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Journal of Theoretical Biology 288 (2011) 1–8

Contents lists available at ScienceDirect

Journal of Theoretical Biology

journal homepage: www.elsevier.com/locate/yjtbi

The population dynamical consequences of density-dependent prophylaxis

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ARTICLE INFO

Article history:
Received 7 February 2011
Received in revised form
18 July 2011
Accepted 28 July 2011
Available online 5 August 2011

Keywords:
DDP
Mathematical model
Population cycles
Host-pathogen
Time delay

ABSTRACT

When infectious disease transmission is density-dependent, the risk of infection will tend to increase with host population density. Since host defence mechanisms can be costly, individual hosts may benefit from increasing their investment in immunity in response to increasing population density. Such "density-dependent prophylaxis" (DDP) has now indeed been demonstrated experimentally in several species. However, it remains unclear how DDP will affect the population dynamics of the host–pathogen interaction, with previous theoretical work making conflicting predictions. We develop a general host–pathogen model and assess the role of DDP on the population dynamics. The ability of DDP to drive population cycles is critically dependent on the time delay between the change in density and the subsequent phenotypic change in the level of resistance. When the delay is absent or short, DDP destabilises the system. As the delay increases, its destabilising effect first diminishes and then DDP becomes increasingly stabilising. Our work highlights the significance of the time delay and suggests that it must be estimated experimentally or varied in theoretical investigations in order to understand the implications of DDP for the population dynamics of particular systems.

1. Introduction

Given the ubiquity of parasites and pathogens in nature, and the fitness costs associated with disease, there is a clear advantage to the host in investment in defence. However, it is well established that the activation and deployment of the immune system may be costly (e.g. McKean et al., 2008; Schmid-Hempel, 2003) and indeed a significant part of the disease that many infectious agents cause results from immuno-pathology (Graham et al., 2005; Long et al., 2008; Moret and Schmid-Hempel, 2000; Sadd and Siva-Jothy, 2006). In addition, there is good evidence that there are evolutionary costs to the maintenance of defence in the absence of parasites and pathogens (e.g. Boots and Begon, 1993; Kraaijeveld and Godfray, 1997). Hence, we would expect natural selection to favour individuals that invest more when there is the greatest threat of disease. Individuals should benefit from tailoring their allocation of resources to immunity in order to match the perceived risk of exposure to disease.

If transmission is positively density-dependent (Anderson and May, 1979; Ryder et al., 2005, 2007), the risk of infection may increase at high density leading to the idea that it may be optimal to invest more in defence in crowded conditions (Barnes and Siva-Jothy, 2000; Wilson and Reeson, 1998; Wilson et al., 2002). There is now experimental evidence of such "density-dependent prophylaxis" (DDP) in a number of systems, with further evidence coming from comparative studies of social and solitary species (Barnes and Siva-Jothy, 2000; Cotter et al., 2004; Hochberg, 1991a; Reeson et al., 1998; Wilson and Reeson, 1998; Wilson et al., 2002). For example, larvae of both the Oriental armyworm *Mythimna separata* and the African armyworm *Spodoptera exempta* show increased viral resistance when reared at high population densities (Kunimi and Yamada, 1990; Reeson et al., 1998). Mealworm beetles (*Tenebrio molitor*) reared at high larval densities show lower mortality when exposed to a generalist entomopathogenic fungus, compared to those reared singly (Barnes and Siva-Jothy, 2000). Similarly, Wilson et al. (2002) found that desert locusts (*Schistocerca gregaria*) reared under crowded conditions were significantly more resistant to an entomopathogenic fungus than solitary locusts. Furthermore, a recent study on adult bumble-bee workers (*Bombus terrestris*) concluded that there is rapid plasticity in immunity levels dependent on social context (Ruiz-González et al., 2009). This demonstration of DDP in adults suggests that it may be a widespread phenomenon, and considerably broadens its potential significance. It is therefore important to examine the impact that DDP may have on the population dynamics of both the host and the parasite.

There has been some theoretical examination of the effect of DDP on host–parasite population dynamics. White and Wilson (1999)

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doi:10.1016/j.jtbi.2011.07.029

used a discrete-time model, representing non-overlapping insect generations, and found that if the density-dependent effect is sufficiently small, it stabilises the dynamics. Reilly and Hajek (2008) developed a framework with a continuous-time model for host and pathogen within the season and a discrete-time map between seasons with a model structure related to gypsy moth–virus interactions. In contrast to White and Wilson (1999), they reported that DDP has a destabilising effect on the population. Here, we present a general continuous-time model framework that allows the effects of DDP to be understood in more detail. There is a well established literature on continuous models (e.g. Anderson and May, 1981; Bowers et al., 1993; White et al., 1996), so a continuous framework is used here to ensure that comparisons can be drawn with other studies. Our model enables us to produce specific and widely applicable conclusions. The aim is to thoroughly examine the implications of DDP for population dynamics and reconcile the current differences in the predictions of the theoretical studies.

2. The model

Our aim is to produce a general theoretical framework and we therefore choose a classic model framework for representing hosts infected by free-living stages. Much of the evidence for DDP has been found in invertebrate systems and therefore we use a baseline model without acquired immunity. We examine the effects of DDP on the stability of the system by examining the likelihood of population cycles. Our framework is an extension of Anderson and May's (1981) Model G that includes self-regulation of the host (Bowers et al., 1993). The Bowers et al. (1993) model was developed to investigate the possible role of pathogens in the cyclic dynamics of forest insect pests. We consider a system in which the host population is composed of susceptibles, with density X, and infecteds, with density Y (total density $H=X+Y$), and with a free-living pathogen with density of infective stages W. The dynamics are represented by the following system of differential equations:

$$\frac{dH}{dt} = rH\left(1-\frac{H}{K}\right)-\alpha Y, \tag{1}$$

$$\frac{dY}{dt} = \beta W(H-Y)-(\alpha+b)Y, \tag{2}$$

$$\frac{dW}{dt} = \lambda Y-\mu W. \tag{3}$$

Here we choose to use the differential equation for total host density (Eq. (1)), but we could interchange this with one for the susceptible host density (Eq. (4)). For clarity, the model in terms of X, Y and W consists of Eqs. (2) and (3) together with:

$$\frac{dX}{dt} = (r+b)(X+Y)-bX-r\frac{(X+Y)^2}{K}-\beta WX. \tag{4}$$

The model assumes that host self-regulation acts on birth rate and that both susceptible and infected hosts can die naturally. Susceptible hosts can become infected through contact with free-living infective stages of the pathogen, and once infected experience additional mortality due to the disease. Infected hosts also release infective stages at a constant rate and these stages are lost through natural decay. Descriptions of the parameters in the model are given in Table 1. We have used as our reference parameter values those from Bowers et al. (1993). The effective rate of production of infective stages, λ, is large in relation to the other rate parameters because pathogens are typically highly productive (Anderson and May, 1981). Throughout this study, units of time are years and units of abundance are individuals per unit area.

Under DDP, when host density H is high, individuals invest more in resistance mechanisms, and therefore the transmission rate of the disease is reduced. To represent this density-dependent response, we modify the above model by changing β from a constant parameter to a density-dependent term. For simplicity, we take β to be a simple linear function that decreases as $H(t)$ increases:

$$\beta = \beta_0\left(1-\frac{p}{100\,K}H(t)\right). \tag{5}$$

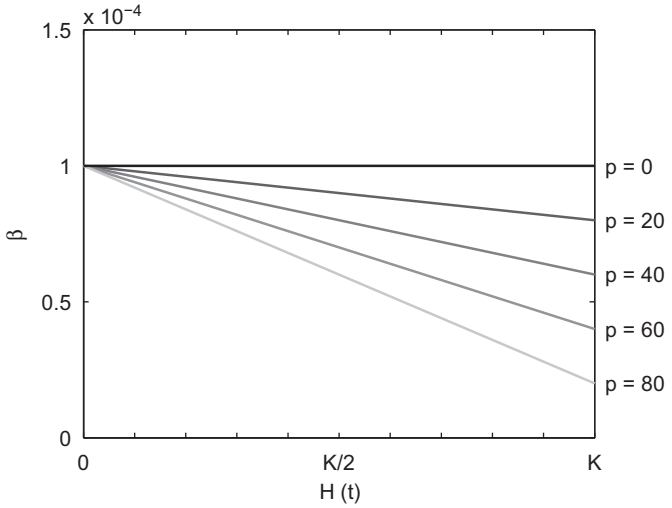

Fig. 1. The disease transmission rate β is a function of $H(t)$. This figure shows β for DDP of varying strengths, i.e. different p values. The horizontal line ($p=0$) represents no prophylactic response.

Table 1
Model parameter definitions. Values of the parameters that remain unchanged for all figures are: $r=1$, $K=1$ and $\beta_0=0.0001$. Units of time are years and units of abundance are individuals per unit area; see Bowers et al. (1993) for details.

Parameter	Meaning
r	Intrinsic rate of net increase of the host (birth rate – death rate b)
K	Host carrying capacity
α	Rate of disease-induced mortality
β	Transmission coefficient of the disease
b	Natural host death rate
γ	Recovery rate of the host (included in an extension of the model: see Discussion)
λ	Rate at which an infected host produces infective stages of the pathogen
μ	Decay rate of the infective stages of the pathogen
p	Measure of the reduction in β caused by DDP
β_0	Transmission coefficient of the disease when there is no DDP
τ	Delay in onset of DDP, as a proportion of the average host lifespan ($1/b$)

Here β_0 is a constant and p represents the percentage reduction in β caused by the prophylactic response when $H(t)=K$. For example, when $p=20$, there is a 20% reduction in β at $H(t)=K$ (see Fig. 1). Note that as $H(t)\le K$, the function β is always non-negative.

3. Population dynamics

The model framework (Eqs. (1)–(3)) has three steady states: the trivial state ($H=0$, $Y=0$, $W=0$), which is always unstable since we assume $r>0$, the disease-free state ($H=K$, $Y=0$, $W=0$) and an infected state (H^*, Y^*, W^*) where

$$Y^*=\frac{r}{\alpha}H^*\left(1-\frac{H^*}{K}\right),$$

$$W^*=\frac{\lambda}{\mu}Y^*$$

and H^* is a solution to the cubic equation

$$(H^*)^3\left(\frac{pr}{100\alpha K^2}\right)-(H^*)^2\left(\frac{r}{\alpha K}+\frac{pr}{100\alpha K}-\frac{p}{100\,K}\right)+H^*\left(\frac{r}{\alpha}-1\right)+\frac{\mu(\alpha+b)}{\lambda\beta_0}=0. \quad (6)$$

This cubic equation always has one negative root, which is not ecologically relevant. The two roots that remain can both be complex, in which case there is pathogen extinction. Otherwise there are two positive, real roots. In most cases, one is less than K and one is greater than K, the latter not being relevant. Both can be greater than K, so neither is relevant: in this case pathogen extinction occurs. For some parameters, both roots are less than K. This means that both are potentially relevant to ecological applications. However, the larger root corresponds to a steady state that is always unstable. We focus on the smaller of the two roots when this case arises (see Appendix A for further discussion).

The basic reproduction rate of the pathogen is

$$R(X)=\frac{\lambda\beta_0\left(1-\frac{p}{100}\frac{X}{K}\right)X}{\mu(\alpha+b)}.$$

The maximum of this, denoted by R_{max}, depends on the strength of DDP as follows:

$$R_{max}=\begin{cases}R(X=K) & \text{for } p<50,\\ R(X=50\,K/p) & \text{for } p\ge 50.\end{cases}$$

Pathogen extinction occurs for $R_{max}<1$. R_{max} decreases as p increases, so DDP makes it more difficult for the disease to persist. (See Appendix A for further details.)

For certain parameter values the infected state is unstable, and then one expects population cycles of host and pathogen to occur (Anderson and May, 1981; Bowers et al., 1993; White et al., 1996). To investigate the effect of DDP on the population dynamics, we explore the boundary in parameter space between the occurrence of cycles and the endemic equilibrium being stable.

4. Results

We examine how DDP affects the propensity of cycles in disease parameter space. Fig. 2(a) shows $\alpha-\lambda$ parameter space partitioned into the regions where cycles and no cycles occur. Parameters α and λ are key to the characterisation of the disease, since α is the disease-induced mortality rate, and λ is the rate at which an infected host produces infective stages of the disease. When there is no DDP ($p=0$), the boundary is equivalent to that calculated in Bowers et al. (1993). As the strength of the prophylactic response increases (p increases), the parameter region giving cycles becomes larger, and so the system is destabilised. We therefore conclude that DDP that depends on current host density acts to induce cycles.

5. Delay in onset of DDP

Thus far we have incorporated DDP by setting the transmission rate of the disease to be a function of current host density. In reality, there is likely to be a delay between the assessment of density and the subsequent adjustment in the investment in defence. Experimental evidence indicates that this delay may be short, with DDP being elicited rapidly in adults (Ruiz-González et al., 2009), or relatively long, with early instar density determining the level of defence in later instars or adults (e.g. Reeson et al., 1998). Previous

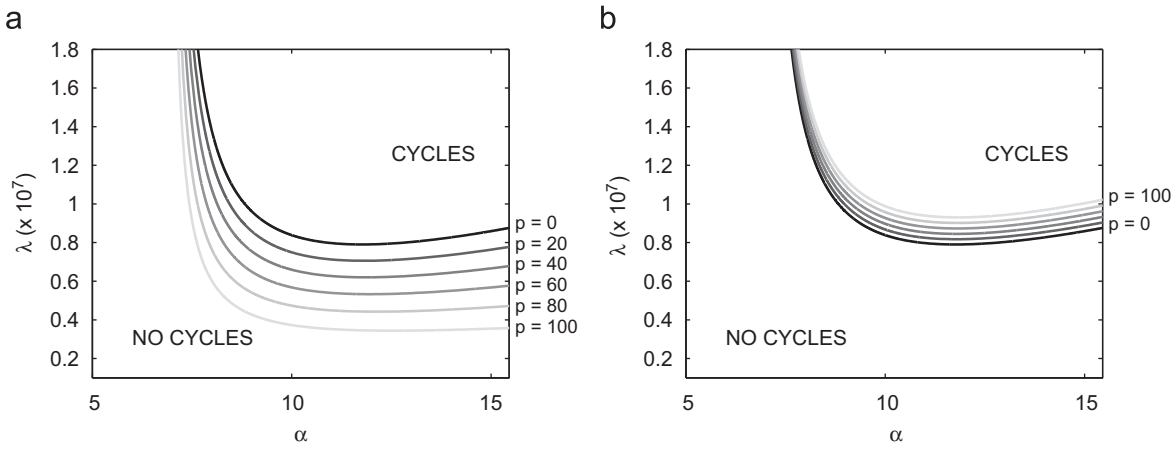

Fig. 2. The divisions in $\alpha-\lambda$ parameter space between cyclic behaviour and no cycling, for a series of p values. In (a) there is no delay ($\tau=0$); in (b) there is a within generational delay ($\tau=0.99$). For the $p=0$ case, as we have no delay term, we can find the boundary between the two regions by consideration of the Routh–Hurwitz stability criteria. (With the characteristic equation in the form $z^3+Az^2+Bz+C=0$, cycles occur when $AB-C<0$; this partitions parameter space.) However, with $p\neq 0$, the model comprises delay differential equations, and the characteristic equation can no longer be solved algebraically. Instead, we take a point on the $p=0$ curve and use this as a starting point for numerical continuation in p up to a particular value of p, for instance $p=20$, tracking the passing of eigenvalues across the imaginary axis. Once a point on the $p=20$ boundary curve is obtained, we change to numerical continuation in α, keeping p fixed. In this way, we can trace the stability boundary curves through parameter space. In this figure, $b=3.3$ and $\mu=3$.

theoretical studies (White and Wilson, 1999; Reilly and Hajek, 2008) include a delay (implicitly or explicitly), but only consider a single fixed delay length. Our aim is to examine in detail how the delay may affect the population dynamics. To include the delay in DDP in our model, we change the dependence on $H(t)$ in Eq. (5) to a dependence on $H(t-\tau/b)$, with delay τ/b. Here, the parameter τ represents the delay as a proportion of the average lifespan of the host ($1/b$), and is therefore between 0 and 1.

Fig. 2(b) shows the results when the proportional time delay $\tau=0.99$. At this time delay, increases in the strength of DDP act to reduce the size of the region of parameter space that gives rise to population cycles, and therefore DDP stabilises the system. As the time delay is increased there is a transition from the situation where DDP has a destabilising effect (Fig. 2(a)) to one where DDP has a stabilising effect (Fig. 2(b)). A change in the time delay can cause the effect of DDP to be reversed. Therefore a key new result is that the effect of DDP depends critically on the length of the delay.

In order to examine the effects of changing the time delay in more detail, we look at the interactions between τ and other parameters in the model. Non-dimensionalisation reveals that there are only three independent parameter groupings, in addition to p and τ. Variations in these parameter groupings can be considered via changes in α, μ and λ (see Appendix B for mathematical details). Figs. 3 and 4 show the boundaries in parameter space between regions of cycles and no cycles, for different parameter combinations and different strengths of the DDP response. Cycles occur for low values of the pathogen decay rate (Fig. 3(a)) and for high values of the rate at which infected hosts produce infective stages of the pathogen (Fig. 3(b)). These results support previous findings that did not involve a prophylactic response or a time delay (Anderson and May, 1981; Bowers et al., 1993; White et al., 1996), but also emphasize how the region of parameter space giving rise to cycles is modified by DDP. Additionally, intermediate values of disease-induced mortality favour cycles, provided the time delay before the onset of DDP is not large (Fig. 4).

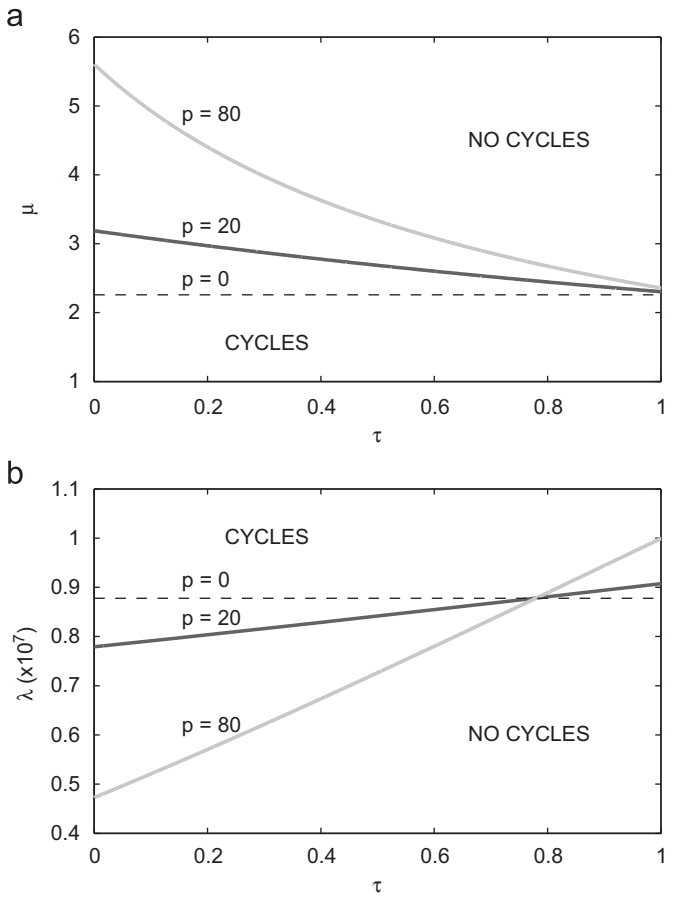

Fig. 3. The effects of the parameters (a) μ and (b) λ on the transition to cyclic dynamics. For each figure, one parameter is varied and others are fixed. Reference values: $\lambda=8\times10^6$, $\mu=3$, $\alpha=15.5$ and $b=3.3$. In each plot, the curves for two values of p are depicted, plus the curve for $p=0$. In this way, the effects of changing both p and τ are shown, so that conclusions can be drawn about how both the strength of prophylaxis and the length of delay affect the population dynamics. In (a), there are cycles below each line and no cycles above; in (b), there are cycles above each line and no cycles below. The time delay τ is expressed as a proportion of the average lifespan of the host, ($1/b$).

Figs. 3 and 4 additionally allow an examination of the effects of the delay τ on the population dynamics. There is a consistent trend that as the time delay τ increases, the parameter region in which cycles are produced diminishes. Thus increasing the delay stabilises the system. These figures also clarify the effects of increasing the strength of DDP (increasing p). The value of the delay at which the lines where $p=20$ and 80 intersect is significant. When τ is below this value, an increase in the DDP strength p destabilises the population; when τ is above the intersection value, an increase in p stabilises the population. This corresponds to a transition from a pattern such as that seen in Fig. 2(a) to that in Fig. 2(b). The delay at which the curves intersect does have a very slight dependence on the p values chosen, but this is negligible for practical purposes (less than 0.2%).

In summary, for short delays, an increase in the strength of DDP is destabilising, and can significantly expand the parameter region over which population cycles are exhibited. As the delay increases, this destabilising effect of DDP is reduced, until a critical delay is reached. For delays longer than this critical value, an increase in the strength of DDP is stabilising. As the delay increases, the extent of this stabilising effect increases.

Fig. 4 indicates how the dynamics are affected by changing underlying model parameters. As pathogen production λ increases, the parameter region giving cycles becomes larger, for both p values (compare Fig. 4(a)–(c)). In contrast, as pathogen decay μ increases, the region giving cycles becomes smaller (compare Fig. 4(d), (b) and (f)). Therefore, increasing the rate at which an infected host produces infective stages of the pathogen destabilises the dynamics, whereas increasing the pathogen decay rate is stabilising. In addition to studying the effects of changing the disease parameters, we also look at changing the natural host death rate b. Increasing b reduces the average lifespan of the host. As the host death rate increases, the region of cycles becomes smaller, and therefore the system is stabilised (compare Fig. 4(b) and (e)). This figure shows that the critical point where the $p=20$ and 80 lines intersect is parameter-dependent: it increases as b gets larger and as μ gets smaller. However, it is relatively insensitive to changes in λ. The implication of this is that for high pathogen decay rates and small host death rates (i.e. long lifespan), the effect of increasing the strength of DDP reverses at time delays that are relatively short as a proportion of the average host lifespan.

Typical population dynamics for parameters in the cycling region are shown in Fig. 5. Cycles arise because as host density increases, an epidemic is triggered, and there is a rapid increase in pathogen numbers. This causes an increase in infection, and a subsequent fall in host density. This leads to a decline in pathogen numbers, allowing host density to increase once again. For a fixed parameter set, an increase in the level of DDP can change the nature of the cycles generated (Fig. 5). For all other parameters fixed, changing the DDP strength p moves the boundary of cycles. Changing the boundary so the point in parameter spaces lies deeper within the cycle region tends to increase both the period and amplitude of the cycles (Anderson and May, 1981).

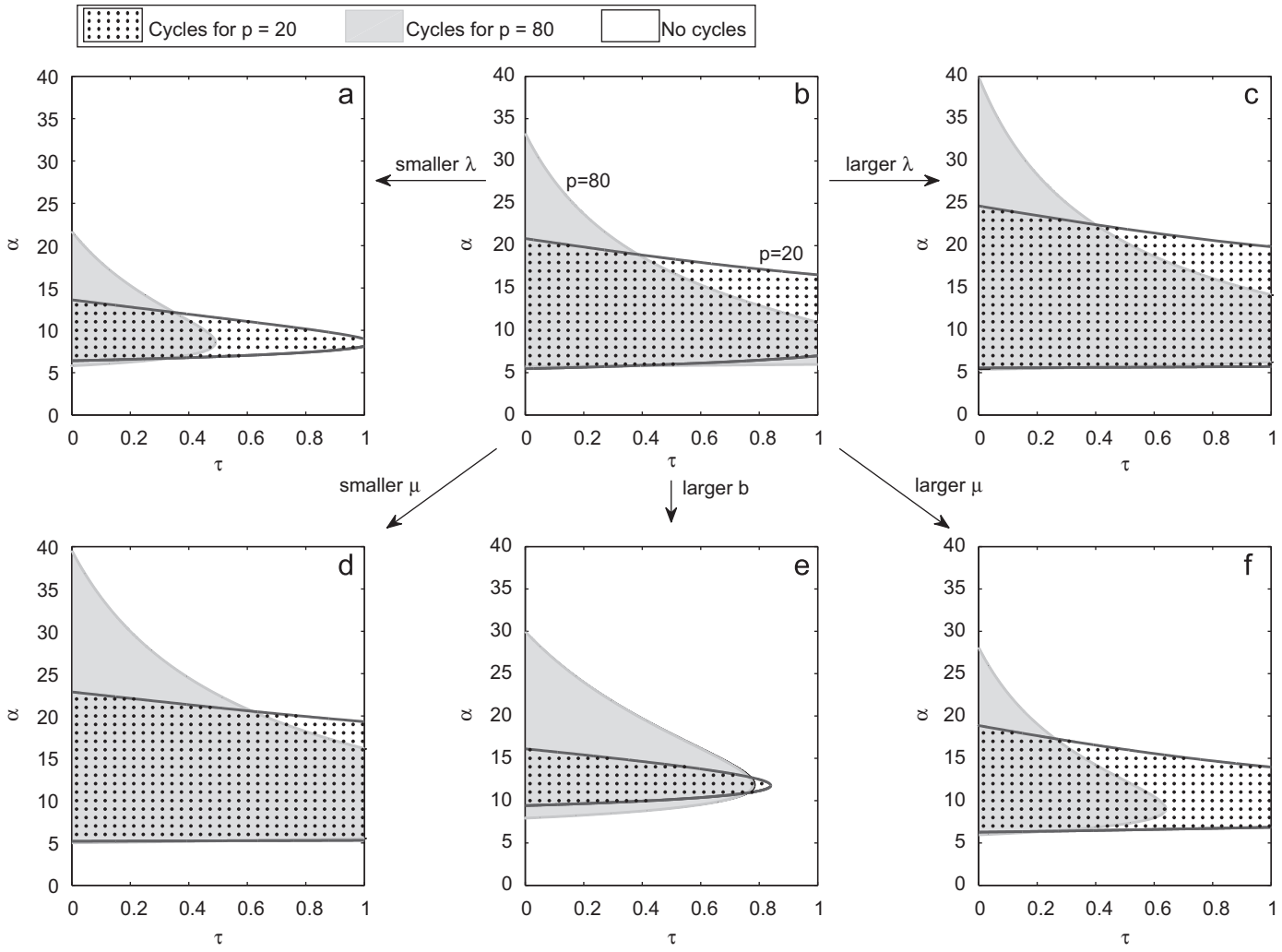

Fig. 4. The effects of parameter α on the transition to cyclic dynamics, and how these change when other parameters are varied. For (b) the fixed parameters are $\mu=3$, $\lambda=8\times10^6$ and $b=1.65$. The remaining panels show the results of changing each of these parameters in turn from this reference parameter set. Parameter values: (a) $\lambda=5\times10^6$; (c) $\lambda=10\times10^6$; (d) $\mu=2$; (e) $b=3.3$; (f) $\mu=4$. Note that the value of b in (e) is the value used in previous figures. The time delay τ is expressed as a proportion of the average lifespan of the host, $(1/b)$. The regions of cycles for $p=20$ are dotted black and the regions of cycles for $p=80$ are shaded grey.

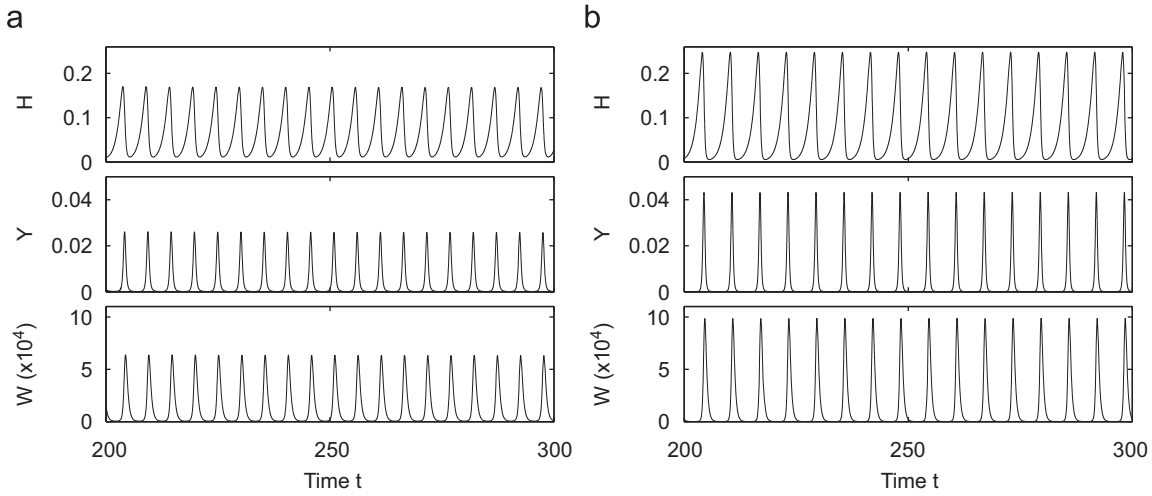

Fig. 5. Cyclic dynamics at equilibrium. Parameter values: $\tau=0.33$, $\alpha=14$, $\lambda=1\times10^7$, $b=3.3$, $\mu=3$ and (a) $p=20$, (b) $p=80$. The cycles in (b) are of higher amplitude and have a longer period. These simulations are produced by MATLAB using the delay differential equation solver dde23. Solutions are shown after running for 200 time units to ensure decay of transients. The initial conditions were $H=0.2$, $Y=0.01$ and $W=1\times10^2$, but the long-term dynamics shown are not sensitive to initial conditions.

6. Discussion

Density-dependent prophylaxis (DDP) is hypothesised to be a widespread phenomenon in natural systems (Wilson and Reeson, 1998). However, the impact of DDP on the population behaviour of outbreaking species is yet to be critically evaluated (Klemola et al., 2007). In this study we develop a theoretical framework to explore the population dynamical impact of DDP. We have shown that increasing the strength of the prophylactic response can be either stabilising and destabilising, depending on the delay between the assessment of density and the adjustment in resistance. When the delay is absent or short, DDP is destabilising; as the delay increases, its destabilising effect diminishes and, once a threshold in the delay is exceeded, it becomes increasingly stabilising. This highlights the importance of the delay and indicates that it is essential to either estimate the delay in natural/laboratory systems or vary the delay in mathematical models to understand the influence of DDP on population dynamics in any given system.

Previous theoretical studies that have examined DDP have (implicitly or explicitly) considered a single fixed delay for the onset of DDP (White and Wilson, 1999; Reilly and Hajek, 2008). These studies report conflicting findings for the impact of DDP, with it either stabilising (White and Wilson, 1999) or destabilising (Reilly and Hajek, 2008) the population behaviour. Our analysis shows that the dynamical outcomes depend critically on the delay length and this could explain the apparent contradiction between these studies.

DDP is most commonly reported in insect–pathogen systems in which the infection is often lethal and therefore in the above analysis we considered a model without recovery from infection. However, to test the generality of our findings, we also studied an extension of our model framework that includes recovery (γ) (see legend to Fig. 6 for details). Our conclusions are unaffected by the inclusion of recovery: there is a parameter-dependent delay value below which an increase in the strength of DDP is destabilising, and above which such an increase is stabilising (Fig. 6). Recovery decreases the size of the region of α–λ parameter space where cycles arise (Fig. 6) and therefore increasing recovery is generally stabilising. This agrees with our intuition and is consistent with previous findings that indicate that recovery, in the absence of DDP effects, reduces the likelihood of cycles (Norman et al., 1994).

It has been postulated that DDP is likely to be manifested particularly in insect species exhibiting population cycles and/or outbreaks (Wilson and Reeson, 1998). Indeed, several of the species for which DDP has been experimentally demonstrated are prone to outbreaks which can cause widespread damage to natural vegetation and crops, for example the desert locust *S. gregaria* (Wilson et al., 2002), the African armyworm *S. exempta* (Reeson et al., 1998) and the Oriental armyworm *M. separata* (Kunimi and Yamada, 1990). Changes in disease-transmission rate due to density-dependence are known to strongly influence population dynamics (Hochberg, 1991b), and it has been predicted that the lower rates of transmission among high-density populations caused by DDP may destabilise host–pathogen interactions and contribute to the large outbreaks characteristic of the insect populations concerned (Reeson et al., 1998). Our findings confirm that DDP does have a significant impact on the population dynamics, and could be a key factor driving outbreaks and cycles, providing the delay in its onset is sufficiently small. When the time until the onset of DDP is short, individuals can rapidly increase resistance at high host densities, resulting in lower than expected rates of transmission and reducing the capacity for the pathogen to regulate the population. This destabilises the host–pathogen interaction and may contribute to the boom-and-bust nature of the population dynamics (Reeson et al., 1998). Furthermore, our results indicate that the peak and period of population cycles are affected by the extent of DDP. Therefore, DDP may have important implications for the duration and size of outbreaks and will need to be considered when developing biological control strategies to manage pest species.

Pathogens are important agents in the regulation of host populations and there has been extensive debate into their role in driving and modulating host outbreaks (e.g. Berryman, 1996; Klemola et al., 2007; Sherratt and Smith, 2008). For cyclic insect populations it has been suggested that although pathogens may promote population oscillations they are unlikely to be the sole driver of cycles since in model systems the population density at the peak of the oscillations is well below outbreak levels (Bowers et al., 1993; White et al., 1996). Extensions to these models that include a time delay in host self-regulation or include additional model complexity to better represent insect–pathogen systems show an increased propensity to cycle (Bonsall et al., 1999; Xiao et al., 2009). Our findings show that the inclusion of DDP could operate in a similar manner. In particular, provided the

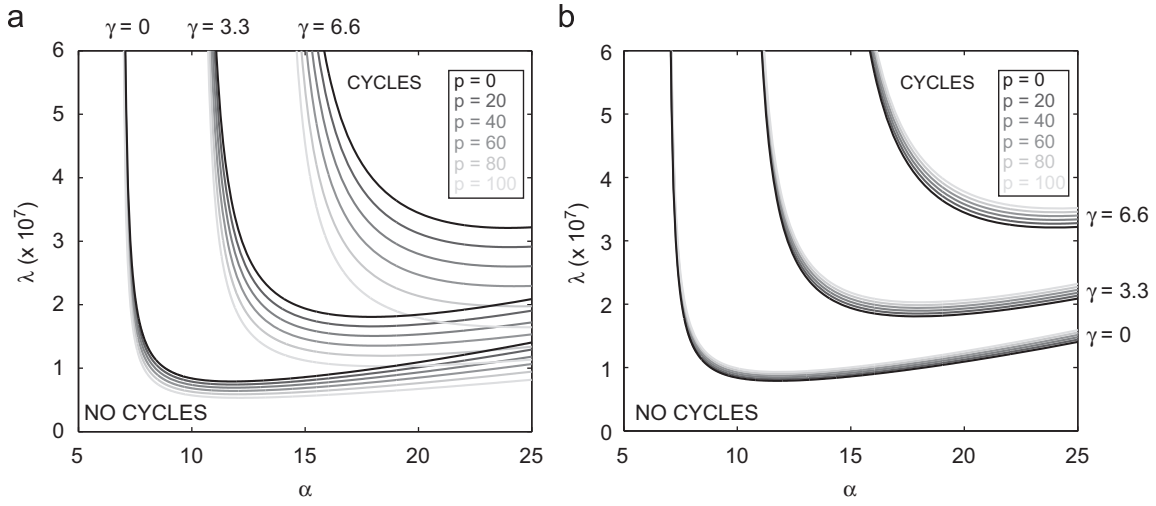

Fig. 6. Recovery γ stabilises the disease dynamics. (a) shows the results for delay $\tau = 0.33$ and (b) for $\tau = 0.99$. To add recovery to the model, we add a $-\gamma Y$ term to Eq. (2), giving $dY/dt = \beta W(H-Y)-(\alpha+b+\gamma)Y$. Curves are shown for two non-zero values of recovery: $\gamma = 3.3$ and $\gamma = 6.6$, and for a range of p values. As γ increases, the cycling region is reduced. Increasing p gives the same trends for $\gamma > 0$ as for $\gamma = 0$. In this figure, $b = 3.3$ and $\mu = 3$ and the time delay τ is expressed as a proportion of the average lifespan of the host, $(1/b)$.

delay before the onset of DDP is short, we predict an increase in the parameter regions over which cycles are exhibited and an increase in the amplitude of population oscillations.

Our key result is that the time delay between the assessment of population density and the change in host defence is critical in determining the influence of DDP on population dynamics. It would be relatively straightforward to design laboratory experiments to estimate this delay. This would be highly informative: quantitative predictions could be made about the impact of DDP and this would further inform the debate on the role of pathogens in driving population cycles. Outbreak pest species continue to cause major economic problems and one of the best studied examples of DDP is in a classic outbreak pest species, the locust (Wilson et al., 2002). It is of great importance to understand whether their natural parasites through processes such as DDP help to generate their unstable population dynamics. Furthermore, pathogens are increasingly proposed as control agents for insect pests where there is the need for stable control. What our work emphasises is that it is the delay between increases in density and increased investment in immunity that is critical. Where it is not possible to measure this delay experimentally, any models built to assess the role of parasites and pathogenic control agents in specific systems need to assess the role of the delay. We have found that DDP can be stabilising or destabilising. Short-lived host species faced with long-lived free-living parasites are most likely to be destabilised by DDP, but the delay is critical to the outcome.

Acknowledgements

JJHR was funded by a studentship from EPSRC. JAS was funded in part by a Research Fellowship from the Leverhulme Trust.

Appendix A

In this appendix we explain the conditions under which there is pathogen extinction. For the model *without* DDP, the basic reproductive rate, R, of the pathogen is

$$R(X)=\frac{\lambda\beta X}{\mu(\alpha+b)},$$

where β is constant. When $R<1$ the disease cannot persist (the disease-free steady state is stable). In the absence of DDP, disease persistence is determined by assessing R in a disease-free population at the host carrying capacity, $R_0=R(K)$. Disease extinction occurs if $R_0<1$.

For our model, with density-dependent β, R can be written

$$R(X)=\frac{\lambda\beta_0\left(1-\frac{p}{100}\frac{X}{K}\right)X}{\mu(\alpha+b)}.$$

To determine when $R<1$ holds, we seek the largest value of $R(X)$, which we denote R_{max}. In the absence of DDP this occurred when $X=K$, however with a density-dependent β the maximum need not occur at the carrying capacity. We differentiate R with respect to X and set to zero to give

$$X=\frac{50\,K}{p}.$$

For $p\geq 50$, $50K/p$ is on $X=[0,K]$. So

$R_{max}=R(X=50K/p)$ for $p\geq 50$.

(Note for $p=50$, $50K/p=K$.) For $p<50$, $50K/p>K$, which is not relevant. The maximum on $X=[0,K]$ is at $X=K$ (see Fig. 7), so

$R_{max}=R(X=K)$ for $p<50$.

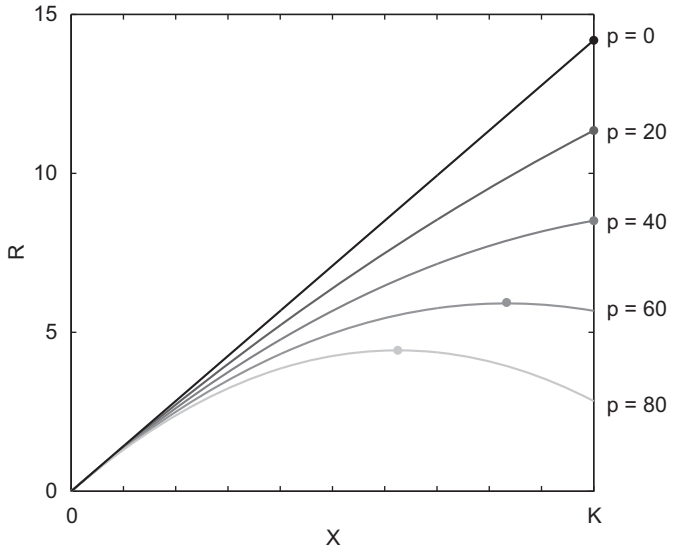

Fig. 7. The basic reproductive rate of the infection (R) needs to be calculated at different values of the density of susceptible hosts (X) depending on the strength of DDP (i.e. the value of p). This figure shows function $R(X)$ for different values of p, for representative parameter values, which are $\lambda=8\times10^6$, $\mu=3$, $\alpha=15.5$ and $b=3.3$. For $p<50$, the maximum of $R(X)$ occurs for $X>K$, which is not relevant. So we take $R_{max}=R(K)$ as this is the maximum within $X=[0,K]$. For $p\geq 50$, the maximum of $R(X)$ lies within $X=[0,K]$ at $X=50\,K/p$. The R_{max} value for each p is indicated with a dot.

From Fig. 7, for any given X, as p increases, $R(X)$ decreases, and so pathogen extinction becomes more likely. Thus DDP acts to make disease persistence more difficult.

For sufficiently large p, and for appropriate values of the other parameters, a stable disease-free steady state coexists with an ecologically relevant infected steady state. This links to the roots of cubic equation (6): this case occurs when there are two positive roots less than K. Numerical studies suggest that there is a separatrix in phase space, passing through the (unstable) steady state which corresponds to the larger cubic root. This separatrix determines the basins of attraction for the two steady states. We are interested in the dynamics when disease is present, so we focus on this region of phase space, rather than behaviour in the basin of attraction of the disease-free steady state.

Appendix B

In this appendix, mathematical details of the non-dimensionalisation of the model (Eqs. (1)–(3)) are given. This non-dimensionalisation is used to determine which parameters should be varied when undertaking a sensitivity analysis of the findings. We first set the following dimensionless variables:

$$H'=H/H_s,\quad Y'=Y/Y_s,\quad W'=W/W_s\quad\text{and}\quad t'=t/t_s.$$

Now we can re-express the model equations as

$$\frac{dH'}{dt'}=rH't_s\left(1-\frac{H'H_s}{K}\right)-\frac{\alpha Y'Y_st_s}{H_s},$$

$$\frac{dY'}{dt'}=\frac{\beta W'W_st_s}{Y_s}(H'H_s-Y'Y_s)-(\alpha+b)Y't_s,$$

$$\frac{dW'}{dt'}=\frac{\lambda Y'Y_st_s}{W_s}-\mu W't_s.$$

Parameters can be eliminated by an appropriate selection of t_s, H_s, Y_s and W_s. Choosing

$$t_s = 1/r, \quad H_s = Y_s = K \quad \text{and} \quad W_s = r/\beta$$

gives

$$\frac{dH'}{dt} = H'(1-H') - \frac{\alpha}{r}Y',$$

$$\frac{dY'}{dt'} = W'(H'-Y') - \frac{(\alpha+b)}{r}Y',$$

$$\frac{dW'}{dt'} = \frac{\lambda K\beta}{r^2}Y' - \frac{\mu}{r}W'.$$

This dimensionless form shows that there are four independent parameter groupings:

$$\alpha/r, \quad b/r, \quad \mu/r \quad \text{and} \quad \lambda K\beta/r^2.$$

To cover all cases, it is therefore enough to consider variations in α, b, μ and λ. Note that in the Discussion, we comment on an extended model which includes recovery γ. Changing γ is akin to changing b and keeping r constant. Thus, since we look at the effects of changing γ, we are left with only three other parameters that we need to vary: α, λ and μ.

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