Coinfection and the Evolution of Parasite Virulence
Author(s): Robert M. May and Martin A. Nowak
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Coinfection and the evolution of parasite virulence

ROBERT M. MAY AND MARTIN A. NOWAK

Department of Zoology, University of Oxford, South Parks Road, OX1 3PS, Oxford, U.K.

SUMMARY

Analyses of the selection pressures acting on parasite virulence are made more complicated when individual hosts can simultaneously harbour many different strains or genotypes of a parasite. Here we explore the evolutionary dynamics of host–parasite associations in which individual hosts can be coinfectcd with many different parasite strains. (We take coinfection to mean that each strain transmits at a rate unaffected by the presence of others in the same host.) This study thus represents the opposite extreme to our earlier work on superinfection in which there is a dominance hierarchy such that only the most virulent strain present in a host is transmitted. For highly diverse populations of parasite strains, we find that such coinfection leads to selection for strains whose virulence-levels lie in a relatively narrow band close to the maximum consistent with the parasite's basic preproductive ratio, $R_0$, exceeding unity.

1. INTRODUCTION

Recently, many papers have been published on the subject of the evolution of parasite virulence (with parasite defined broadly to include viruses, bacteria, and protozoans along with the conventional helminth and arthropod parasites: see May & Anderson 1990; Anderson & May 1991; Nowak 1991; Frank 1992; Antia et al. 1993; Ewald 1993; Yamamura 1993; Bonhoeffer & Nowak 1994; Levin & Bull 1994; Rand et al. 1994; Lipsitch et al. 1995a, b; empirical studies include Bull et al. 1991, 1992; Herre 1993; Ebert 1994; for review articles we refer to Bull 1995; Herre et al. 1995). On the theoretical side, one of the most complicated issues is understanding how parasite diversity within individual hosts alters the selective forces determining virulence. Essentially, parasites compete and evolve at two different levels: within a host and between hosts.

We recently studied the evolution of virulence in mathematical models where already-infected hosts can be 'superinfected' by other parasites (May & Nowak 1994; Nowak & May 1994). There we assumed a competitive hierarchy among the different parasite strains such that a more virulent parasite can infect and 'take over' a host that is already infected by a less virulent strain; multiply-infected hosts transmit only the most virulent of the strains they harbour. Here we analyse the opposite extreme of this scenario. We assume that individual hosts can be 'coinfected' by a large number of different parasites and that there is no competition among different parasites in the same host; each strain produces transmission stages, and hence new infections, at a rate that is unaffected by the presence of any other strains coinfecting its hosts. We thus use the term 'coinfection' to indicate a stable coexistence of different parasites (or strains) in the same host. Hence, the coinfection model describes situations where a host species is infected with strains of a given parasite species, or with a number of different parasite species.

This study of coinfection and our earlier studies of superinfection represent the two opposite extremes in situations where hosts experience multiple infection with many different strains of a parasite. By studying these two extremes, we hope to 'bracket' the more general range of possible situations.

Both these simplified extremes are amenable to analytical understanding. Eventually our aim is to combine the full scenario of multiple infections in a single host with the selection dynamics for evolution within and among hosts. Such studies will mostly rely on computer simulations, and therefore we regard it as important to understand the simple cases first.

In what follows, we first define a simple model for the dynamics of a host–parasite association with coinfection. We then present numerical studies of this system, along with supporting analytic understanding, for the case where all strains have the same transmission rate. Next we extend the numerical studies and supporting analytic approximations to the more general case where more virulent strains have higher transmission rates. We conclude by comparing these results with our earlier studies of superinfection and discuss the implications for evolutionary trends in parasite virulence.

2. A BASIC MODEL FOR COINFECTION

A simple model for coinfection is the following:

$$\frac{dy_i}{dt} = y_i[\beta_i(1-y_i) - u - e_i], \quad \text{with} \quad i = 1, \ldots, n.$$  (1)

There are $n$ strains of parasite. The total population size of hosts is assumed to be held constant by other ecological factors, and may be normalized to unity. The fraction of hosts infected by strain $i$ is given by $y_i$. 

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Several parasites can be present in the same host and so the sum over all $y_i$ will in general exceed the fraction of all hosts that are infected. The infectivity (transmission rate) of strain $i$ is denoted by $\beta_i$. Strain $i$ can infect any host which is not already infected by strain $i$. The infectivity of a strain is unaffected by the presence of other strains in the same host, which indeed represents our definition of ‘coinfection’. Thus $\beta_i y_i(1-y_i)$ is the rate at which new infections with strain $i$ occur.

There is a natural death rate, $u$, and a disease induced death rate, $v_i$, which denotes the average death rates of hosts infected by strain $i$. Given that hosts may simultaneously harbour several parasite strains, we assume that the death rate of an infected host is determined by the most virulent strain present. In a single infection, strain $i$ has virulence $v_i$. We label the strains such that $v_i < v_{i+1}$ for all $i$; thus 1 is the least virulent and $n$ the most virulent strain.

We define $P_i$ as the probability that a host is not infected with a strain more virulent than $i$. That is,

$$P_i = \prod_{j=i+1}^{n} (1-y_j).$$  \hfill(2)

Note that $P_n = 1$ and $P_i = (1-y_{i+1})P_{i+1}$. The fraction of hosts that are uninfected is given by $P_0 = \prod_{i=1}^{n} (1-y_i)$. The average virulence of strain $i$ is now given by

$$v_i = v_n \left(1 - \sum_{j=i}^{n-1} P_j \Delta v_j \right),$$ \hfill(8)

with $\Delta v_j = (v_{j+1} - v_j)/v_n$. From equations (6) and (8) we get

$$v(1-P_0) = v_n \left(1 - \sum_{j=1}^{n-1} P_j \Delta v_j \right) - v_1 P_0.$$ \hfill(9)

It is reasonable to assume that $P_0$ becomes small for large $n$ (this will be proved below). Hence a good approximation is

$$v \approx v_n \left(1 - \sum_{j=1}^{n-1} P_j \Delta v_j \right).$$ \hfill(10)

We now proceed to obtain analytic approximations for the average virulence, $v_\bar{e}$, and for the relative abundances of the various strains, $y_i$ (and thence for $P_i$), as a function of the number of strains originally present, $n$, and other relevant variables. We do this first for the case where $\beta_i$ is the same for all $i$ and second for the more general case where $\beta_i$ increases with increasing $v_i$. These analytic results provide insight into our numerical explorations of the dynamics of the basic model (1)-(3), as summarized below.

3. STRAIN-INDEPENDENT TRANSMISSION RATE, $\beta_i = \text{const}$

We assume we are given the virulence values, $v_i$. All strains have the same transmission rate, $\beta$. We now seek expressions for $y_i$ and $P_i$ in terms of the given $v_i$. Hence, via equation (10), we can calculate $v_\bar{e}$.

Returning to equation (4), we see that the equation for $y_n$ puts a limit on $v_n$, the most virulent strain:

$$y_n \geq 0 \implies v_n \leq v_\beta = \beta - u.$$ 

This upper limit to the virulence spectrum corresponds to the limit $R_0 = \beta/(v_\beta + u) \rightarrow 1$.

More generally, from equation (4) with $\beta_i = \beta$, we get a relation between $y_i$ and $v_\bar{e}$:

$$y_{i+1} - y_i = - (v_{i+1} - v_i)/\beta.$$ \hfill(11)

Substituting from equation (7) in the right hand side of equation (11), we obtain a relation among $y_i$, $P_i$ and $v_\bar{e}$:

$$y_{i+1} - y_i = - P_i (v_{i+1} - v_i)/\beta.$$ \hfill(12)

In the continuous limit, which will represent a good approximation as the spacing between adjacent strains along the virulence axis becomes small, equation (12) becomes

$$[dy(v)/dv] = -P(v)/\beta.$$ \hfill(13)

We need a further relation between $y_i$ and $P_i$ (or $y(v)$ and $P(v)$) to close this system. Such a relation is supplied by the definition of $P_i$, equation (2), which can be rewritten

$$\ln P_i = \ln \left(1 - y_i \right).$$ \hfill(14)
If the individual abundances, \( y_i \), are small (as they will be seen to be for \( n \gg 1 \), below), we may approximate equation (14) by

\[
\ln P_i \simeq - \sum_{j=1}^{n} y_j.
\]

In the continuous limit, this gives

\[
\ln P(v) \simeq - \frac{n}{\Delta} \int_v^{v+} y(v') dv'.
\]

Here we have used the facts that: (i) \( v \equiv v_i \equiv \beta - u \); (ii) there are \( n \) strains in the virulence interval of width \( \Delta \equiv v_i - v_0 \) (where \( v_i = \beta - u \) is the most virulent possible persisting strain, and \( v_0 = 0 \) the least virulent one), so that there are on average \( (n/\Delta) \) strains in an interval of width \( \Delta \). Notice that here, where \( v_0 = 0 \), we have \( \Delta = v_i \); we preserve the notational distinction between \( \Delta \) and \( v_i \), however, because in the more general case when \( \beta \) varies with \( v_i \) (as in the next section) \( v_0 \neq 0 \) and \( \Delta < v_i \).

We now proceed to get a relation between \( P(v) \) and \( v \), from equations (13) and (16), in the continuous limit. Expressions for \( v^- \) and for \( y(v) \) follow easily.

It is convenient to introduce \( Z(v) \equiv \ln P(v) \). Differentiating both sides of equation (16) twice with respect to \( v \), we get

\[
d^2Z/dv^2 = \frac{n}{\Delta} \frac{dy(v)}{dv}. \tag{17}
\]

Substituting from equation (13) on the right hand side, and using \( d^2f/dx^2 = 1/2 (df/dx)^2 \), we arrive at

\[
d^2Z/dv^2 = -2(2n/\beta \Delta)^2 \theta. \tag{18}
\]

Integrating from \( v \) to the maximum value \( v+ = \beta - u \), and noting that \( Z(v_+ = \ln P_+ = 0 \) and \( dZ(v_+)/dv = (n/\Delta) \), we get

\[
(dZ/dv)^2 = (2n/\beta \Delta) (1 - \theta^2). \tag{19}
\]

Re-expressing equation (19) in terms of \( P(v) \) rather than \( Z(v) \), we arrive at

\[
(1/P) (dP/P) = (2n/\beta \Delta)^2 (1 - P)^3. \tag{20}
\]

Figure 1. The average level of virulence versus the number of different parasite strains in the population for the coinfection model given by equations (1-3). The individual parasite strains have randomly assigned levels of virulence ranging from 0 to 1. All parasite strains have the same transmission rate, \( \beta = 2 \). The natural death rate is \( u = 1 \). For different numbers of strains, \( n \), the equilibrium population structure is computed according to equation (4). The figure shows that for large \( n \) there is excellent agreement between the numerical calculations (the points, \( \times \)) and the theoretical curve, given by equation (23).

We now return to equation (10) for \( \bar{v} \), and express it in the continuous limit:

\[
\bar{v} \simeq v_+ \left[ 1 - \int_{v_0}^{v_+} P(v') dv'/v_+ \right]. \tag{21}
\]

Substituting directly from equation (20) for \( Pdv \), we get

\[
\bar{v} \simeq v_+ \left[ 1 - \frac{\beta \Delta}{2 v^+} \right] \left[ 1 - \frac{1}{(1 - P)^3} dP \right]. \tag{22}
\]

Performing the integration, and recalling that \( \Delta = v_+ = \beta - u \), we get

\[
\bar{v} \simeq v_+ \left[ 1 - \left( \frac{\beta \Delta}{2 v^+} \right)^3 \int_{v'}^{v_+} (1 - P)^{-3} dP \right]. \tag{23}
\]

With \( \epsilon = (2\beta^2)/\beta^2 \),

This result, equation (23), agrees well with the extensive numerical simulations summarized in figure 1, especially as \( n \) becomes very large.

Returning to equation (20), we may integrate from \( v = v \) to \( v = v_+ = \beta - u \), to get

\[
\int_{v}^{v_+} \left[ dP/P(1 - P)^3 \right] = (2n/\beta \Delta)^2 \int_{v}^{v_+} \frac{dv}{\theta}. \tag{24}
\]

Here we have defined

\[
\theta = \frac{2n}{\beta \Delta} (1 - v/v_+), \tag{25a}
\]

or, equivalently,

\[
\theta = \frac{2n}{\beta \Delta} (1 - 1/n), \tag{25b}
\]

where \( i \) is the index ‘counting’ the \( n \) persisting strains, from least \( (v_0 = 0) \) to most \( (v_+ = \beta - u) \) virulent. Integrating the left hand side of equation (24) gives

\[
\ln \left[ (1 + (1 - P)^3)/(1 - (1 - P)^3) \right] = \theta. \tag{26}
\]

And thence, after some manipulation,

\[
P(v) = \cosh (\theta/2)^{-2}. \tag{27}
\]

Equation (27) describes the behaviour of \( P(v) \), or equivalently \( P_0 \), as we move down the virulence spectrum, away from values of \( v \) close to \( v_{\text{max}} \) (i.e. values of \( i \) close to \( n \)). \( P(v) \) will remain close to unity so long as \( \theta \) is small, which is to say \( (v_+ - v) \approx \theta \approx n \), or \( 1 - (i/n) \ll n \). This corresponds to a narrow band of strains with virulence-values close to \( v_+ \), representing a fraction of order \( n^{-2} \) of all strains, or a total of order \( n^4 \) of the \( n \) persisting strains. For strains with \( v \)-values below this narrow band, the probability that they are the most virulent in a given host becomes very small; \( P(v) \approx 4e^{-\theta} \), with \( \theta > 1 \) for \( v \)-values not close to \( v_+ \), for \( n > 1 \). In particular,

\[
P_0 \approx 4 \exp \left[ -2n(\beta - u)/\beta \right]. \tag{27a}
\]

This, incidentally, justifies our earlier approximation that \( P_0 \ll 1 \) for \( n \gg 1 \).

These insights translate into a corresponding understanding for the patterns of relative abundance of the various strains, \( y(v) \). Equation (16) gives us \( y(v) = \Delta/n \) \( d \ln P/vdv \), or, using equation (25), \( y(v) = \frac{1}{n} \frac{dP}{\ln P} \). Thence equation (27) gives

\[
y(v) = \frac{2 \Delta/n \theta}{1 - \tanh (\theta/2)}. \tag{28}
\]

Unless we are very close to \( v_+ \), \( y \approx \frac{2}{n} \beta - u \theta \). Within a narrow band of \( v \)-values close to \( v_+ \), \( y \approx (v_+ - v) \approx \beta - u \), we have \( \theta \) small, and \( y \) falls from \( (2\Delta/n) \theta \)
212 R. M. May and M. A. Nowak Coinfection and virulence

Figure 2. Equilibrium distributions of the coinfection model as specified by equations (1–3). The individual parasite strains have randomly assigned levels of virulence ranging from 0 to 1. All parasite strains have the same transmission rate, $\beta \equiv 2$. The natural death rate is $u = 1$. (a) $n = 20$ strains of parasite. The figure shows the frequency of hosts, $y_i$, infected by parasite strain $i$, which has virulence $v_i$. The most virulent strain is the least abundant, but all strains survive (as long as their virulence is smaller than 1). We obtain an average virulence, as defined by equation (5), of $\bar{v} = 0.5856$ and a fraction of uninfected hosts of $P_0 = 0.0397$. The frequency of hosts infected by the least virulent parasite is $y_1 = 0.2178$. The analytic approximations of equations (23), (27), and (28) give $\bar{v} \approx 0.55$, $P_0 \approx 0.04$, and $y_1 \approx 0.22$, respectively. (b) $n = 200$ strains of parasite. We obtain an average virulence of $\bar{v} = 0.863$ and a fraction of uninfected hosts of $P_0 = 2.08 \times 10^{-6}$, and for the least virulent parasite $y_1 = 0.0684$. Here the corresponding analytic approximations are $\bar{v} \approx 0.86$, $P_0 \approx 2.9 \times 10^{-6}$, and $y_1 \approx 0.071$. (c) The basic reproductive ratio, $R_0$, as a function of virulence.

Figure 3. Equilibrium distribution of the coinfection model with a trade-off between transmission rate $\beta_i$ and virulence $v_i$. We chose $\beta_i = 5v_i/(1 + v_i)$. This gives a one humped curve for the basic reproductive rate as a function of virulence. The natural death rate is $u = 1$. The parasites have levels of virulence uniformly distributed between 0 and 3. We observe that all parasite strains persist with a level of virulence above a certain minimum $v_{\min}$ and the maximum level of virulence that corresponds to $R_0 = 1$, i.e. $v = (3 + \sqrt{5})/2$. (a) $n = 20$ parasite strains. We obtain an average virulence of $\bar{v} = 1.9246$ and a fraction of uninfected hosts of $P_0 = 0.5716$. (b) $n = 200$ parasite strains. We obtain an average virulence of $\bar{v} = 2.3039$ and a fraction of uninfected hosts of $P_0 = 0.1952$. The persisting strains occupy a band of virulence-values of width $\Delta v = 0.87$; the roughly approximate equation (39) gives $\Delta v \approx 0.86$ (note that here we should put $\Delta = 3$ for $n = 200$). (c) The basic reproductive ratio, $R_0$, as a function of virulence.

4. TRANSMISSION RATE INCREASING WITH VIRULENCE

We now turn to the more general case where the transmission rate for strain $i$ is not constant, but increases with increasing virulence, $v_i$.

Specifically, we assume a functional relation between $\beta(v)$ and $v$ of the form

$$\beta(v) = \beta(v)/(\gamma + v).$$

Here $\beta$ is a constant. The results of the previous section are recovered as the limit $\gamma \to 0$. From equation (1) or equation (4) we can see that the basic reproductive ratio for strain $i$, $R_{0,i}$, is now

$$R_{0,i} = \beta e/[(\gamma + v)(u + v)].$$

$R_0$ is thus maximized by the strain with virulence $v_m = (\gamma u)/(\gamma + u)$, and is $R_{0,\text{max}} = \beta/(u + \gamma)^2$. The minimum and maximum virulence-values for strains that have the potential to maintain themselves within the host population, $v_-$ and $v_+$, respectively, are given by setting $R_{0,i} = 1$:

$$v_- = (\beta - u - 4\gamma)^1/2.$$
equation (16) (which relate \( P(v) \) and \( y(v) \)) do not involve \( \beta_i \), and so remain valid. The difficulties caused by a non-constant \( \beta_i \) (or \( \beta(v) \)) arise in the steps which in the previous section took us from equation (11) to equations (12) and (13). As we shall now see, once \( \beta(v) \) varies with \( v \) the second relation between \( P(v) \) and \( y(v) \) is substantially more complicated than the simple derivative with respect to \( v \):

\[
\frac{dy}{dv} = -P/\beta(v),
\]

which contrast with figure 2.

When \( n > 1 \), we can take the continuous limit to get

\[
\frac{dy}{dv} = \left[ \frac{1}{\beta(v)} \right] \left[ -P(v) \right] \frac{d\beta(v)}{dv}.
\]

This approximation gives an intuitive feeling for the numerical results of figure 3, and shows that in the limit \( n \gg 1 \) only a relatively narrow band of strains persist (a fraction of order \( n^{-2} \), or a total of order \( n^2 \), of the original set of \( n \) strains with \( v \)-values such that \( R_0 > 1 \)).

This crude approximation also provides a rough estimate of \( P_0 \), the fraction of uninfected hosts, for systems of this kind with \( n \gg 1 \). For such a system, equation (16) gives

\[
\ln P_0 \approx \left\{ -\frac{(n/\Delta)^2}{v_{+}-v_{-}} \right\} \frac{d[y(v')dv']}{\beta(v)}.
\]

Following the very rough approximation outlined above, we can now write:

\[
y(v) \approx \left(2\Delta/n\beta(v)^2\right)^{1/2} \left[ \frac{2}{\sinh(\theta/2)} - \ln \left( \beta(v)/\beta(v) \right) \right]
\]

in equation (40), to arrive (after considerable manipulation) at:

\[
P_0 \approx e^{-\phi \cosh^{-2}(v)} v_{+} - v_{-} \frac{n}{e^v - 1}
\]

with \( v_{+} = (v_{+} + v_{-})/2 \). This fraction is roughly independent of \( n \) in the limit \( n \gg 1 \). As \( n \) increases, the width of the band of surviving strains scales as \( n^{-\phi} \), with the abundance of each strain scaling roughly as \( n^{2\phi} \); hence the overall probability for a host to escape infection tends to some \( n \)-independent constant. Contrast this to the constant-\( \beta \) case of the previous section, where all \( n \) strains coexist, so that \( P_0 \) scales as \( e^{-(c/\theta)} \) in the limit of large \( n \) (see equation (27a)).

5. DISCUSSION

Suppose we are dealing with a situation where more and more strains appear, by mutation, as time goes on. From the preceding analysis, we would expect the persisting strains to be confined to an ever narrower band of \( v \)-values, of width \( \sim n^{-\phi} \), just below the critical value, \( v_{+} \), for which \( R_0(v_{+}) = 1 \) (except in the special
case when all strains have the same transmission rate, and consequently all persist; see figure 2). The total number of strains, however, increases as $n^3$ as $n$ increases. If new mutations appear at a roughly constant rate, $\lambda$, we have $n = \lambda T$ after time $T$, and consequently the total number of persisting strains is expected to increase with $T$ as

$$N(T) \sim T^3.$$  \hspace{1cm} (43)

This analytic expectation is confirmed by the numerical studies illustrated in figure 4.

These findings provide an interesting contrast with our earlier studies of ‘superinfection’ models. For superinfection, we assumed a rigorous dominance hierarchy, so that only the most virulent strain in a given host was transmitted. As explained earlier (Nowak & May 1994; May & Nowak 1994), this resulted in effective ‘limits to similarity’ among strains, which emerged from the dynamics of the model (see also Tilman et al. 1994), and which meant that many new mutants could not establish themselves; if they did, they tended to displace existing strains. Consequently, the superinfection models showed the total number or diversity of strains rising only slowly with time (i.e. with number of mutants): $N_{\text{superinfection}} \sim \ln T$. On the other hand, these same limits to similarity resulted in a wide range of virulence-values persisting in the system. By contrast, the present coinfection models have no limits to similarity, and surviving strains are packed ever closer as time goes on (see figure 4). These coexisting strains are, however, constrained to lie in a very narrow band of virulence-values, close to the maximum consistent with persistence ($R_0=1$). This effectively represents competitive exclusion of most strains; less virulent strains cannot realize their potentially superior $R_0$-values, because hosts are killed by more virulent strains which have higher transmission rates, although lower $R_0$-values.

Our simple models for superinfection (transmission only by the most virulent strain within a host) and for coinfection (all strains transmit, albeit at different rates, independent of other strains present in the host) represent extremes that are likely to bracket the reality of polymorphic parasites. In both cases, we find the anticipated tendency towards the predominance of strains which are significantly more virulent than those which maximize parasite reproductive success in singly infected hosts. The numbers and virulence range of persisting strains, however, depend on the details: coinfection tends to favour a larger number of coexisting strains, but more closely grouped around a maximum virulence level, than does superinfection. There are suggestive parallels with notions of ‘scramble’ (coinfection) and ‘contest’ (superinfection) in ecological theory (Begon et al. 1986).

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**Figure 4.** The number of surviving strains, $s$, versus the total number of strains which have been generated by mutation, $n$ ($n = \lambda T$, where $\lambda$ is the mutation rate, and $T$ the elapsed time), for the coinfection model assuming a trade-off between virulence and transmission rate. As for figure 3 we have $\beta_i = 5n_i/(1+n_i)$; the natural death rate is $u = 1$. **Proc. R. Soc. Lond. B (1995)**


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