

Assessing the effects of quantitative resistance on the life-history traits of sporulating parasites with growing lesions - Math-Stat Supplementary Information

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MS-1 Analytical expression of the sporulation model

Let $\delta = t_0 - t_1$ be the possible delay between the onset of sporulation and lesion formation. Equation (3) in the main text can be expressed as: for all $t \geq t_1$,

$$s(t) = \int_0^t \ell(t + \delta - a)\sigma(a)da.$$

Let $\tau = t + \delta - a$. For all $t \geq t_1 = t_0 - \delta$,

$$s(t) = \int_{\delta}^{t+\delta} \ell(\tau)\sigma(t + \delta - \tau)d\tau.$$

Taking our simple lesion growth model, we have:

$$\ell(t) = \begin{cases} 0 & \text{if } t \leq t_0 < T_1 < T_2, \\ \ell_1(t) = \pi\rho^2(t - t_0)^2 & \text{if } t_0 \leq t < T_1 < T_2, \\ \ell_2(t) = \pi R_1\rho(t - t_0) & \text{if } t_0 < T_1 \leq t < T_2, \\ L = \pi R_1 R_2 & \text{if } t_0 < T_1 < T_2 \leq t, \end{cases}$$

with, for $i = 1, 2$,

$$T_i = t_0 + \frac{R_i}{\rho}.$$

Let

$$s_1(t, T) = \int_{t_0}^{T+\delta} \ell_1(\tau)\sigma(t + \delta - \tau)d\tau, \quad s_2(t, T) = \int_{T_1}^{T+\delta} \ell_2(\tau)\sigma(t + \delta - \tau)d\tau,$$

and

$$s_3(t) = \int_{T_2}^{t+\delta} L\sigma(t + \delta - \tau)d\tau = L \int_0^{t+\delta-T_2} \sigma(a)da.$$

Using these notations, $s(t)$ can be expressed as

$$s(t) = \begin{cases} 0 & \text{if } t \leq t_0 - \delta = t_1, \\ s_1(t, t) & \text{if } t_0 - \delta \leq t < T_1 - \delta, \\ s_1(t, T_1 - \delta) + s_2(t, t) & \text{if } T_1 - \delta \leq t < T_2 - \delta, \\ s_1(t, T_1 - \delta) + s_2(t, T_2 - \delta) + s_3(t) & \text{if } T_2 - \delta \leq t. \end{cases} \quad (\text{S-1})$$

We consider the Rayleigh probability distribution function as a sporulation function, i.e. :

$$\sigma(a) = S \times \frac{a}{\mu^2} \exp\left(-\frac{a^2}{2\mu^2}\right), \quad (\text{S-2})$$

where S is the sporulation capacity, i.e. the maximum number of spores per unit area, and μ is the mode of the distribution i.e. the time at which spore production reaches its maximum value.

Using the Rayleigh cumulative distribution function leads to

$$s_3(t) = LS \left(1 - \exp\left(-\frac{(t + \delta - T_2)^2}{2\mu^2}\right)\right). \quad (\text{S-3})$$

Then, we obtain :

$$\begin{aligned} s_2(t, T) &= S\pi R_1 \rho \left((T + \delta - t_0) \exp\left(-\frac{(t - T)^2}{2\mu^2}\right) - (T_1 - t_0) \exp\left(-\frac{(t + \delta - T_1)^2}{2\mu^2}\right) \right) \\ &+ S\pi R_1 \rho \left(\sqrt{\frac{\pi}{2}} \mu \left(\operatorname{erf}\left(\frac{t - T}{\sqrt{2}\mu}\right) - \operatorname{erf}\left(\frac{t + \delta - T_1}{\sqrt{2}\mu}\right) \right) \right), \end{aligned} \quad (\text{S-4})$$

and

$$\begin{aligned} s_1(t, T) &= S\pi \rho^2 \left(((t + \delta - t_0)^2 + 2\mu^2) \exp\left(-\frac{(T - t)^2}{2\mu^2}\right) - 2\mu^2 \exp\left(-\frac{(t + \delta - t_0)^2}{2\mu^2}\right) \right) \\ &+ S\pi \rho^2 \left(-\sqrt{2\pi} \mu (t + \delta - t_0) \left(\operatorname{erf}\left(\frac{t + \delta - t_0}{\sqrt{2}\mu}\right) + \operatorname{erf}\left(\frac{T - t}{\sqrt{2}\mu}\right) \right) \right). \end{aligned} \quad (\text{S-5})$$

where erf is the Gauss error function.

MS-2 Statistical analyses

The effects of pathogen isolate {BP3, BP6} and host genotype {Bintje, Möwe, Désirée} on the epidemiological parameters of models (1) and (3) were assessed through pairwise comparisons as proposed by ?. The statistical analysis is based on the comparison of two versions of the fitted models that differ in the number of parameters allowed to change with the treatments or modalities. If we consider two treatments M_1 and M_2 the simplest version of the model is a common model CM fitted to the common data while the version with the most free parameters is the case where all the parameters have separate values for each of the two treatments (i.e. separate models SM_1 and SM_2). These models are then compared to intermediate models X in which only some parameters are allowed to differ between treatments. The statistical comparison of the treatments is then

tested through approximated F -tests which allow the determination of parameters and processes that contribute the most to the differences between treatments :

$$F = \frac{[RSS_{CM} - RSS_X]/[df_{CM} - df_X]}{[RSS_{SM_1} + RSS_{SM_2}]/df_{SM}}$$

where RSS is the residual sum of squares and df the degree of freedom of each model.