.

The next-generation method (Diekmann et al., 1990; Hurford et al., 2010) is the most efficient derivation of these reproduction numbers and proceeds as follows.

C.1 General reproduction number

First, we isolate the ODEs of the infected compartments from the rest of the system (here system (S1)) to obtain

$$\begin{cases} \frac{\mathrm{d}E}{\mathrm{d}t} &= \left(\beta_I I + \beta_D D + \beta_C \frac{C}{N}\right) S - \omega E, \\ \frac{\mathrm{d}I}{\mathrm{d}t} &= \omega E - \gamma I, \\ \frac{\mathrm{d}D}{\mathrm{d}t} &= \alpha\theta\gamma I - \varepsilon D, \\ \frac{\mathrm{d}C}{\mathrm{d}t} &= (1-\alpha)\,\gamma I - \sigma C. \end{cases} \tag{S12}$$

Second, we write the Jacobian matrix $\mathbf{J}$ that corresponds to this sub-system (S27), by deriving each time-derivative $(\frac{\mathrm{d}E}{\mathrm{d}t}, \frac{\mathrm{d}I}{\mathrm{d}t}, \frac{\mathrm{d}D}{\mathrm{d}t}, \frac{\mathrm{d}C}{\mathrm{d}t})$ with respect to each infected compartment density

(E, I, D, C):

$$\mathbf{J} = \begin{bmatrix} -\beta_C \frac{CS}{N^2} - \omega & \left(\beta_I + \beta_C \frac{C}{N^2}\right) S & \beta_D S & \left(1 - \frac{C}{N}\right) \beta_C \frac{S}{N} \\ \omega & -\gamma & 0 & 0 \\ 0 & \alpha\gamma\theta & -\varepsilon & 0 \\ 0 & (1-\alpha)\,\gamma & 0 & -\sigma \end{bmatrix},$$

reminding that $N \coloneqq S + E + I + R + C$.

Third, we arbitrarily decompose $\mathbf{J}$ as a sum of an 'inflow' matrix $\mathbf{F}$ and an 'outflow' matrix $-\mathbf{V}$ provided that $\mathbf{V}$ is non-singular (that is $\mathbf{V}^{-1}$ exists), $\mathbf{F}$ and $\mathbf{V}^{-1}$ are non-negative elementwise and the real parts of all eigenvalues of $-\mathbf{V}$ are negative. Here, we conveniently choose two matrices that fulfil these requirements:

$$\mathbf{F} = \begin{bmatrix} 0 & \left(\beta_I + \beta_C \frac{C}{N^2}\right) S & \beta_D S & \beta_C \frac{S}{N} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \text{ and } \mathbf{V} = \begin{bmatrix} -\beta_C \frac{CS}{N^2} - \omega & 0 & 0 & -\beta_C \frac{CS}{N^2} \\ \omega & -\gamma & 0 & 0 \\ 0 & \alpha\gamma\theta & -\varepsilon & 0 \\ 0 & (1-\alpha)\,\gamma & 0 & -\sigma \end{bmatrix}.$$

Finally, the general reproductive number $\mathcal{R}$ is given by the largest modulus of all eigenvalues of the $\mathbf{F}.\mathbf{V}^{-1}$ matrix. Elementary calculations result in the following general result

$$\mathcal{R} = \frac{\left((1-\alpha)\,\gamma\varepsilon\beta_C + \left(\varepsilon\beta_I + \alpha\gamma\theta\beta_D\right) N\right) \omega S N}{\left(\gamma\sigma\beta_C CS + \left((1-\alpha)\,\gamma\beta_C CS\left(\beta_C CS + N^2\gamma\right)\sigma\right)\omega\right)\varepsilon}. \tag{S13}$$

C.2 Basic reproduction number

The basic reproduction number $\mathcal{R}_0$ is obtained from $\mathcal{R}$ by setting the densities to their values at the disease free equilibrium (DFE), namely $S = N = \frac{\lambda}{\mu}$ and $C = 0$, hence

$$\mathcal{R}_0 = \left(\frac{\beta_I}{\gamma} + \frac{\alpha\theta\beta_D}{\varepsilon} \right) S_0 + \frac{(1-\alpha)\,\beta_C}{\sigma}, \tag{S14}$$

Any strain introduced in a fully susceptible host population spreads if and only if $\mathcal{R}_0 > 1$.

C.3 Relative reproduction number

As for the relative reproduction number $\mathcal{R}_\mathrm{m}$, it is obtained from $\mathcal{R}$ by setting the densities to their values at an alternative strain endemic equilibrium (EE), namely $S = \widetilde{S}$, $N = \widetilde{N}$ and $C = 0$ (notice that in such setting $N = S + R + E_\mathrm{r} + I_\mathrm{r} + C_\mathrm{r} + E + I + C$ where the r index denotes compartments of individuals infected by the previously established ('resident'), which may not be empty at EE, making $\widetilde{S} < \widetilde{N}$), hence

$$\mathcal{R}_\mathrm{m} = \left(\frac{\beta_I}{\gamma} + \frac{\alpha\theta\beta_D}{\varepsilon} + \frac{(1-\alpha)\,\beta_C}{\sigma\widetilde{N}} \right) \widetilde{S}.$$

It follows that a rare mutant strain of CFR x that appears in a host population endemically infected by a resident strain of CFR y spreads and persists if and only if

$$\mathcal{R}\,(x, y) \coloneqq \left(\frac{\beta_I\,(x)}{\gamma} + \frac{x\theta\beta_D\,(x)}{\varepsilon} + \frac{(1-x)\,\beta_C\,(x)}{\sigma\widetilde{N}\,(y)} \right) \widetilde{S}\,(y) > 1. \tag{S15}$$

Moreover, it is possible to eliminate $\widetilde{S}(y)$ using equation (S5), leading to

$$\mathcal{R}(x,y) = \frac{\frac{\beta_I(x)}{\gamma} + \frac{x\theta\beta_D(x)}{\varepsilon} + \frac{(1-x)\beta_C(x)}{\sigma\widetilde{N}(y)}}{\frac{\beta_I(y)}{\gamma} + \frac{y\theta\beta_D(y)}{\varepsilon} + \frac{(1-y)\beta_C(y)}{\sigma\widetilde{N}(y)}}. \tag{S16}$$

This formula shows in particular that, because of the two occurrences of $\widetilde{N}(y)$, the relative reproduction number is not the ratio between the two basic reproduction numbers, as it is in simpler models (Dieckmann, 2002).

We can finally apply approximation (S10) $\widetilde{N}(y) \approx (1-y)S_0 + \frac{\gamma\varepsilon y}{\varepsilon\beta_I(y)+\gamma\theta y\beta_D(y)}$ to obtain a closed-form expression for $\mathcal{R}(x,y)$ (not shown here).

D Evolutionary analysis of virulence

Investigating the evolutionary trends require to consider trade-offs. From now on, we will then always apply the transmission-virulence trade-off assumed in equation (2) and keep in mind that the β_H constant case can be retrieved if $p = 0$.

D.1 Virulence effect on basic reproduction number

It is worth noticing that unless $p = 0$, we have $\mathcal{R}_0 = 0$ when $\alpha = 0$. Therefore not all CFR/virulence levels are able to give rise to an epidemic and persist in the population. Indeed, $\mathcal{R}_0(\alpha)$ may not be greater than 1 for all $\alpha \in [0; 1]$. First, let us then study how $\mathcal{R}_0$ is affected by α, by calculating its derivative

$$\begin{aligned}\frac{\mathrm{d}\mathcal{R}_0}{\mathrm{d}\alpha}(\alpha) &= \frac{\mathrm{d}}{\mathrm{d}\alpha}\left(\left(\left(\frac{b_I}{\gamma} + \frac{\alpha\theta b_D}{\varepsilon}\right) S_0 + \frac{(1-\alpha)\, b_C}{\sigma}\right)\alpha^p\right), \\ &= \left(\left(\frac{\theta b_D S_0}{\varepsilon} - \frac{b_C}{\sigma}\right)\alpha + p\left(\left(\frac{b_I}{\gamma} + \frac{\alpha\theta b_D}{\varepsilon}\right) S_0 + \frac{(1-\alpha)\, b_C}{\sigma}\right)\right)\alpha^{p-1},\end{aligned}$$

which cancels only if $\alpha = 0$ or

$$\alpha = \frac{\frac{b_C}{\sigma} + \frac{b_I S_0}{\gamma}}{\frac{b_C}{\sigma} - \frac{\theta b_D S_0}{\varepsilon}} \times \frac{p}{1+p} =: \alpha^\circ,$$

which lies in $]0, 1[$ if and only if $\theta < \frac{\varepsilon b_C}{\sigma b_D S_0} \approx 2.3\%$ and $p < \frac{\frac{b_C}{\sigma S_0} - \frac{\theta b_D}{\varepsilon}}{\frac{b_I}{\gamma} + \frac{\theta b_D}{\varepsilon}} \underset{\theta=0}{\approx} 5.6 \cdot 10^{-3}$ (numerical values are given according to Table 1 calibration). If these conditions are not fulfilled, then $\mathrm{d}\mathcal{R}_0/\mathrm{d}\alpha$ is positive for all CFR.

Given these conditions, the value of α° can be approximated by

$$\alpha^\circ \underset{\theta\to 0}{\approx} \frac{\sigma b_I S_0}{\gamma b_C} p.$$

The basic reproduction number at this value is

$$\mathcal{R}_0\left(\alpha^\circ\right) = \left(\left(\frac{b_I}{\gamma} + \frac{\alpha\theta b_D}{\varepsilon}\right) S_0 + \frac{(1-\alpha)\, b_C}{\sigma}\right)\left(\frac{\sigma b_I S_0}{\gamma b_C} p\right)^p \underset{\theta\to 0}{\approx} \frac{b_I S_0}{\gamma},$$

which is a maximum on $]0,1[$ (inequality $\frac{\mathrm{d}^2\mathcal{R}_0}{\mathrm{d}\alpha^2}\left(\alpha^\circ\right) < 0$ has been checked after calculations not shown).

Besides, evaluating $\mathcal{R}_0$ for $\alpha = 1$ leads to

$$\mathcal{R}_0\left(1\right) = \left(\frac{b_I}{\gamma} + \frac{\theta b_D}{\varepsilon}\right) S_0 \geq \frac{b_I S_0}{\gamma},$$

the lower bound being greater than one according to Table 1 estimates, and this holds even with almost half of the b_I value and smaller values of γ.

To conclude, for any given values of p and θ, there is always a CFR interval $[\alpha_{\min}, 1]$ in which any strain can spread.

Notice also that for $\alpha = 0$ and $p = 0$,

$$\mathcal{R}_0 = \frac{b_I S_0}{\gamma} + \frac{b_C}{\sigma} \geq \frac{b_I S_0}{\gamma},$$

and likewise this is greater than one for estimated parameters. Consequently, all CFR values can spread in absence of trade-off.

D.2 Minimum spreadable CFR approximation

$\alpha_{\min} \in [0,1]$ is the minimum CFR of EBOV required to spread, i.e. $\mathcal{R}_0(\alpha_{\min}) \coloneqq 1$. However, it is not possible to find the exact closed form of $\alpha_{\min}$ (as the equation $\mathcal{R}(x) = 1$ involves irreducible terms of both x^p and x). It is nonetheless possible to analytically find a lower bound for $\alpha_{\min}$, which we denote by α_- ($0 \leq \alpha_- \leq \alpha_{\min} \leq 1$). First, notice that

$$\mathcal{R}_0(\alpha) \coloneqq \left(\frac{\beta_I}{\gamma} + \frac{\alpha\theta\beta_D}{\varepsilon}\right) S_0 + \frac{(1-\alpha)\beta_C}{\sigma} \leq \left(\frac{\beta_I}{\gamma} + \frac{\theta\beta_D}{\varepsilon}\right) S_0 + \frac{\beta_C}{\sigma} =: \mathcal{R}_{0,+}(\alpha), \tag{S17}$$

where $\mathcal{R}_{0,+}(\alpha)$ is an over-estimate of $\mathcal{R}_0(\alpha)$. Applying the trade-off from equation (2), we get

$$\mathcal{R}_{0,+}(\alpha) = \left(\left(\frac{b_I}{\gamma} + \frac{\theta b_D}{\varepsilon}\right) S_0 + \frac{b_C}{\sigma}\right) \alpha^p.$$

Let α_- be the CFR such that $\mathcal{R}_{0,+}(\alpha_-) = 1$, that is

$$\alpha_- = \left(\left(\frac{b_I}{\gamma} + \frac{\theta b_D}{\varepsilon}\right) S_0 + \frac{b_C}{\sigma}\right)^{\frac{-1}{p}}. \tag{S18}$$

From equation (S17) and as $\mathcal{R}_0$ and $\mathcal{R}_{0,+}$ are increasing functions of α, it follows that

$$\mathcal{R}_0(\alpha_-) \leq \mathcal{R}_{0,+}(\alpha_-) = 1 = \mathcal{R}_0(\alpha_{\min}) \leq \mathcal{R}_{0,+}(\alpha_{\min}),$$

thus α_- is an analytical under-estimate of $\alpha_{\min}$.

Notice that in absence of trade-off, the closed form $\alpha_{\min}$ can be easily found as

$$\alpha_{\min} = \frac{1 - \frac{b_I S_0}{\gamma} - \frac{b_C}{\sigma}}{\frac{\theta b_D S_0}{\varepsilon} - \frac{b_C}{\sigma}}. \tag{S19}$$

D.3 Virulence effect on stationary densities

From now one, we will assume that $\alpha \in [\alpha_{\min}, 1]$.

We apply definition from equation (2) to equation (S9), that is

$$\widetilde{S} \approx \frac{\gamma\varepsilon}{(\varepsilon b_I + \gamma\theta b_D \alpha)\,\alpha^p}.$$

Its derivative with respect to α is

$$\frac{\mathrm{d}\widetilde{S}}{\mathrm{d}\alpha}(\alpha) \approx \frac{-\left(\gamma\theta b_D \alpha + p\left(\varepsilon b_I + \gamma\theta b_D \alpha\right)\right)\gamma\varepsilon\alpha^{p-1}}{\left(\varepsilon b_I + \gamma\theta b_D \alpha\right)^2} < 0.$$

Thus, it comes from equation (S8), that

$$\frac{\mathrm{d}\widetilde{N}}{\mathrm{d}\alpha}(\alpha) = -S_0 + \widetilde{S}(\alpha) + \alpha\frac{\mathrm{d}\widetilde{S}}{\mathrm{d}\alpha}(\alpha).$$

Since $\widetilde{S}(\alpha) < S_0$ for $\alpha \geq \alpha_{\min}$ (any EBOV strain that spreads decreases the number of susceptible individuals), $\frac{\mathrm{d}\widetilde{N}}{\mathrm{d}\alpha}(\alpha) < 0$, that is $\widetilde{N}(\alpha)$ is a decreasing function of α, we have

$$\widetilde{N}(\alpha) \geq \widetilde{N}(1) = \frac{\gamma\varepsilon}{\varepsilon b_I + \gamma\theta b_D}.$$

D.4 Virulence selection gradient

We can finally investigate the virulence selection gradient, Δ, by deriving the relative reproduction number from equation (S16) with respect to the first argument (*i.e.* the mutant's virulence), which leads to $\partial_1\mathcal{R}$, and equalizing the mutant and resident's virulence. After some calculations, we find

that

$$\Delta(y) \coloneqq \partial_1 \mathcal{R}(y,y) = \frac{p}{y} + \frac{\frac{\theta b_D}{\varepsilon}\widetilde{N}(y) - \frac{b_C}{\sigma}}{(1-y)\frac{b_C}{\sigma} + \left(\frac{b_I}{\gamma} + \frac{\theta b_D}{\varepsilon} y\right)\widetilde{N}(y)}.$$

Since the CFR is bounded by 1, it is expected to evolve towards lower values if and only if $\Delta(1) < 0$, that is

$$\Delta(1) \approx p + \frac{\theta b_D \gamma}{\varepsilon b_I + \gamma \theta b_D} - \frac{b_C}{\sigma} < 0.$$

By investigating burial control under the most favourable trade-off, which is no trade-off ($p = 0$), we find that this condition is equivalent to (for $b_C \ll \sigma$):

$$\theta < \frac{b_I b_C \varepsilon}{\gamma \sigma b_D} \approx 4\%.$$

By investigating trade-off shape under the most favourable burial control ($\theta = 0$), we find that the condition is equivalent to

$$p < \frac{b_C}{\sigma} \approx 10^{-2}.$$

Moreover, investigating the selection gradient at the lowest spreadable CFR $y = \alpha_{\min}$, we notice that the following lower bound

$$\Delta(\alpha_{\min}) \geq \frac{\frac{\theta b_D}{\varepsilon}\widetilde{N}(1) - \frac{b_C}{\sigma}}{(1-\alpha_{\min})\frac{b_C}{\sigma} + \left(\frac{b_I}{\gamma} + \frac{\theta b_D}{\varepsilon}\alpha_{\min}\right)\widetilde{N}(1)}$$

is positive if $\theta > \frac{b_I b_C \varepsilon}{\gamma \sigma b_D}$. Therefore a necessary condition for having a negative selection gradient on the lowest spreadable CFRs is $\theta < \frac{b_I b_C \varepsilon}{\gamma \sigma b_D}$.

D.5 Evolutionary attracting virulence estimation

Unless it is equal to the 0 or 1 boundaries (the determination of which only requires the invariant sign of the selection gradient), the evolutionary attracting virulence $\alpha^\star$ is an intermediate CFR value in $]0,1[$ such that $\Delta(\alpha^\star) = 0$ (singularity condition), $\partial_{1,1}\mathcal{R}(\alpha^\star, \alpha^\star) < 0$ (evolutionary stability condition) and $\frac{\mathrm{d}\Delta}{\mathrm{d}\alpha}(\alpha^\star) < 0$ (convergent stability condition), according to the adaptive dynamics framework (Geritz et al., 1998). We therefore investigate the singularity condition that provides an equation $\alpha^\star$ has to satisfy.

By writing the selection gradient under a condensed form and defining $\eta \coloneqq \frac{b_I}{\gamma}, \phi \coloneqq \frac{b_D}{\varepsilon}, \psi \coloneqq \frac{b_C}{\sigma}$, we find that

$$\begin{aligned} \Delta(\alpha^\star) = \frac{p}{\alpha^\star} + \frac{\theta\phi\widetilde{N}(\alpha^\star) - \psi}{(1-\alpha^\star)\psi + (\eta + \theta\phi\alpha^\star)\widetilde{N}(\alpha^\star)} &= 0, \\ \iff (p - (1+p)\alpha^\star)\psi + (p\eta + (p+\alpha^\star)\theta\phi)\widetilde{N}(\alpha^\star) &= 0. \end{aligned} \tag{S20}$$

As noticed in the previous subsection, this equation has a solution only if p is small enough (for the first term to be negative) and θ is small enough (for the second term not to be too positive). Hereafter, and because we are seeking for an intermediate evolutionary attracting virulence, we assume that p and θ are small enough such that this equation has a solution in $]0,1[$.

The complexity of $\widetilde{N}(\alpha^\star)$ prevents us from having a closed-form expression of $\alpha^\star$. However, $\alpha^\star$ can be bounded by an underestimate $\alpha^\star_-$ on the one hand, and an overestimate $\alpha^\star_+$ on the other hand.

First, notice that the left hand side of equation (S20) has the following upper bound, replacing $\widetilde{N}(\alpha^\star)$ by its maximum $S_0 = \frac{\lambda}{\mu}$,

$$(p - (1+p)\,\alpha^\star)\,\psi + (p\eta + (p+\alpha^\star)\,\theta\phi)\,S_0,$$

which cancels out only if $\alpha^\star$ is replaced by a greater value we denote by $\alpha^\star_+$ (since the first term is a decreasing function of the CFR). This leads to

$$\alpha^\star_+ = \frac{((\eta+\theta\phi)\,S_0 + \psi)\,p}{(1+p)\,\psi - \theta\phi S_0}. \tag{S21}$$

Notice that $\alpha^\star_+ > 0$ requires that $\psi\,(1+p) > \theta\phi S_0$ that is θ small.

Second and analogously, the left hand side of equation (S20) has the following lower bound, replacing $\widetilde{N}\,(\alpha^\star)$ by its minimum $\widetilde{N}\,(1) = \frac{1}{\eta+\theta\phi}$,

$$(p - (1+p)\,\alpha^\star)\,\psi + \frac{p\eta + (p+\alpha^\star)\,\theta\phi}{\eta+\theta\phi},$$

which cancels out only if $\alpha^\star$ is replaced by a smaller value we denote $\alpha^\star_-$ (since the first term is a decreasing function of the CFR). This leads to

$$\alpha^\star_- = \frac{(1+\psi)\,p}{(1+p)\,\psi - \frac{\theta\phi}{\eta+\theta\phi}}. \tag{S22}$$

Notice that $\alpha^\star_- < 1$ requires that $p < \psi - \frac{\theta\phi}{\eta+\theta\phi}$. Since $\frac{\widehat{b_C}}{\widehat{\sigma}} = 10^{-2}$, the approximations $1+\psi \approx 1$ and $1+p \approx 1$ holds, which makes this expression even simpler:

$$\alpha^\star_- \approx \frac{p}{\psi - \frac{\theta\phi}{\eta+\theta\phi}},$$

which in turn is positive only if $\theta < \frac{\psi\eta}{(1+\psi)\phi} \approx \frac{\psi\eta}{\phi}$. Therefore, the two conditions on p and θ related to the cancellation of Δ are retrieved.

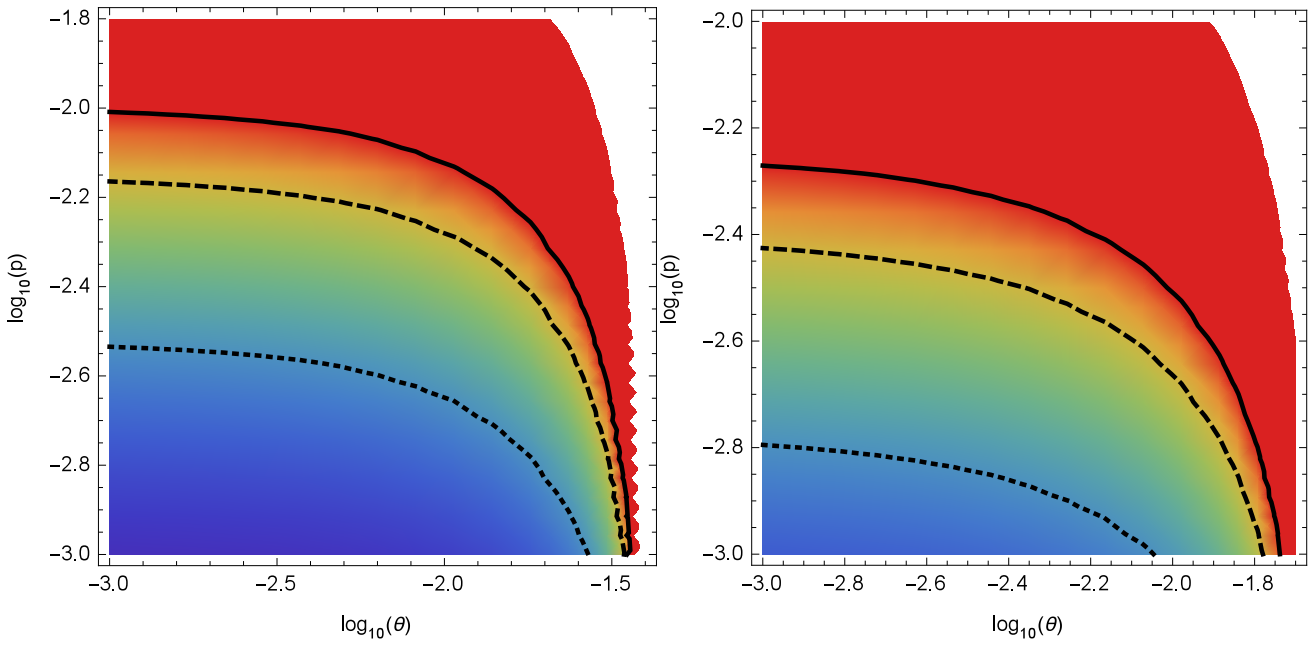

Figure S1: **Boundaries of the evolutionary attracting values of CFR.** Underestimate ($\alpha^\star_-$, left) and the overestimate ($\alpha^\star_+$, right) values of the evolutionary attractor $\alpha^\star$ as a function of unsafe burial ratio θ and trade-off exponent p. The solid, the dashed and the dotted lines correspond to $\alpha^\star = 1, 0.7$ and 0.3 respectively. Other parameter values are default (Table 1).

As one can see by comparing Figure S1 with Figure 3, $\alpha^\star_+$ but moreover $\alpha^\star_-$ are accurate estimates of $\alpha^\star$.

E Sensitivity analysis

For the sake of both generality and graphical readability, we reduced the dimensionality of the parameter space by defining:

$$\eta \coloneqq \frac{b_I}{\gamma}, \delta \coloneqq \frac{b_D}{\varepsilon} \cdot \frac{\gamma}{b_I}, \kappa \coloneqq \frac{b_C}{\sigma} \cdot \frac{\gamma}{b_I}, \tag{S23}$$

where η is the average number of infectious contacts between one susceptible and one symptomatic individual over the symptomatic individual's symptomatic period, δ is the ratio between the equivalent of η for dead bodies and η itself, and κ is the ratio between the equivalent of η for convalescent individuals and η itself. Quantity η is equal to the symptomatic individual relative (that is normalised by S_0) contribution to the basic reproduction number, and is used for defining both δ and κ. Therefore, η is a primary scaling factor that can be eliminated through any estimated value of the $\mathcal{R}_0$. δ and κ are secondary scaling factors that can be studied independently.

First, the basic reproduction number can be rewritten using definitions (S23),

$$\mathcal{R}_0 = \left(\left(1 + \alpha\theta\delta\right) S_0 + \left(1 - \alpha\right) \kappa\right) \eta\alpha^p.$$

Therefore, any given a set of estimated epidemiological data $(\widehat{\alpha}, \widehat{\theta}, \widehat{S_0}, \widehat{\mathcal{R}_0})$ can be used to scale η, while keeping undetermined the trade-off exponent p, that is to say

$$\widehat{\eta} = \frac{\widehat{\mathcal{R}_0}\widehat{\alpha}^{-p}}{\left(1 + \widehat{\alpha}\widehat{\theta}\delta\right) \widehat{S_0} + \left(1 - \widehat{\alpha}\right) \kappa}. \tag{S24}$$

Rewriting the selection gradient at $\alpha = 1$ with definitions (S23),

$$\Delta(1) \approx p + \frac{\theta\delta}{1+\theta\delta} - \kappa\eta,$$

and imputing estimated data with equation (S24),

$$\Delta(1) \approx p + \frac{\theta\delta}{1+\theta\delta} - \frac{\widehat{\mathcal{R}_0}\widehat{\alpha}^{-p}\kappa}{\left(1+\widehat{\alpha}\widehat{\theta}\delta\right)\widehat{S_0} + (1-\widehat{\alpha})\,\kappa},$$

we find that

$$\begin{aligned}\Delta(1) < 0 &\iff ((1+\theta\delta)\,p + \theta\delta)\left(\left(1+\widehat{\alpha}\widehat{\theta}\delta\right)\widehat{S_0} + (1-\widehat{\alpha})\,\kappa\right) < (1+\theta\delta)\,\widehat{\mathcal{R}_0}\widehat{\alpha}^{-p}\kappa,\\ &\iff ((1+\theta\delta)\,p + \theta\delta)\left(1+\widehat{\alpha}\widehat{\theta}\delta\right)\widehat{S_0} < \left((1+\theta\delta)\,\widehat{\mathcal{R}_0}\widehat{\alpha}^{-p} - ((1+\theta\delta)\,p + \theta\delta)\,(1-\widehat{\alpha})\right)\kappa.\end{aligned}$$

Further investigation requires to study the inequality

$$\widehat{\mathcal{R}_0} \gtrless \left(p + \frac{\theta\delta}{1+\theta\delta}\right)(1-\widehat{\alpha})\,\widehat{\alpha}^p.$$

Elementary calculus then shows that for any couple $(p, \widehat{\alpha}) \in \mathbb{R}_+ \times [0,1]$, we have the following upper bound

$$\left(p + \frac{\theta\delta}{1+\theta\delta}\right)(1-\widehat{\alpha})\,\widehat{\alpha}^p \leq (p+1)\,(1-\widehat{\alpha})\,\widehat{\alpha}^p \leq 1,$$

By definition, epidemiological data originate from outbreaks for which $\widehat{\mathcal{R}_0} > 1$, therefore we get the inequality used to plot our figure

$$\Delta(1) < 0 \iff \frac{\kappa}{\widehat{S_0}} > \frac{((1+\theta\delta)\,p + \theta\delta)\left(1+\widehat{\alpha}\widehat{\theta}\delta\right)}{(1+\theta\delta)\,\widehat{\mathcal{R}_0}\widehat{\alpha}^{-p} - ((1+\theta\delta)\,p + \theta\delta)\,(1-\widehat{\alpha})}, \tag{S25}$$

with values $\widehat{\alpha} = 0.7$, $\widehat{\theta} = 0.25$, $\widehat{S_0} = 4.44444 \cdot 10^6$ and $\widehat{\mathcal{R}_0} \in [1.26, 2.53]$, according to reference (World Health Organization Ebola Response Team, 2014; Nyenswah et al., 2016; Abbate et al., 2016) respectively.

F Application of the Price equation

Introducing a diversity of $n \in \mathbb{N}^\star$ non-coinfecting strains of EBOV, system (S1) becomes a set of $4n+1$ ordinary differential equations, where for all $i \in \{1, \ldots, n\}$,

$$\begin{cases} \frac{\mathrm{d}S}{\mathrm{d}t} &= \lambda - \mu S - \sum_{i=1}^{n} \left(\beta_{I,i} I_i + \beta_{D,i} D_i + \beta_{C,i} C_i\right) S, \\ \frac{\mathrm{d}E_i}{\mathrm{d}t} &= \left(\beta_{I,i} I_i + \beta_{D,i} D_i + \beta_{C,i} C_i\right) S - \omega_i E_i, \\ \frac{\mathrm{d}I_i}{\mathrm{d}t} &= \omega_i E_i - \gamma_i I_i, \\ \frac{\mathrm{d}D_i}{\mathrm{d}t} &= \alpha_i \theta \gamma_i I_i - \varepsilon_i D_i, \\ \frac{\mathrm{d}C_i}{\mathrm{d}t} &= (1-\alpha_i)\, \gamma_i I_i - \sigma_i D_i. \end{cases} \tag{S26}$$

780 The total population size of each class, denoted by $X_\bullet \coloneqq \sum_{i=1}^{n} X_i$, therefore satisfies

$$\begin{cases} \frac{\mathrm{d}S}{\mathrm{d}t} &= \lambda - \mu S - \left(\overline{\beta_I}^{I} I_\bullet + \overline{\beta_D}^{D} D_\bullet + \overline{\beta_C}^{C} C_\bullet\right) S, \\ \frac{\mathrm{d}E_\bullet}{\mathrm{d}t} &= \left(\overline{\beta_I}^{I} I_\bullet + \overline{\beta_D}^{D} D_\bullet + \overline{\beta_C}^{C} C_\bullet\right) S - \overline{\omega}^{E} E_\bullet, \\ \frac{\mathrm{d}I_\bullet}{\mathrm{d}t} &= \overline{\omega}^{E} E_\bullet - \overline{\gamma}^{I} I_\bullet, \\ \frac{\mathrm{d}D_\bullet}{\mathrm{d}t} &= \theta \overline{\alpha\gamma}^{I} I_\bullet - \overline{\varepsilon}^{D} D_\bullet, \\ \frac{\mathrm{d}C_\bullet}{\mathrm{d}t} &= \overline{\gamma}^{I} I_\bullet - \overline{\alpha\gamma}^{I} I_\bullet - \overline{\sigma}^{D} D_\bullet. \end{cases} \tag{S27}$$

By definition, an average value of a trait x in a compartment H is given by $\overline{x}^{H} = \sum_{i=1}^{n} x_i \frac{H_i}{H_\bullet}$.

If we assume that the trait value of a strain is constant and neglect mutational variance (*i.e.*

$\frac{\mathrm{d}x_i}{\mathrm{d}t} = 0$), the dynamics of any trait x in the I compartment are thus given by

$$\begin{aligned}
\frac{\mathrm{d}\overline{x}^I}{\mathrm{d}t} &= \sum_{i=1}^{n}\left(\frac{1}{I_\bullet}\frac{\mathrm{d}I_i}{\mathrm{d}t} - \frac{I_i}{I_\bullet^2}\frac{\mathrm{d}I_\bullet}{\mathrm{d}t}\right)x_i, \\
&= \sum_{i=1}^{n}\left(\left(\omega_i E_i - \gamma_i I_i\right)\frac{1}{I_\bullet} - \left(\overline{\omega}^E E_\bullet - \overline{\gamma}^I I_\bullet\right)\frac{I_i}{I_\bullet^2}\right)x_i, \\
&= \sum_{i=1}^{n}\left(\omega_i\frac{E_i}{E_\bullet} - \overline{\omega}\frac{I_i}{I_\bullet}\right)x_i\frac{E_\bullet}{I_\bullet} - \sum_{i=1}^{n}\left(\gamma\frac{I_i}{I_\bullet} - \overline{\gamma}\frac{I_i}{I_\bullet}\right)x_i, \\
&= \frac{E_\bullet}{I_\bullet}\sum_{i=1}^{n}\left(\omega_i\frac{E_i}{E_\bullet} - \overline{\omega}\frac{E_i}{E_\bullet} + \overline{\omega}\frac{E_i}{E_\bullet} - \overline{\omega}\frac{I_i}{I_\bullet}\right)x_i - \sum_{i=1}^{n}\left(\gamma - \overline{\gamma}\right)x_i\frac{I_i}{I_\bullet}, \\
\frac{\mathrm{d}\overline{x}^I}{\mathrm{d}t} &= \left(\mathrm{cov}_E\left(x,\omega\right) + \left(\overline{x}^E - \overline{x}^I\right)\overline{\omega}^E\right)\frac{E_\bullet}{I_\bullet} - \mathrm{cov}_I\left(x,\gamma\right), \qquad \text{(S28)}
\end{aligned}$$

where cov indicates a genetic covariance between two traits, $\overline{x}^H$ is the average value of trait x in host compartment X and $\overline{xy}^H$ is the average value of the product xy in the same compartment. This illustrates that it might be difficult to disentangle a trait of interest x with the duration of the latent period ($1/\omega$) if this latter trait varies for different virus genotypes.

Similarly, in the E compartment we have

$$\begin{aligned}
\frac{\mathrm{d}\overline{x}^E}{\mathrm{d}t} &= \sum_{i=1}^{n}\left(\frac{1}{E_\bullet}\frac{\mathrm{d}E_i}{\mathrm{d}t} - \frac{E_i}{E_\bullet^2}\frac{\mathrm{d}E_\bullet}{\mathrm{d}t}\right)x_i, \\
&= \sum_{i=1}^{n}\left(\left(\left(\beta_i^I I_i + \beta_i^D D_i + \beta_i^C C_i\right)S - \omega_i E_i\right)\frac{1}{E_\bullet}\right. \\
&\quad \left. - \left(\left(\overline{\beta^I}^I I_\bullet + \overline{\beta^D}^D D_\bullet + \overline{\beta^C}^C C_\bullet\right)S - \overline{\omega}E_\bullet\right)\frac{E_i}{E_\bullet^2}\right)x_i, \\
&= \frac{S}{E_\bullet}\sum_{i=1}^{n}\left(\left(\beta_i^I I_i + \beta_i^D D_i + \beta_i^C C_i\right) - \left(\overline{\beta^I}^I I_\bullet + \overline{\beta^D}^D D_\bullet + \overline{\beta^C}^C C_\bullet\right)\frac{E_i}{E_\bullet}\right)x_i \\
&\quad - \sum_{i=1}^{n}\left(\omega_i - \overline{\omega}\right)x_i\frac{E_i}{E_\bullet}, \\
&= \frac{S}{E_\bullet}\left(\sum_{H\in\{I,D,C\}} H_\bullet \sum_{i=1}^{n}\left(\beta_i^H\frac{H_i}{H_\bullet} - \overline{\beta_H}^H\frac{H_i}{H_\bullet} + \overline{\beta_H}^H\frac{H_i}{H_\bullet} - \overline{\beta_H}^H\frac{E_i}{E_\bullet}\right)x_i\right) - \mathrm{cov}_E\left(x,\omega\right), \\
\frac{\mathrm{d}\overline{x}^E}{\mathrm{d}t} &= \frac{S}{E_\bullet}\left(\sum_{H\in\{I,D,C\}}\left(\mathrm{cov}_H\left(x,\beta_H\right) + \left(\overline{x}^H - \overline{x}^E\right)\overline{\beta_H}^H\right)H_\bullet\right) - \mathrm{cov}_E\left(x,\omega\right). \qquad \text{(S29)}
\end{aligned}$$

If we now focus on the dead hosts, we have

$$\begin{aligned}
\frac{\mathrm{d}\overline{x}^D}{\mathrm{d}t} &= \sum_{i=1}^{n}\left(\frac{1}{D_\bullet}\frac{\mathrm{d}D_i}{\mathrm{d}t} - \frac{D_i}{D_\bullet^2}\frac{\mathrm{d}D_\bullet}{\mathrm{d}t}\right)x_i,\\
&= \sum_{i=1}^{n}\left(\left(\alpha_i\theta\gamma_i I_i - \varepsilon_i D_i\right)\frac{1}{D_\bullet} - \left(\theta\overline{\alpha\gamma}^I I_\bullet - \overline{\varepsilon}D_\bullet\right)\frac{D_i}{D_\bullet^2}\right)x_i,\\
&= \theta\frac{I_\bullet}{D_\bullet}\sum_{i=1}^{n}\left(\alpha_i\gamma_i\frac{I_i}{I_\bullet} - \overline{\alpha\gamma}^I\frac{D_i}{D_\bullet}\right)x_i - \sum_{i=1}^{n}\left(\varepsilon_i - \overline{\varepsilon}\right)x_i\frac{D_i}{D_\bullet},\\
&= \theta\frac{I_\bullet}{D_\bullet}\sum_{i=1}^{n}\left(\alpha_i\gamma_i\frac{I_i}{I_\bullet} - \overline{\alpha\gamma}^I\frac{I_i}{I_\bullet} + \overline{\alpha\gamma}^I\frac{I_i}{I_\bullet} - \overline{\alpha\gamma}^I\frac{D_i}{D_\bullet}\right)x_i - \sum_{i=1}^{n}\left(\varepsilon_i - \overline{\varepsilon}\right)x_i\frac{D_i}{D_\bullet},\\
\frac{\mathrm{d}\overline{x}^D}{\mathrm{d}t} &= \left(\mathrm{cov}_I\left(x,\alpha\gamma\right) + \left(\overline{x}^I - \overline{x}^D\right)\overline{\alpha\gamma}^I\right)\theta\frac{I_\bullet}{D_\bullet} - \mathrm{cov}_D\left(x,\varepsilon\right). \qquad \text{(S30)}
\end{aligned}$$

Finally, in the convalescent hosts, we have

$$\begin{aligned}
\frac{\mathrm{d}\overline{x}^C}{\mathrm{d}t} &= \sum_{i=1}^{n}\left(\frac{\mathrm{d}C_i}{\mathrm{d}t}\frac{1}{C_\bullet} - \frac{\mathrm{d}C_\bullet}{\mathrm{d}t}\frac{C_i}{C_\bullet^2}\right)x_i,\\
&= \sum_{i=1}^{n}\left(\left(\left(1-\alpha_i\right)\gamma_i I_i - \sigma_i C_i\right)\frac{1}{C_\bullet} - \left(\left(\overline{\gamma}^I - \overline{\alpha\gamma}^I\right)I_\bullet - \overline{\sigma}^C C_\bullet\right)\frac{D_i}{D_\bullet^2}\right)x_i,\\
&= \frac{I_\bullet}{C_\bullet}\sum_{i=1}^{n}\left(\gamma_i\frac{I_i}{I_\bullet} - \alpha_i\gamma_i\frac{I_i}{I_\bullet} - \left(\overline{\gamma}^I - \overline{\alpha\gamma}^I\right)\frac{C_i}{C_\bullet}\right)x_i - \sum_{i=1}^{n}\left(\sigma_i - \overline{\sigma}^C\right)x_i\frac{C_i}{C_\bullet},\\
&= \frac{I_\bullet}{C_\bullet}\sum_{i=1}^{n}\left(\frac{I_i}{I_\bullet}\left(\gamma_i - \overline{\gamma}^I - \alpha_i\gamma_i + \overline{\alpha\gamma}^I\right) + \overline{\gamma}^I\frac{I_i}{I_\bullet} - \overline{\gamma}^I\frac{C_i}{C_\bullet} + \overline{\alpha\gamma}^I\frac{C_i}{C_\bullet} - \overline{\alpha\gamma}^I\frac{I_i}{I_\bullet}\right)x_i - \sum_{i=1}^{n}\left(\sigma_i - \overline{\sigma}^C\right)x_i\frac{C_i}{C_\bullet},\\
\frac{\mathrm{d}\overline{x}^C}{\mathrm{d}t} &= \frac{I_\bullet}{C_\bullet}\left(\mathrm{cov}_I\left(x,\gamma\right) - \mathrm{cov}_I\left(x,\alpha\gamma\right) + \left(\overline{x}^I - \overline{x}^C\right)\overline{\gamma}^I - \left(\overline{x}^I - \overline{x}^C\right)\overline{\alpha\gamma}^I\right) - \mathrm{cov}_C\left(x,\sigma\right). \qquad \text{(S31)}
\end{aligned}$$

G Numerical simulations

We explored 8 scenarios. For each, we assume that we have $n = 100$ EBOV strains. The standing genetic variation for the CFR α_i ($i \in \{1, \dots n\}$) is drawn from a Gaussian distribution with mean $\widehat{\alpha} = 0.7$ and standard deviation $\varsigma = 0.1$

We only explored positive correlations between CFR and transmissions rates, consistently with our trade-off hypothesis. We also did not investigate correlations between CFR and *post mortem* elimination rate because we assume that the period over which an unsafe buried body is still a suitable environment for virion survival is independent from the initial number of virions. Finally, we ignored convalescent-related variables received since this component of EBOV transmission is much smaller than the others two.

The description of the 9 scenarios is as follows:

1. No genetic correlation between the CFR α and other traits ("all constant" panel, also shown in the main text).

2. Addition of a negative correlation between α and the rate of end of latency period ω.

3. Addition of a positive correlation between α and the transmission rates β_H ("+bH" panel) that will be kept for the next six scenarios.

4. Addition of a positive correlation between α and the inverse of the latency period ω ("+bH+O" panel).

5. Reversing the correlation between α and ω ("+bH-O" panel).

6. positive correlations between α and β_H, α and ω and α and the inverse of the symptomatic period γ ("+bH+O+G" panel)

7. positive correlations between α and β_H and between α and γ, negative correlation between α and ω ("+bH-O+G" panel)

8. positive correlations between α and β_H and between α and ω, negative correlation between α and γ ("+bH+O-G" panel)

9. positive correlation between α and β_H, negative correlations between α and ω and between α and γ ("+bH-O-G" panel)

Positively and negatively correlated traits were drawn according to the formulas $x_i = \left(\varrho \frac{\alpha_i}{\widehat{\alpha}} + (1-\varrho)\,\xi_i\right)\widehat{x}$ and $x_i = \left(\left(-\left(\max(\alpha) - \widehat{\alpha}\right)\frac{\alpha_i}{\widehat{\alpha}} + \max(\alpha) - \min(\alpha)\right)\frac{\varrho}{\widehat{\alpha}-\min(\alpha)} + (1-\varrho)\,\xi_i\right)\widehat{x}$ respectively, where $\widehat{x}$ the estimated value of $x \equiv \beta_H, \omega, \gamma$ according to Table 1, $\varrho = 0.5$ denotes the strength of the correlation and ξ_i a Gaussian random variable with mean 1 and standard deviation $\varsigma = 0.1$. Initial conditions are given by $S(0) = \frac{\lambda}{\mu} \approx 4.4 \cdot 10^6$ ind and $H_i(0) = 1$ ind for all $i \in \{1, \ldots, n\}$ and all $H \equiv E, I, D, C$.

Results for 8 of the scenarios are shown in Figure S2 (scenario 2 is only shown in the main text for space constraint reasons).

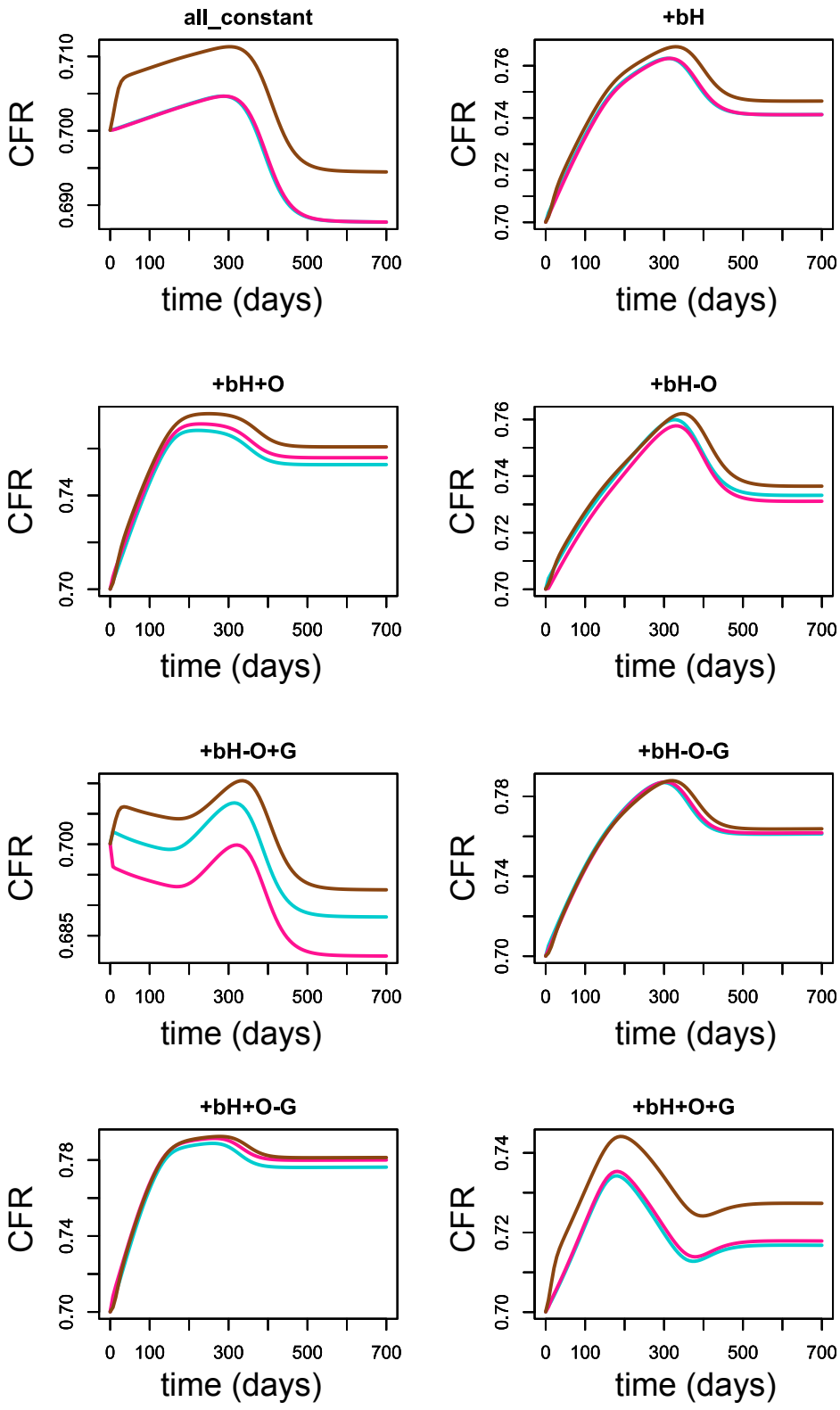

Figure S2: **Short-term evolution of CFR with standing genetic variation**.
The CFR averaged over the exposed individuals ($\overline{\alpha}^E$) is depicted in cyan, over the symptomatic individuals ($\overline{\alpha}^I$) in pink and over the infectious dead bodies ($\overline{\alpha}^D$) in brown.

H Virulence and transmission routes

We have showed that EBOV' reproduction numbers can be split into three additive components that correspond to each of the three transmission routes namely symptomatic (through regular contact with symptomatic individuals), *post mortem* (through contact with unsafe buried infectious dead bodies) and sexual (through sexual contact with convalescent individuals). According to our trade-off assumption, the intensity of each of these components is modulated by virulence: both symptomatic and *post mortem* components always increase with virulence while sexual component is maximum for an intermediate virulence level (unless there is no trade-off, in which case the symptomatic component is constant and the sexual component decreases with virulence), as in Figure S3.

This come from the fact that virulence increases all transmission rates and infectious bodies inflows, while decreasing the convalescent individuals inflow. Virulence then also acts as an investment cursor between the exclusive *post mortem* and sexual transmission routes. It thus appears that the cost of virulence is strictly limited to loss in sexual transmission. Therefore, it is only if the sexual component is the dominant route of the virus' life cycle that this cost can really balances with the overall transmission

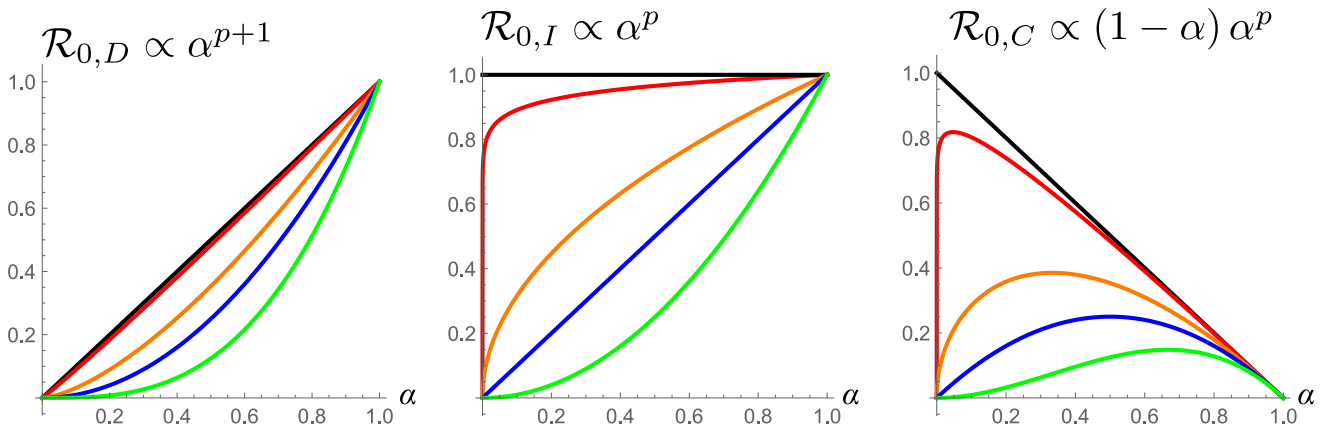

Figure S3: **Relative variation of transmission route component intensity as a function of virulence and trade-off shape.**
Post mortem (left), symptomatic (middle), and sexual (right) transmission components as a function of virulence and trade-off shape ($p = 0$ in black, 0.05 in red, 0.5 in orange, 1 in blue and 2 in green).