Ecological factors driving the long-term evolution of influenza’s host range

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The evolution of a pathogen’s host range is shaped by the ecology of its hosts and by the physiological traits that determine host specificity. For many pathogen traits, there is a trade-off: a phenotype suitable for infecting one set of hosts poorly infects another. Introducing and analysing a simple evo-epidemiological model, here we study how such a trade-off is expected to affect evolution of the host ranges of influenza viruses. We examine a quantitative trait underlying host specificity, given by an influenza virus’s degree of adaptation to certain conformations of sialic acid receptors, and investigate how this receptor preference evolves in a minimal network of host species, including humans, that differ in life history and receptor physiology. Using adaptive dynamics theory, we establish thresholds in interspecific transmission rates and host population sizes that govern the emergence and persistence of human-adapted viruses. These ecological thresholds turn out to be largely independent of the strength of the evolutionary trade-off, underscoring the importance of ecological conditions in determining a disease’s host range.

Keywords: influenza; host range; adaptive dynamics; emerging infectious diseases

1. INTRODUCTION

Several challenges complicate the task of predicting evolution. One is the presence of evolutionary constraints: it may not be possible to optimize two phenotypic traits simultaneously, because a high value in one trait rules out high values in the other. Another problem concerns attainability: pathways of phenotypic evolution may lead through regions of low fitness or, especially if mutations interact epistatically, the genotypes required along these pathways may be unlikely or even impossible to appear. Yet another class of problems arises from the environment or ecology in which evolution occurs: the fitness of a trait may be frequency dependent, being influenced by the phenotypes of other individuals. Fitness can also be affected by population size, spatial interactions and extrinsic factors, and these relationships can be nonlinear and dynamic.

Predicting evolution of host ranges in pathogens requires confronting several of these problems at once. Many pathogens show adaptations to specific host or tissue types and are unable to infect other hosts or tissues without undergoing extensive adaptation (Baranowski et al. 2001; Webby et al. 2004). Such adaptation often comes at the expense of the ability to infect an original host type, and thus presents an evolutionary constraint in the form of a trade-off. Pathogens tend to undergo extreme changes in population size during the same period in which rapid evolution occurs. Host immunity and host demography furthermore often impose frequency-dependent selection.

Given this complexity, it is not surprising that there is little general theory for the evolution of host ranges in pathogens. This is unfortunate, considering the ubiquity of zoonoses: most pathogens of humans infect at least one other species (Woolhouse & Gowtage-Sequeria 2005). Existing models address host range indirectly. For example, Parker et al. (2003) used optimization principles to show how parasitic helminths may expand their host range through trophic transmission to acquire complex life cycles. Gandon (2004) developed predictions for the evolution of virulence and transmission in a multi-host environment. Some insights might also be gained by interpreting host range as a resource-choice problem for pathogens. In Levin’s (1962) classic approach, consumers are predicted to specialize under strong trade-offs and to adopt generalist strategies when trade-offs are weak. His model, like Parker’s, assumes that the optimal strategy will prevail. When selection is frequency dependent, however, optimization principles are likely to give qualitatively incorrect predictions (Dieckmann et al. 2002; Egas et al. 2004; Koelle et al. 2005).

Our goal in this study is to develop basic predictions for the evolution of influenza’s host range. Host range here refers to the specificity and diversity of pathogens in the host community. We choose influenza because of its importance to the health of animal populations and its interesting constraints and ecology. At the same time, the methods of analysis presented here are general and might be of interest also with regard to many other pathogens. Our analysis focuses on how host ecology and a trade-off in host specialization are expected to influence
evolutionary outcomes in the long run. We do not consider the mechanistic details of evolutionary attainability here, since the genotype-to-phenotype maps relevant to influenza’s host range are poorly known (Baigent & McCauley 2003). Like Levin’s approach, ours ignores environmental variation, such as seasonality, and assumes that viral population dynamics roughly equilibrate between successful invasions of pathogen strategies. These simplifications allow us to obtain general results about the structure of host ranges in a heterogeneous host environment, when adaptation is restricted by a single evolutionary constraint. We find that: (i) specialists are favoured for a broad range of both weak and strong trade-offs, (ii) the scope for specialist coexistence sensitively depends on interspecific transmission rates and host population sizes, whereas (iii) these dependencies are only weakly affected by trade-off strength.

2. BACKGROUND
The host range of many viruses is constrained by cell recognition (Baranowski et al. 2001). Influenza viruses all bind to cell-surface oligosaccharides with a terminal sialic acid. Sialic acids fall into one of two general types of conformations: the Neu5Ac(2,3)-Gal linkage or the Neu5Ac(2,6)-Gal linkage. The intestinal and/or respiratory epithelia of waterfowl, horses and dogs contain mainly cells with α2,3-linked sialic acids, whereas the upper respiratory epithelia of cats and humans are dominated by α2,6-linked sialic acid receptors (Baigent & McCauley 2003). Pigs, the alleged ‘mixing vessels’ of influenza viruses (Webster et al. 1992), contain both types of receptors in their respiratory tracts (Scholitses et al. 1998). Chickens also possess both types of receptors (Gambaryan et al. 2002). Experiments have shown that most viruses cannot replicate in host tissue of dissimilar receptor type, and viruses preferring one receptor type can often sustain some replication in any host possessing that type, even if they are adapted to another species (e.g. Kida et al. 1994; Ito et al. 1999). Thus, the chemistry of receptor binding creates a trade-off between the ability of influenza viruses to invade cells of one type or the other.

The distribution of α2,3- and α2,6-linked receptors in the host community presents an interesting evolutionary challenge. In a population of diverse potential hosts, under what circumstances will viruses evolve new receptor preferences? The emergence of avian influenza subtype H5N1 in humans has been ascribed to high interspecific mixing in backyard farms, large population sizes in the expanding commercial poultry industry and the presence of intermediate hosts (pigs or chickens) that serve as ecological and evolutionary bridges between waterfowl and humans (Bulaga et al. 2003; Liu et al. 2003; Webster 2004; Webster & Hulse 2004). How easily could α2,6-adapted mutant viruses invade in these different environments, and would they be able to coexist in the long run with α2,3-adapted resident viruses?

Here we analyse how the host range of influenza changes with trade-off strength in a simple evo-epidemiological model in which influenza viruses can adapt their receptor preference. We first assume that host species are epidemiologically equivalent except for their receptor types. Subsequently, we adopt more realistic assumptions and explore how the evolutionary dynamics of influenza viruses are modulated by two major components of influenza’s ecology, interspecific transmission rates and the relative abundances of different host species.

3. MATERIAL AND METHODS
(a) Epidemiological dynamics
We consider a community with three host populations. One population, with abundance $N_l$, represents the waterfowl reservoir and has only α2,3-receptors. Another population, with abundance $N_m$, represents the ‘target’ population (e.g. cats or humans) and has only α2,6-receptors. The third population, with abundance $N_r$, represents intermediate hosts such as pigs and chickens that possess both receptor types. We assume there are contacts between the reservoir and intermediate hosts ($N_l$ and $N_m$) and between the intermediate and target hosts ($N_m$ and $N_r$), but not between the reservoir and the target hosts (figure 1a).

Whether a contact between infected and susceptible host individuals results in transmission of the influenza virus depends on the host’s receptor type and the virus’s receptor preference $p$. We define $p$ as the virus’s probability of infecting via an α2,6-receptor; a perfect α2,6-specialist thus has $p = P(α2,6) = 1$. In our model, the virus’s probability of infecting via an α2,3-receptor, $P(α2,3)$, is related to $P(α2,6)$ through a trade-off with strength $s$ (Egas et al. 2004),

$$P(α2,3)^{1/s} + P(α2,6)^{1/s} = 1.$$  

(3.1)

This trade-off can be tuned to be weak ($s < 1$) or strong ($s > 1$). For later reference, we introduce three broad categories of viral phenotypes: α2,6-specialists, α2,3-specialists and generalists. We consider an α2,6-specialist to have a low degree of specialization if $0.5 < P(α2,6) - P(α2,3) < 0.8$ and a high degree of specialization if $P(α2,6) - P(α2,3) ≥ 0.8$. The criteria for α2,3-specialization are analogous. A virus is considered adapted to a receptor if it is specialized to that receptor. Generalist preferences comprise the remaining cases, $|P(α2,6) - P(α2,3)| ≤ 0.5$ (figure 1b).

Epidemiological dynamics follow the susceptible–infected–recovered–susceptible model. The transition of a host from recovered to susceptible indirectly captures two kinds of processes, the replenishment of susceptible hosts via births and deaths and the loss of immunity owing to antigenic evolution by the pathogen. Our model represents these dynamics by six ordinary differential equations. The equations follow the rates $dS/dt$ and $dI/dt$ at which the abundances of susceptible and infected hosts change in each of the three host populations. Since we assume constant population sizes, the rates $dR/dt$ at which the number of recovered hosts changes in each of the three host populations follow from those equations. For each host population, $i = r$ (‘reservoir’), $m$ (‘intermediate’), t (‘target’), the rate of susceptible replenishment is given by $γ_r$, the rate of infection by $λ$, and the rate of recovery by $ν$. Below, we explicitly show the equations for each state of the intermediate host,

$$\frac{dS_m}{dt} = γ_m R_m - λ_m S_m.$$  

(3.2a)

$$\frac{dI_m}{dt} = λ_m S_m - ν_m I_m.$$  

(3.2b)

and

$$\frac{dR_m}{dt} = ν_m I_m - γ_m R_m.$$  

(3.2c)

The force of infection in the intermediate host, $λ_m$, equals the sum of the per capita rates of acquiring infections from
contacts with infected members of all host populations, \( \lambda_m = \lambda_{mr} + \lambda_{mm} + \lambda_{mr} \). We initially assume that transmission rates are frequency dependent (Keeling \& Rohani 2007). This leads to the following form of the transmission term, illustrated here for the rate of new infections in the intermediate host caused by contact with reservoir hosts,

\[
\lambda_m S_m = \max[P(\alpha_{2,3}), P(\alpha_{2,6})] \beta_m \frac{e_{mr} S_m}{N_r + e_{mr} N_m} I_r.
\]

where \( \beta_m \) is the baseline rate at which an infected individual in host population \( j \) transmits infection to a susceptible individual in host population \( i \). The transmission rate \( \beta_m \) takes into account physical and behavioural differences between the host populations that affect the likelihood of infection given a contact. The effective transmission rate between two different populations is further modified by the appropriate receptor probability (in equation (3.3), \( \max[P(\alpha_{2,3}), P(\alpha_{2,6})] \)), and the fraction of contacted hosts that are susceptible (in equation (3.3), \( \frac{e_{mr} S_m}{N_r + e_{mr} N_m} \)). To specify this susceptible fraction, we introduce \( e_{mar} \), the ratio of the probabilities per unit time of interpopulation (between intermediate and reservoir hosts) and intrapopulation (among reservoir hosts) contact. The denominator, \( N_r + e_{mr} N_m \), is thus proportional to the expected total number of hosts contacted by an infected reservoir host during a given time period, and the numerator, \( e_{mr} S_m \), is proportional to the expected number of susceptible intermediate hosts contacted by an infected reservoir host during the same time period.

For simplicity, we initially assume \( e_q = c_p = c_i \) before relaxing this assumption later. Under this assumption, \( c \) controls the degree of mixing between host populations. For \( c = 0 \), all contacts occur within the separate host populations. In this situation, if \( S_i/N_i \approx 1 \), the effective transmission rate equals the baseline rate \( \beta_m \) and no contacts are potentially wasted on hosts in other populations. The case \( c = 1 \) implies free mixing between reservoir and intermediate hosts and between intermediate and target hosts. As \( c \) approaches infinity, the effective transmission rate between host populations \( i \) and \( j \) equals \( \beta_m \) (again assuming \( S_i/N_i \approx 1 \)), and the effective transmission rate within host populations drops to zero. A more restrictive interpretation of our parametrization is that \( c_q \) represents the fraction of population \( j \) in the range of population \( i \), implying \( c \in [0,1] \); \( c_q \) can also be interpreted as the integrated product of the spatial frequency distributions for hosts \( i \) and \( j \). We further assume that the between-population transmission rates \( \beta_q \) equal the average of the two corresponding within-population transmission rates,

\[
\beta_q = \frac{\beta_m + \beta_p}{2}.
\]

Extending these conventions to infections arising from contacts with infected hosts from all three host populations, we obtain

\[
\lambda_m = \max[P(\alpha_{2,3}), P(\alpha_{2,6})] \times \frac{\beta_m e_{mr} I_m}{N_r + e_{mr} N_m} + \frac{\beta_m e_{mr} I_m}{N_r + e_{mr} N_m} + \frac{\beta_m e_{mr} I_m}{e_{mr} N_m + N_r}.
\]

Equations for the other host populations are analogous (electronic supplementary material, equations (S1) and (S2)). As equation (3.5) illustrates, in our model, infection of the intermediate host occurs via the receptor type to which the infecting virus is better adapted. By modelling all mortality implicitly in the rate of susceptible replenishment, our model assumes that infections are acute and do not kill hosts, and that natural mortality acts only on recovered hosts.

(b) Evolutionary dynamics

To model the evolution of host range, we test the ability of a mutant virus with receptor preference \( p_m \) to invade a community of hosts infected with a resident virus of receptor preference \( p_r \). To constrain the problem, we assume that in each host population, the resident virus has reached its endemic equilibrium, and that the ability of the mutant to invade the resident is given by its instantaneous growth rate when rare in the environment determined by the resident. This growth rate, also known as the mutant’s invasion fitness in the resident’s environment (Metz et al. 1992), is given by the dominant eigenvalue of the Jacobian of the rare mutant’s epidemiological dynamics (see the electronic supplementary material). The endemic equilibrium and the dominant eigenvalue are calculated numerically, since both are determined by polynomial equations of orders in excess of four.

By determining the growth rate of every possible mutant phenotype against every possible resident phenotype, we obtain pairwise invasibility plots (PIPs). PIPs show which phenotypes are uninvasible once attained and which phenotypes can be attained through the succession of small and advantageous mutational steps. The former phenotypes are
called evolutionarily stable, the latter convergence stable. Our assumptions and approach are an application of the theory of adaptive dynamics (Dieckmann & Law 1996; Metz et al. 1996; Geritz et al. 1998).

4. RESULTS

(a) Effects of trade-off strength in a neutral host ecology

We first examine how host range evolves when the host populations are epidemiologically equivalent in every respect but their receptors: hosts share the same population sizes and rates of contact, recovery and susceptible replenishment, but their receptors vary. For simplicity, we assume $c = 1$, implying free mixing between reservoir and intermediate hosts and between intermediate and target hosts.

For very weak trade-offs ($s \leq 0.5$ in figure 2a), a complicated dynamic emerges. The PIPs show two strategies that are both evolutionarily and convergence stable, but only locally. Which strategies are realized depends on the phenotype of the initial resident and on the mutational step size. For $s = 0.5$, starting from a perfect $\alpha_{2,3}$-specialist (i.e. from a resident with $p = 0$), mutants that are slightly better adapted to the target host than the residents can invade up to $p \approx 0.23$ (where $P(\alpha_{2,3} \approx 0.97$). If mutations are always small, this resident, which shows a low degree of $\alpha_{2,3}$-specialization, will persist indefinitely. However, there is evidence that in some subtypes of influenza viruses, single mutations can effect large changes in receptor binding. If mutations are large, mutants with sufficiently high $p$ can still invade when trade-offs are very weak. At $s = 0.5$, invasions by mutants with very high $p$ leads to a resident strategy at $p \approx 0.97$ (where $P(\alpha_{2,3} \approx 0.23$, corresponding to low $\alpha_{2,3}$-specialization). This other attractor is also locally evolutionarily and convergence stable.

As the trade-off strengthens, the two local attractors disappear, and only the repellor previously separating them remains. The two perfect specialists (at $p = 0$ and $p = 1$) thus become evolutionary endpoints. If mutational step sizes are small, only one perfect specialist will arise from a given starting condition. For example, if $s = 0.75$, a resident starting at $p = 0.5$ can be progressively invaded by mutants with smaller $p$ until arriving at perfect $\alpha_{2,3}$-specialization. As before, which specialist appears depends on the phenotype of the initial resident. Figure 2 also shows that if mutational step sizes are large, a mutant better adapted to $\alpha_{2,6}$-receptors (i.e. with $P(\alpha_{2,6}) > 0.7$) can invade a perfect $\alpha_{2,3}$-specialist and evolve increasing $\alpha_{2,6}$-specialization, and vice versa.

Assuming that large mutations can occur and that multiple specialists are able to arise, will they coexist? Reflecting the plots about their main diagonal reveals areas of mutual invisibility, or protected dimorphic coexistence: both the mutant and the resident have positive invasion fitness in the environment of the other type. Evaluating the selection gradient in the regions of coexistence shows whether this coexistence is transient or evolutionarily stable. When the trade-off is very weak ($s = 0.05, 0.25$ and $0.5$), we see the basins of attraction for the equilibria described previously (figure 2b). In addition, we find a third attractor within the region of coexistence that is also locally evolutionarily stable. This kind of attractor is sometimes referred to as a singular coalition (Geritz et al. 1998). At $s = 0.5$, this attractor occurs where one resident is highly $\alpha_{2,6}$-specialized and the other is highly $\alpha_{2,3}$-specialized. For stronger trade-offs ($s = 0.75$ and above), this attractor is absent, and perfect specialists can coexist as evolutionary endpoints.

In summary, if large mutations are possible, a neutral ecology almost always gives rise to pairs of specialists that are able to coexist in the long run; generalists only appear when the trade-off is extremely weak ($s = 0.05$). These results appear robust for reasonable variations in ecological parameters (electronic supplementary material, figures S1 and S2). Our analysis up to this point reveals additional features of the evolution of host range in this system. First, PIPs are not anti-symmetric, that is, they are not invariant under reflection about the main diagonal and the subsequent exchange of signs. This demonstrates that selection for receptor preference is frequency dependent (Meszéna et al. 2001). Second, evolutionary branching, the endogenous generation of two different phenotypes from a single phenotype through frequency-dependent disruptive selection (Metz et al. 1992; Geritz et al. 1998), cannot occur in this system for a wide range of plausible ecological parameters (see the electronic supplementary material). Third, once trade-off strength increases to the point that perfect specialists are evolutionary endpoints, further increases in trade-off strength have virtually no effect on the invasion potential of strong $\alpha_{2,6}$-specialists.

(b) Effects of host ecology

We now explore how a range of relevant ecological features affect our results. First, we allow hosts to vary in their rates of contact, recovery and loss of infectiousness. Second, we investigate a modified version of our model that might better capture the dynamics of faecal–oral and aerosol transmission between and within the reservoir and intermediate hosts. Third, we examine the effects of two possible long-term intervention strategies, changing the sizes of intermediate and target hosts and the degree of mixing between different host populations.

(i) Differences in host demography and epidemiology

Natural host populations differ not only in their receptors but also in their demographic and epidemiologic rates. We therefore investigate two main features of host populations, the rate $\gamma$ at which susceptible hosts are replenished and the pathogen’s basic reproduction ratio $R_0$ in each host population.

The rate $\gamma$ in equations (3.2a) and (3.2c) approximates the net effects of birth, death, immigration, emigration and loss of immunity. We choose relatively high values of $\gamma$ (1/3 and 1/6 month$^{-1}$, respectively) for reservoir and intermediate hosts, implying that a recovered individual will, on average, be replaced every three or six months by a susceptible host. In the intermediate hosts, such replacement mainly occurs through culling or sale. In the reservoir hosts, it occurs mainly through loss of immunity and migration. We initially assume that $\gamma$ is approximately fourfold smaller (1/2 yr$^{-1}$) in the target hosts. This choice reflects influenza’s relatively fast antigenic evolution in humans, the longer lifespan of the
Evolution of influenza’s host range  S. Cobey et al. 5

![Evolution of influenza’s host range](https://rspb.royalsocietypublishing.org/)

Figure 2. Evolutionary outcomes in a neutral host ecology. (a) PIPs for different trade-off strengths $s$ for $N_1 = N_m = N_2$, $c = 1$, $\beta_p = \rho_{m} = \beta_T = 1/3 \text{ day}^{-1}$, $v_r = v_m = v_1 = 1/6 \text{ day}^{-1}$ and $\gamma_r = \gamma_m = \gamma_1 = 1/180 \text{ day}^{-1}$. Black (white) areas indicate where the mutant has a positive (negative) growth rate in the endemic environment determined by the resident. Grey areas indicate regions in which the resident phenotype is not viable. (b) Trait evolution plots for the PIPs in (a). Grey areas indicate phenotype pairs that are mutually invasible and that therefore can coexist and coevolve. Black lines are evolutionary isolines at which the selection pressure on one phenotype vanishes. Circles correspond to evolutionary attractors if filled and to evolutionary repellors if open. Arrows show the directions, at the quadrant level, of positive selection pressures (for better readability, such arrows are shown here only for the largest bounded regions).

**target population and a high rate of immigration and emigration events.**

Better estimates are available for the epidemiological rates of transmission and recovery in influenza’s different host populations (electronic supplementary material, table S1). A standard measure of a pathogen’s fitness in a population is its basic reproduction ratio $R_0$, which measures the expected total number of secondary infections caused by a primary infection in an otherwise fully susceptible host population. For a perfect specialist in a population of intermediate hosts with $c = 1$, the total number of secondary cases in its own population is $R_{0,m,m} = \rho_{m}$. Our parameters yield $R_0$ values that are highest for reservoir hosts ($R_{0,r,r} = 4$ for a perfect $2,3$-specialist), lowest for target hosts ($R_{0,t,t} = 1.5$ for a perfect $2,6$-specialist) and intermediate for intermediate hosts ($R_{0,m,m} = 1.75$ for either perfect specialist). These choices of $R_0$ and $c$ allow the highest disease prevalence to be reached in reservoir hosts and the highest levels of immunity in target hosts.

Changing the demography and epidemiology of the different host populations predictably breaks the symmetry in evolutionary outcomes. In general, if mixing is complete ($c = 1$) and the trade-off is not especially weak ($s$ larger than $c \approx 0.25$), perfect $2,3$-specialists tend to dominate: they are the evolutionary endpoint from the majority of starting conditions, assuming small mutational step sizes (electronic supplementary material, figures S3–S5). Even if large mutations are possible, $2,6$-specialists often cannot invade perfect $2,3$-specialists, or such invasion is feasible only for perfect or nearly perfect $2,6$-specialists. This restriction on $2,6$-specialist invasion is much more sensitive to differences in $R_0$ among host populations than to the rates $\gamma$ of susceptible replenishment (electronic supplementary material, figures S3 and S4).

**(ii) Density-dependent transmission**

In wild waterfowl, influenza viruses appear to be transmitted predominantly by the faecal–oral route via contamination of shared water sources. Water is presumably also the route by which they infect domesticated animals, including pigs and chickens. Pigs and chickens generally crowd at high densities and permit aerosol transmission (see the electronic supplementary material). To test the robustness of our conclusions, we now assume that transmission rates under waterborne and aerosol transmission in reservoir and intermediate hosts scale more closely with the abundances than with the frequencies of infected hosts, resulting in density-dependent transmission (Keeling & Rohani 2007). By contrast, aerosol transmission involving the target hosts is better represented by frequency-dependent transmission, as transmission rates between target and intermediate hosts quickly saturate with respect to population size.

A modified version of our model thus assumes density-dependent transmission within and between reservoir and intermediate hosts, and frequency-dependent transmission within target hosts and between target and intermediate hosts. We also distinguish the amount of mixing between reservoir and intermediate hosts ($c_1$) from that between intermediate and target hosts ($c_2$). Analogous to equation (3.4), the force of infection for the intermediate host is then

$$\lambda_m = \max[P(\alpha_2, 3), P(\alpha_2, 6)] \times \left( \beta_{m1} I_1 + \beta_{mm} I_m + \frac{\beta_{m2} c_2 I_2}{c_2 N_m + N_1} \right). \quad (4.1)$$

The shift from frequency-dependent to density-dependent transmission requires a change in the value and dimensions of $\beta_{ij}$ for $i, j \in \{m,r\}$. We choose $\beta_{ij}$ so that
the initial growth rates in each host are identical to the
frequency-dependent case with \( N_t = N_m = 100 \) individuals.
We assume that transmission is limited by the abundance of
viruses in, and contact opportunities of, infecting hosts, and
thus let the transmission rates equal those of the infecting
host population: \( \beta_m = \beta_{mn} \) and \( \beta_m = \beta_{mt} \). For simplicity,
we also assume that the transmission rate between
intermediate and target hosts equals that within the target
population: \( \beta_m = \beta_{mn} = \beta_{mt} \). A complete description of
this model version is provided by the electronic supplementary
material, equations (S3)–(S5). We now explore the
consequences of this varied form of transmission in the
context of possible intervention strategies.

(iii) Sizes of intermediate and target host populations
The abundances of the intermediate and target hosts have
nonlinear effects on the ability of \( \alpha_{2,6}\)-specialists to
invade perfect \( \alpha_{2,3}\)-specialists. In general, increasing the
size of the intermediate host population diminishes the ability
of \( \alpha_{2,6}\)-specialists to invade when perfect \( \alpha_{2,3}\-
specialists are endemic. By contrast, increasing the size of
the target host population improves the ability of
\( \alpha_{2,6}\)-adapted viruses to invade. These patterns hold for
our frequency-dependent and density-dependent models,
and also for neutral and non-neutral host ecologies
(electronic supplementary material, figures S6–S9).

There are notable quantitative differences in the evol-
uationary outcomes resulting from the two different
transmission modes. Unsurprisingly, frequency-depen-
dent transmission attenuates the effects of increasing
abundances. In otherwise neutral host ecologies, even
when the population of intermediate hosts is twice as
large as the population of target hosts, invasion by \( \alpha_{2,6}\-
adapted viruses with a low degree of specialization is
still possible when perfect \( \alpha_{2,3}\)-specialists are resident.
Interestingly, these conditions are relatively insensitive to
trade-off strength. Except at extremely weak trade-offs,
epidemiological coexistence implies evolutionary coexis-
tence; if perfect specialists cannot coexist evolutionarily,
only weak trade-offs favour generalist strategies. Unexpectedly,
however, weak trade-offs can promote the evolution and
coevolution of viral phenotypes specialized on alternative
receptor types, assuming large mutations are possible.

In that case, both host ecology and trade-off strength non-
linearly affect the ability of \( \alpha_{2,6}\)-adapted mutants to
invade when \( \alpha_{2,3}\)-specialists are resident. The invasion of
\( \alpha_{2,6}\)-adapted viruses is facilitated by low interpopula-
tion transmission rates, low abundances of intermediate
hosts and high abundances of target hosts (figure 3).

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tence; if perfect specialists cannot coexist evolutionarily,
only weak trade-offs permit invasion of \( \alpha_{2,6}\)-adapted viruses.
A greater increase in \( c_2 \) is necessary to cause the same effect.

5. DISCUSSION
We have shown how the evolution of host range, predicated on a single trade-off, can be shaped by
frequency-dependent selection, trade-off strength, trans-
mision mode and host ecology. As expected, very weak
trade-offs favour generalist strategies. Unexpectedly,
however, weak trade-offs can promote the evolution and
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A greater increase in \( c_2 \) is necessary to cause the same effect.
Figure 3. Conditions that permit the coexistence of perfect specialists, assuming frequency-dependent transmission, realistic ecological parameters of host populations (electronic supplementary material, table S1) and a linear trade-off ($s = 1$). Parameter combinations that permit specialist coexistence are in grey. Coexistence is evolutionarily stable for higher trade-offs ($s = 0.75$ and above), but not for weaker trade-offs; however, even at weaker trade-offs, extremely well-adapted viruses are able to coexist (see text, figure 2). (a) Effects of the relative population size $N_{im}/N_t = N_{im}/N_t$ of intermediate hosts and of the degree $c_1$ of mixing between reservoir and intermediate hosts. (b) Effects of the relative population size $N_{t}/N_t = N_{t}/N_t$ of target hosts and of the degree $c_2$ of mixing between intermediate and target hosts.

humans (H1N1 and H3N2) show affinity to either $a2,3$- or $a2,6$-receptors, but not to both simultaneously.

Our results lend strong support to the idea that certain host ecologies facilitate expansions of a disease's host range. We find that, fortunately, coexistence of specialists is much more difficult in influenza's natural ecology than in a neutral one. Low interpopulation transmission rates, small intermediate host populations and large target host populations all increase the fraction of hosts that are susceptible to $a2,6$-mutants by limiting exposure to $a2,3$-viruses in the intermediate host. Low transmission rates between the intermediate and target hosts (low $c_2$) reduce the fraction of target hosts' contacts with intermediate hosts, some fraction of which resist infection owing to previous exposure to $a2,3$-adapted viruses.

This reduction thus opposes a potential ‘dilution effect’ of wasting contacts on incompetent (here, immune) hosts (Schmidt & Ostfeld 2001). While the effect of increasing the population of target hosts is unsurprising, a less intuitive result is that large populations of intermediate hosts, by supporting increased exchange of $a2,3$-adapted viruses with the reservoir, reduce the fraction of hosts potentially susceptible to $a2,6$-adapted viruses. Of course, large populations of intermediate hosts in nature could pose an increased risk for the emergence of $a2,6$-adapted viruses if host abundance correlates positively with the pathogen's genetic diversity. This result nonetheless underscores the major roles of immunity in the intermediate host population and of the rates of contact between target and intermediate hosts.

Investigations of the system's non-equilibrium dynamics could be useful. Influenza outbreaks are seasonal in most animals, and transmission rates are likely to be seasonal. If the amplitude of epidemic oscillations is sufficiently high, equilibria of viral evolution can be different from those predicted here (White et al. 2006). Adaptation is also fundamentally probabilistic. Although we established a threshold for invasion based on positive growth of a mutant when rare, negative growth rates in nature may stochastically generate chains of mutations and transmission that are long enough to allow significant adaptation and ultimately positive growth (Antia et al. 2003; Andre & Day 2005). In other words, it may be possible for $a2,6$-adapted viruses to gain a foothold outside the areas of positive growth in the analyses presented here.

Increasing detail on receptor specificity in different viruses will help address questions of evolutionary attainability. The trade-off between $a2,3$- and $a2,6$-preference provides a rough approximation of patterns in relative binding ability (Gambaryan et al. 2005). Receptor binding ability is only one small, though critical, determinant of a disease's host range (Baigent & McCauley 2003). It might be feasible to model additional adaptations indirectly as a change in trade-off strength, which we might expect to diminish over time as compensatory mutations arise at the receptor-binding site and in other genes.

This work shows that the evolution of host range may be as sensitive to ecological considerations as it is to the physiological details of adaptation. The long-term diversity of influenza viruses, for all realistic trade-offs, is highly sensitive to transmission rates and population sizes. Naturally or artificially acquired immunity in intermediate hosts and the dilution of contacts among competent hosts are key to reducing the long-term ability of $a2,6$-adapted viruses to persist.

We thank two anonymous reviewers, as well as Andrew Dobson, Casey Schneider-Mizell, Katia Koelle and Åke Brännström for useful comments. S.C. was funded by the US National Committee for IIASA, the Rackham Graduate Student Research Grant and an NSF Graduate Research Fellowship. This work was begun while S.C. participated in the Young Scientists Summer Program at IIASA. M.P. received support from the James S. McDonnell Foundation through a Centennial Fellowship. M.P. is an investigator of the Howard Hughes Medical Institute. U.D. gratefully acknowledges support by the European Commission, the European Science Foundation, the Austrian Science Fund, the Austrian Ministry of Science and Research and the Vienna Science and Technology Fund.
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