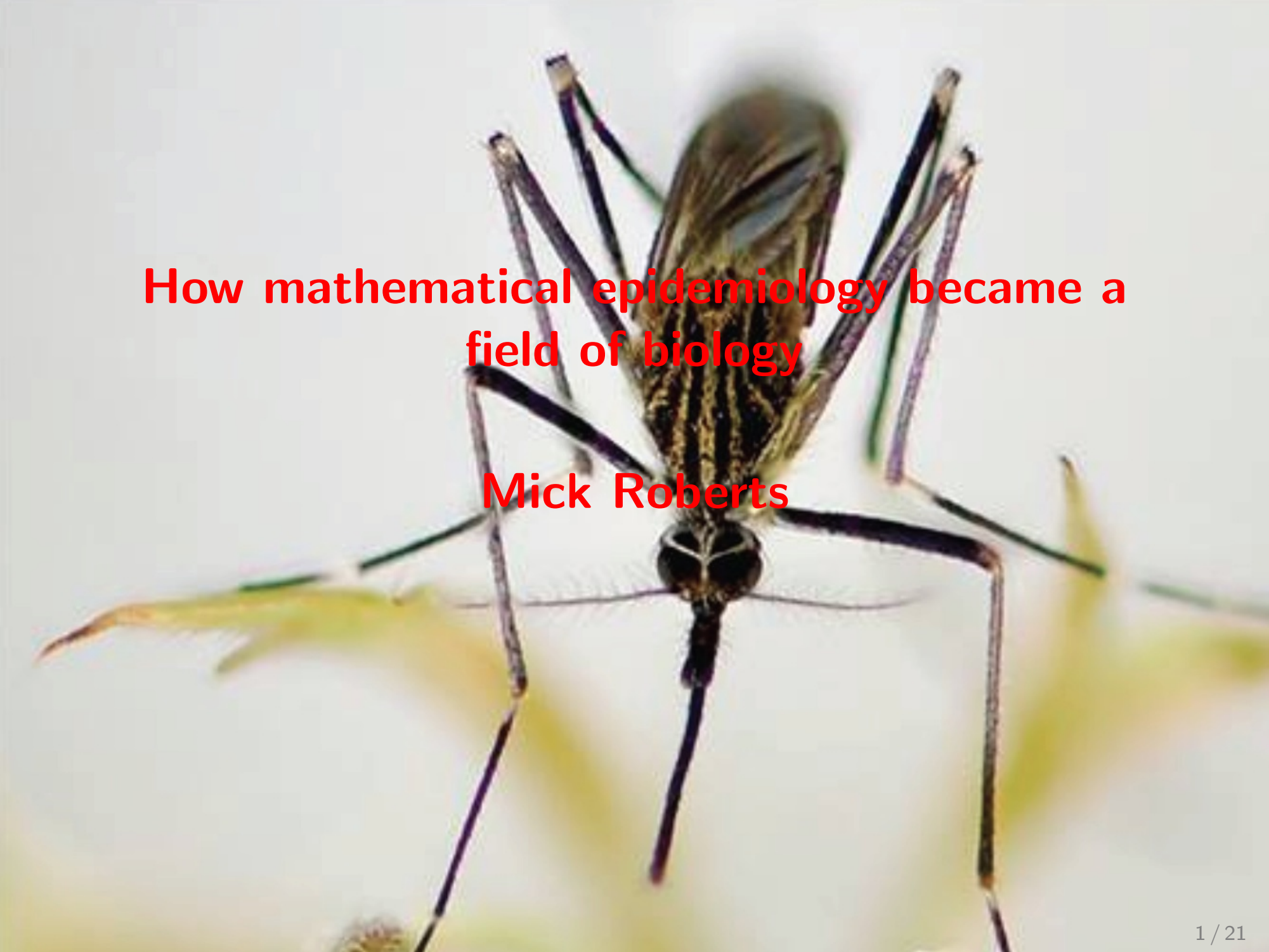
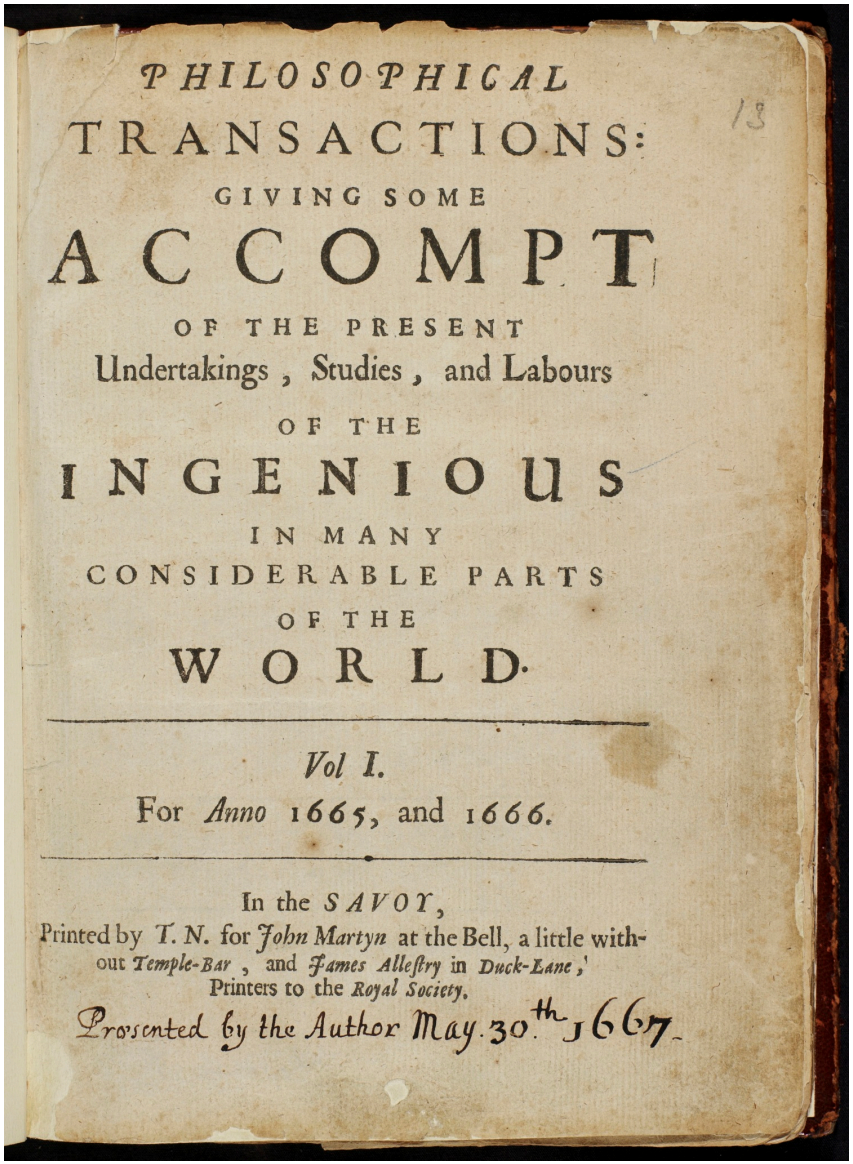


How mathematical epidemiology became a field of biology

Mick Roberts

350 years of scientific publishing



PHILOSOPHICAL
TRANSACTIONS:
GIVING SOME
ACCOMPT
OF THE PRESENT
Undertakings, Studies, and Labours
OF THE
INGENIOUS
IN MANY
CONSIDERABLE PARTS
OF THE
WORLD.

Vol I.
For *Anno* 1665, and 1666.

In the *SAVOY*,
Printed by *T. N.* for *John Martyn* at the Bell, a little without *Temple-Bar*, and *James Allestry* in *Duck-Lane*,
Printers to the *Royal Society*.
Presented by the Author May. 30th 1667.

The original paper: *Phil.Trans.B* (1981) 291:451-524

THE POPULATION DYNAMICS OF MICROPARASITES AND THEIR INVERTEBRATE HOSTS

By R. M. Anderson† and R. M. May, F.R.S.‡

† *Zoology Department, Imperial College, London SW7 2BB, U.K.*

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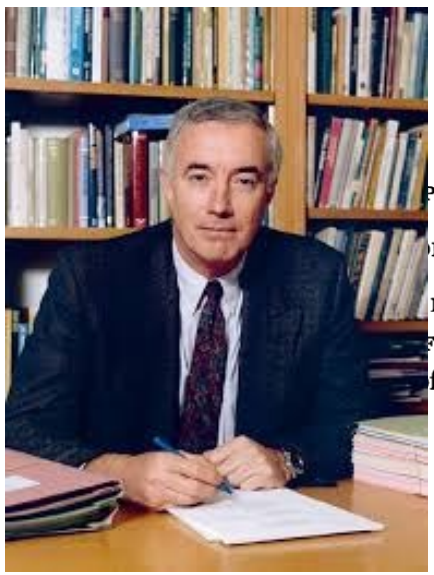

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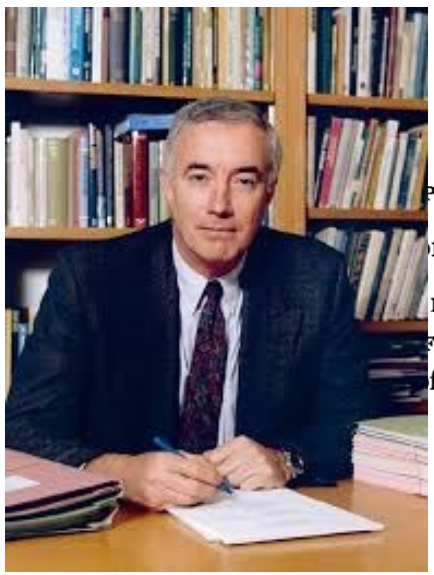

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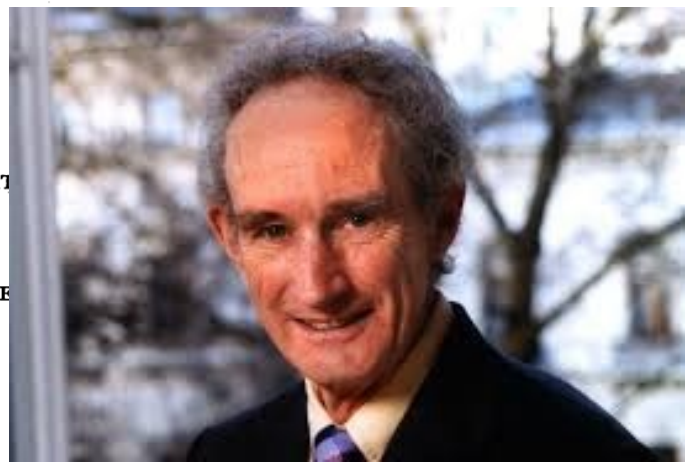

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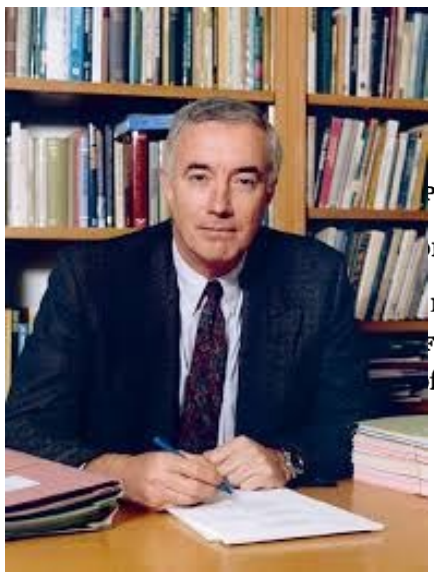

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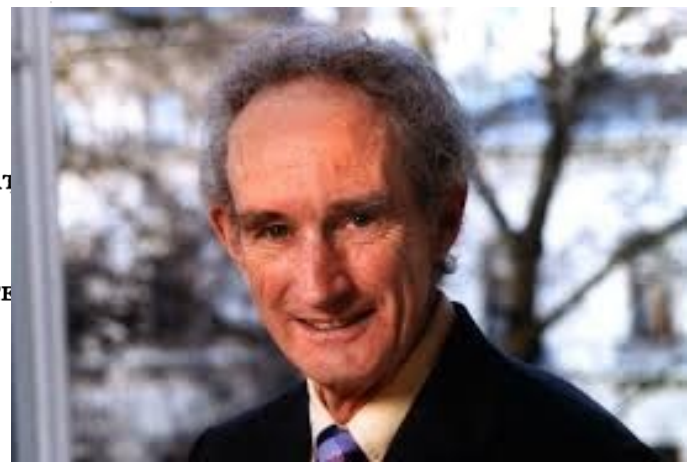

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The Anderson & May timeline

- May 1973. *Stability and Complexity in Model Ecosystems.* Princeton UP.
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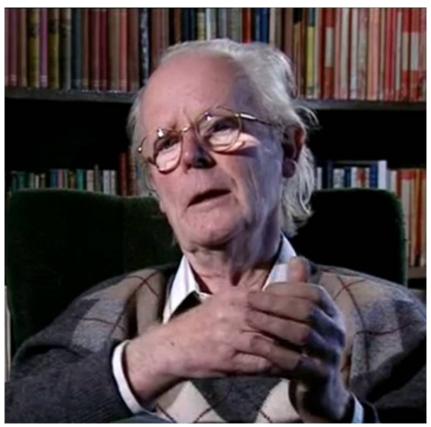
- **The review (John Maynard Smith, 20 June 1980)**
  "Professor Harper asked me if I would look at the enclosed manuscript. I think it is entirely suitable for publication in the 'Transactions'. It is an important contribution to knowledge. It is clearly written, and as brief as it could be in the light of the field covered."



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CONTENTS

- **74 pages, 969 citations**

The commentary *Phil.Trans.B* (2015) 370:20140307

PHILOSOPHICAL TRANSACTIONS B

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Review

Cite this article: Heesterbeek JAP, Roberts MG. 2015 How mathematical epidemiology became a field of biology: a commentary on Anderson and May (1981) 'The population dynamics of microparasites and their invertebrate hosts'. *Phil. Trans. R. Soc. B* **370**: 20140307.
http://dx.doi.org/10.1098/rstb.2014.0307

How mathematical epidemiology became a field of biology: a commentary on Anderson and May (1981) 'The population dynamics of microparasites and their invertebrate hosts'

J. A. P. Heesterbeek[1] and M. G. Roberts[2]

[1]Department of Farm Animal Health, Faculty of Veterinary Medicine, University of Utrecht, Yalelaan 7, Utrecht 3584 CL, The Netherlands
[2]Institute of Natural and Mathematical Sciences, New Zealand Institute for Advanced Study and the Infectious Disease Research Centre, Massey University, Private Bag 102 904, North Shore Mail Centre, Auckland, New Zealand

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The *J. Animal Ecology* papers (1978)

- Parasites of wildlife

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$$\text{Parasites} \qquad \frac{\mathrm{d}P}{\mathrm{d}t} = \frac{\lambda NP}{H+N} - (\mu + d + \alpha)\,P - \alpha\frac{k+1}{k}\frac{P^2}{N}$$

- Parasites are assumed to maintain a negative binomial distribution, with mean P/N and exponent k.

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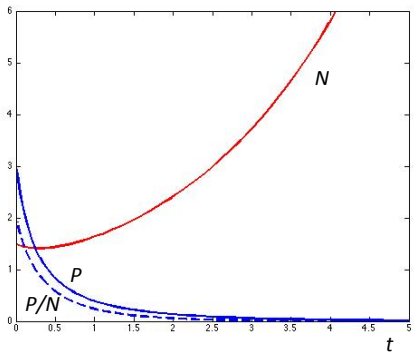

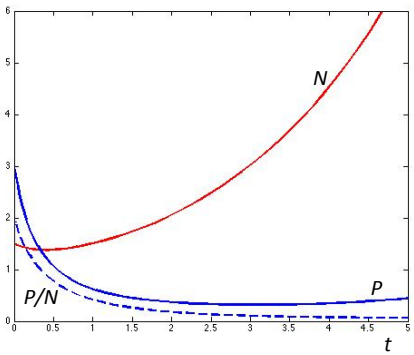

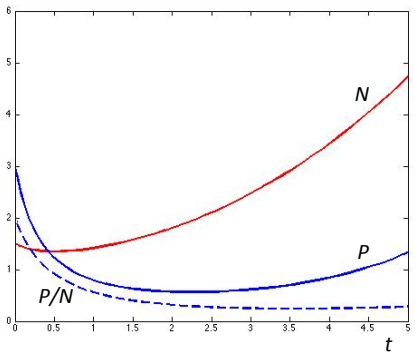

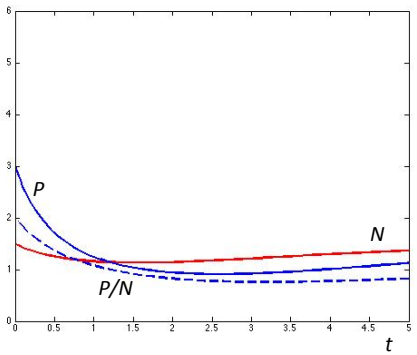

$\Rightarrow\Rightarrow$ Increasing λ $\Rightarrow\Rightarrow$

Anderson & May (1981)

- Assume a constant population size.

$$\text{Susceptibles} \qquad \frac{\mathrm{d}X}{\mathrm{d}t} = b\,(X+Y) - dX - \beta XY + \gamma Y$$

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  - If $R > 1$ the infection persists and approaches $y = 1 - 1/R$ over time.
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- We would now call R the *basic reproduction number* $\mathcal{R}_0$.

Anderson & May (1981) Model A

- In the basic model there is a threshold population size

$$R = \frac{\beta H}{\alpha + d + \gamma} \quad \Rightarrow \quad R = \frac{\beta H}{H_T}$$

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- We would now call H_T the *critical community size*.

Model A continued

- The question: [whether] “natural populations of invertebrates typically have microparasitic infections capable of regulating them”.
- The conclusion: [infections may] “contribute, wholly or in part, to the regulation of their invertebrate host populations.”

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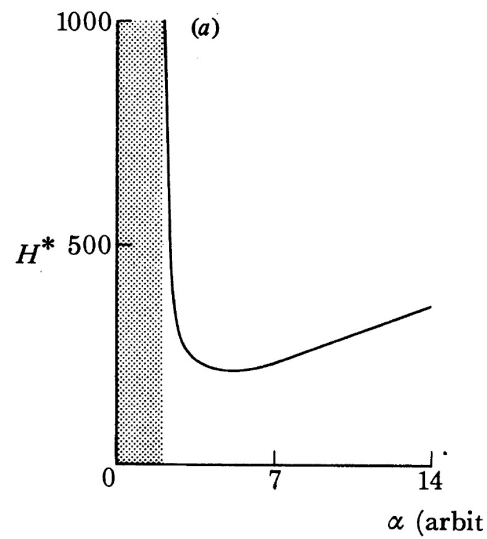
- The spinoff: if a pathogen were to be selected for biological control, rather than seeking the most pathogenic (highest value of α), an intermediate value would result in the lowest population density.



Anderson & May (1981) Model G

- Models B-F elaborated on Model A.
- In Model G the authors introduce a free-living stage

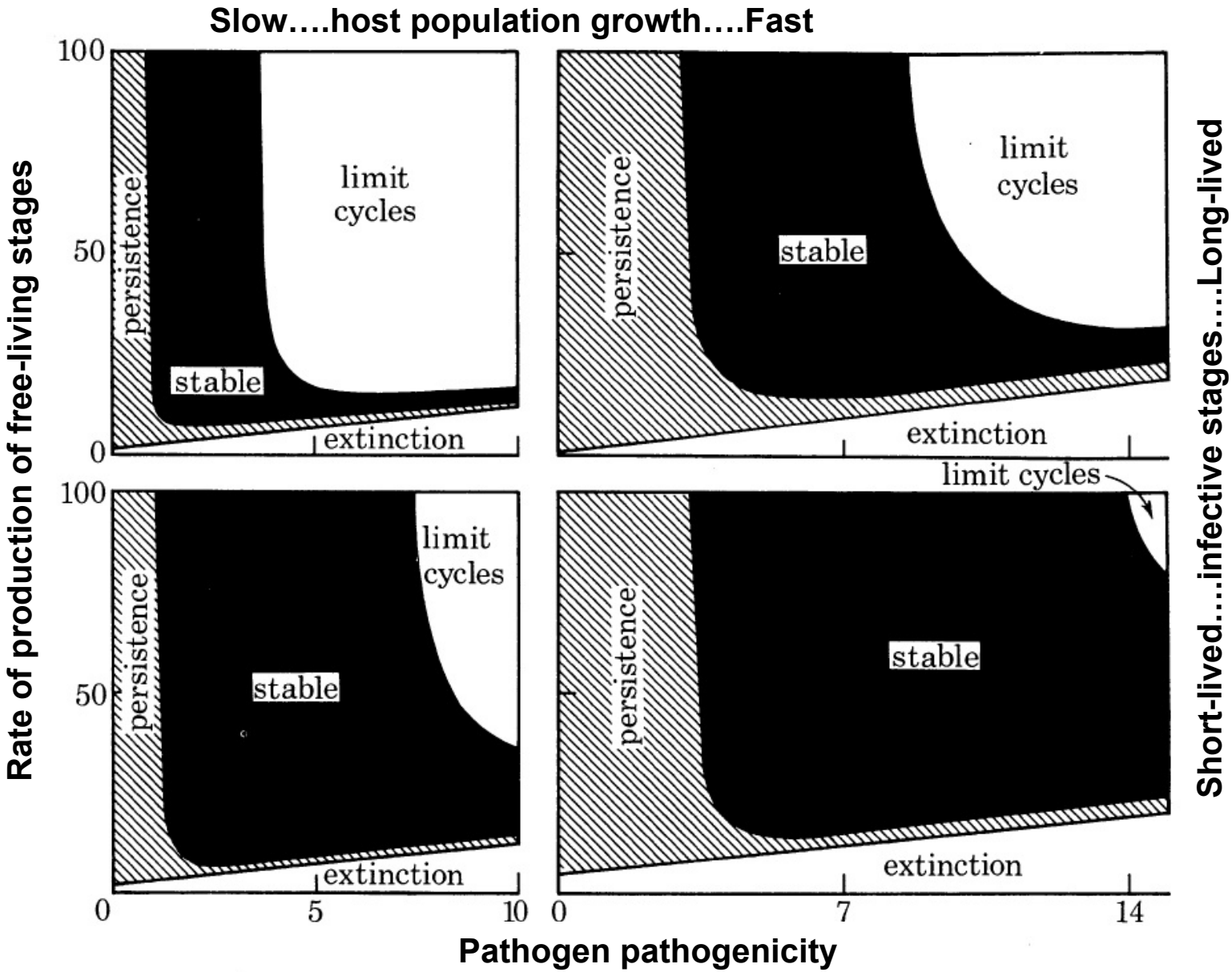
$$\text{Hosts} \qquad \frac{\mathrm{d}H}{\mathrm{d}t} = rH - \alpha Y$$

$$\text{Infecteds} \qquad \frac{\mathrm{d}Y}{\mathrm{d}t} = \nu WY - (\alpha + d + \gamma)\, Y$$

$$\text{Free-living} \qquad \frac{\mathrm{d}W}{\mathrm{d}t} = \lambda Y - (\mu + \nu H)\, W$$

- The conclusion: "highly pathogenic microparasites producing very large numbers of long-lived infective stages are likely to lead to non-seasonal cyclic changes in the abundance of their invertebrate hosts and in the prevalence of infection."

Model G results



Model G conclusions

- [the model is] "sufficient to account at least for most long-term population cycles in forest insects"
- Bowers et al. (1993). Contrary to previous related analyses,
  - "no support is provided for the view that host-pathogen interactions alone are capable of generating cyclic dynamics of the type observed"
  - "parameters from field estimates usually fail to generate cycles"
  - "Even where cycles are generated, ... [in the model] ... disease prevalence tends to peak at too high a value, and host density peaks at a very much lower value than field data suggest."
- The usual explanation - hysteresis effects due to the short insect and long forest timescales.

Why model insect pathogens?

- Climate change could make New Zealand suitable for the *Aedes* mosquitoes that carry dengue and Zika viruses.

Why model insect pathogens?

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- Releasing Wolbachia-infected males suppresses mosquito populations.

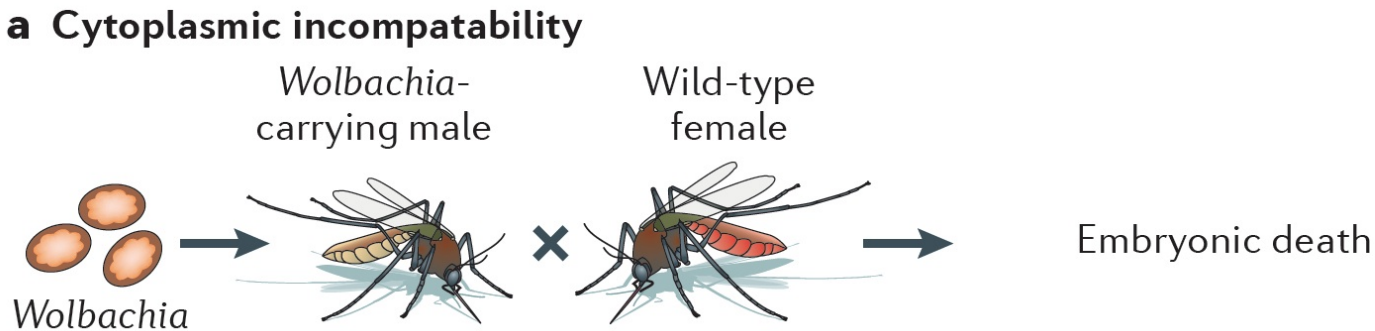
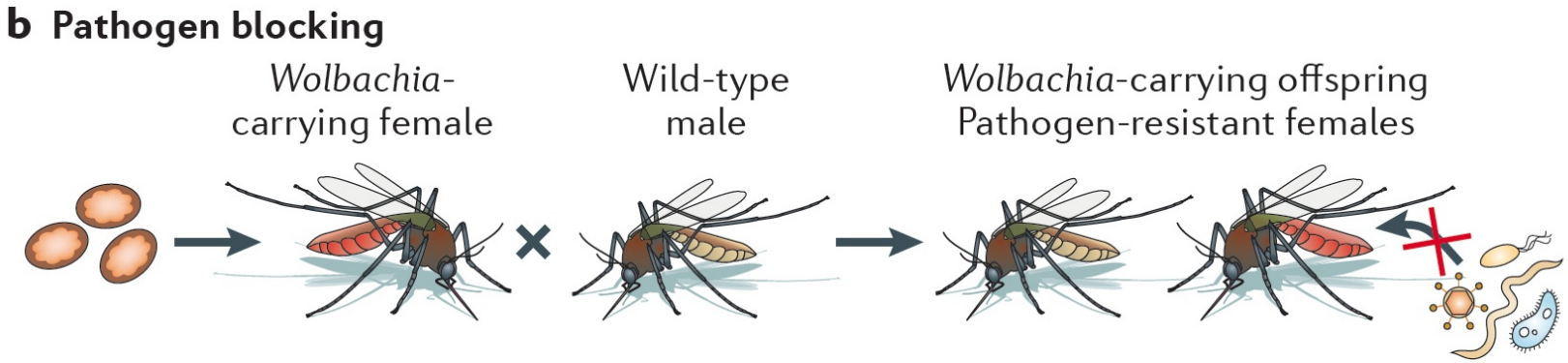


Image from McGraw & O'Neill 2013 *Nature Rev. Microbiol.* **11**, 181-193.

Wolbachia

- Releasing Wolbachia-infected females suppresses dengue transmission.



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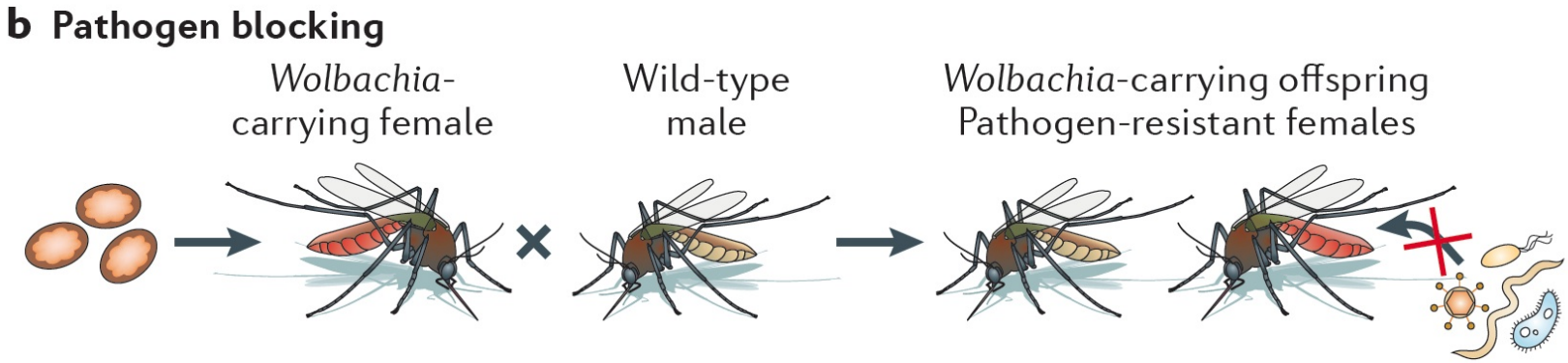

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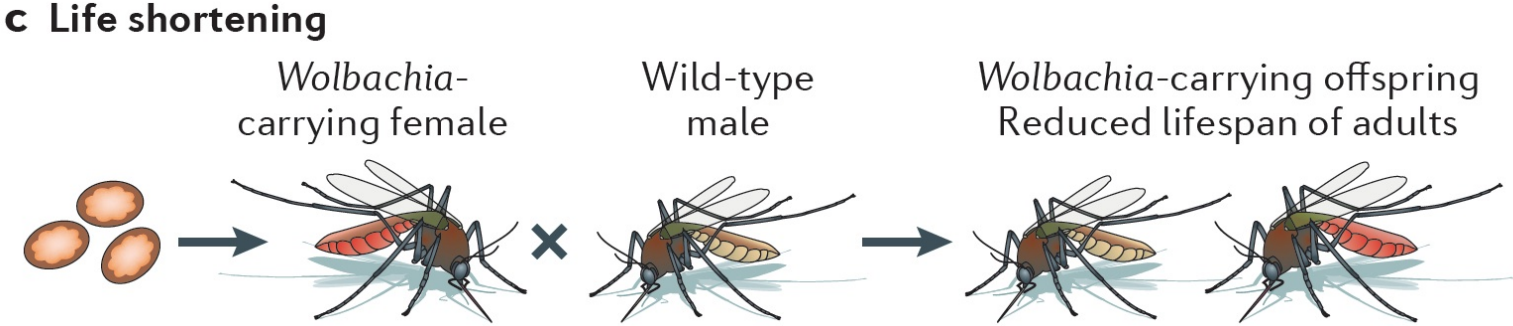
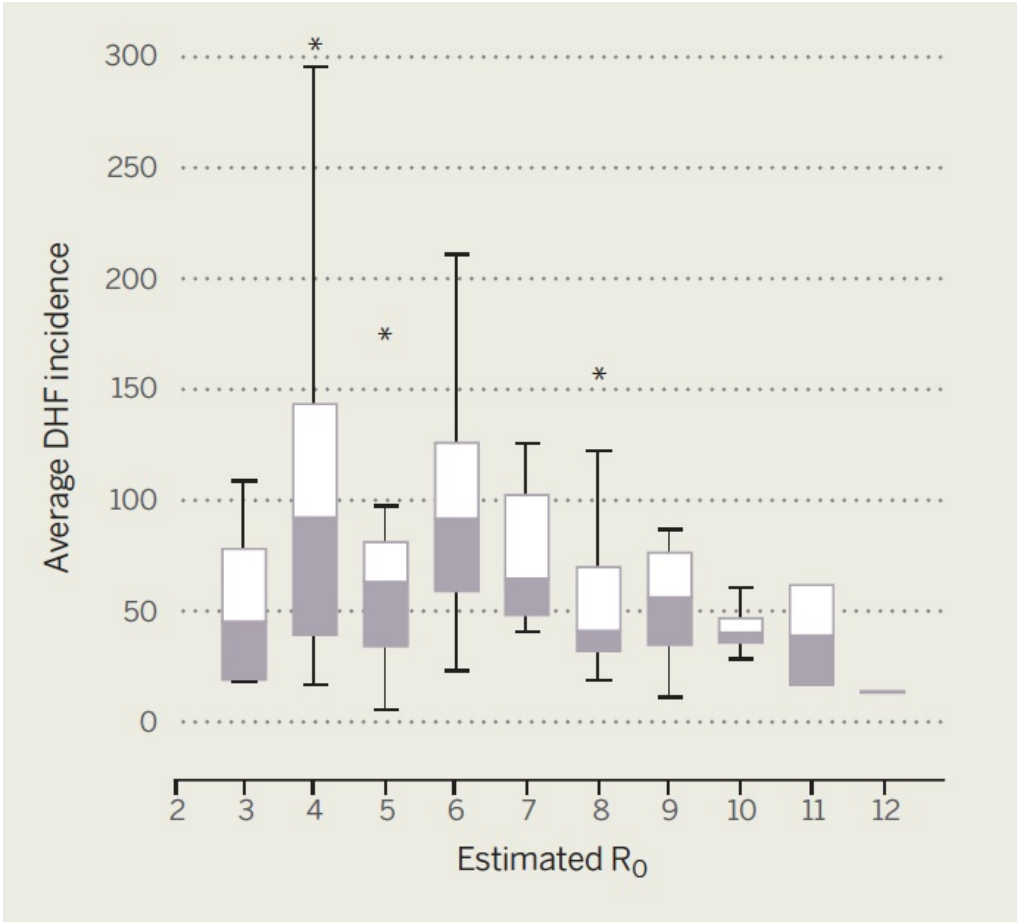


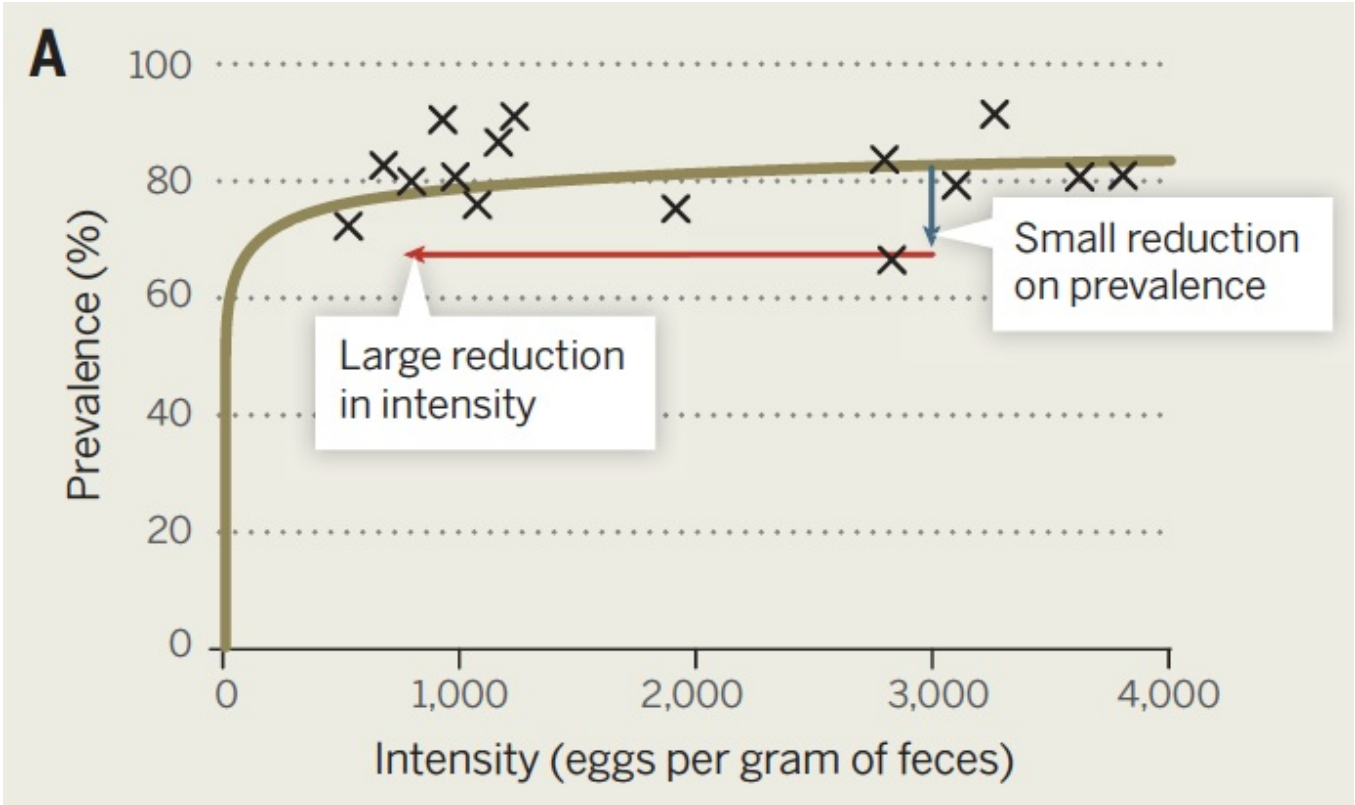
Images from McGraw & O'Neill 2013

Counterintuitive effects - 1



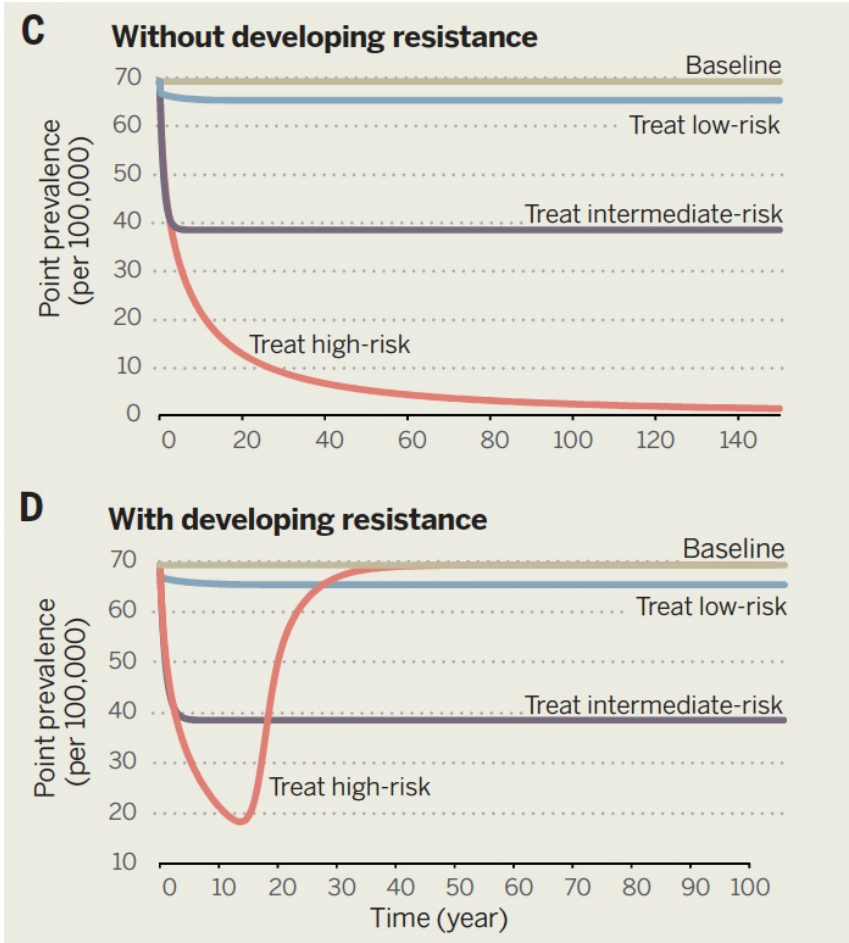
- Control measures may increase the incidence of dengue haemorrhagic fever.

Counterintuitive effects - 2



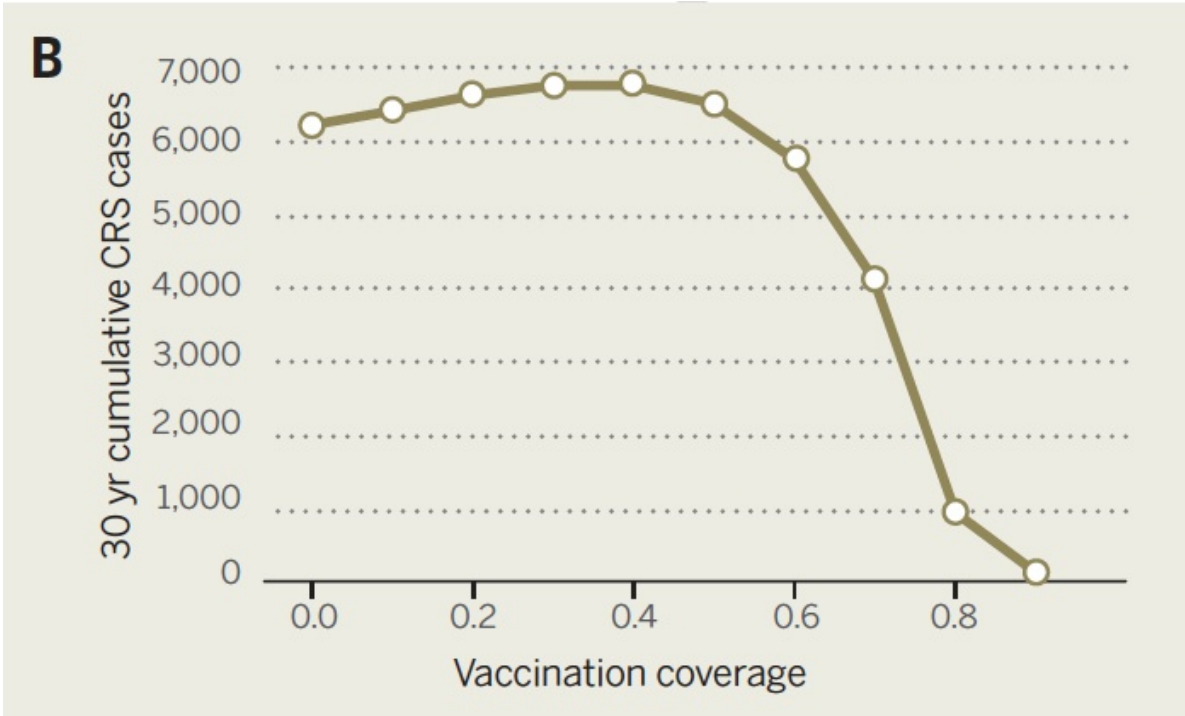
- Reducing parasite intensity may not reduce prevalence.

Counterintuitive effects - 3



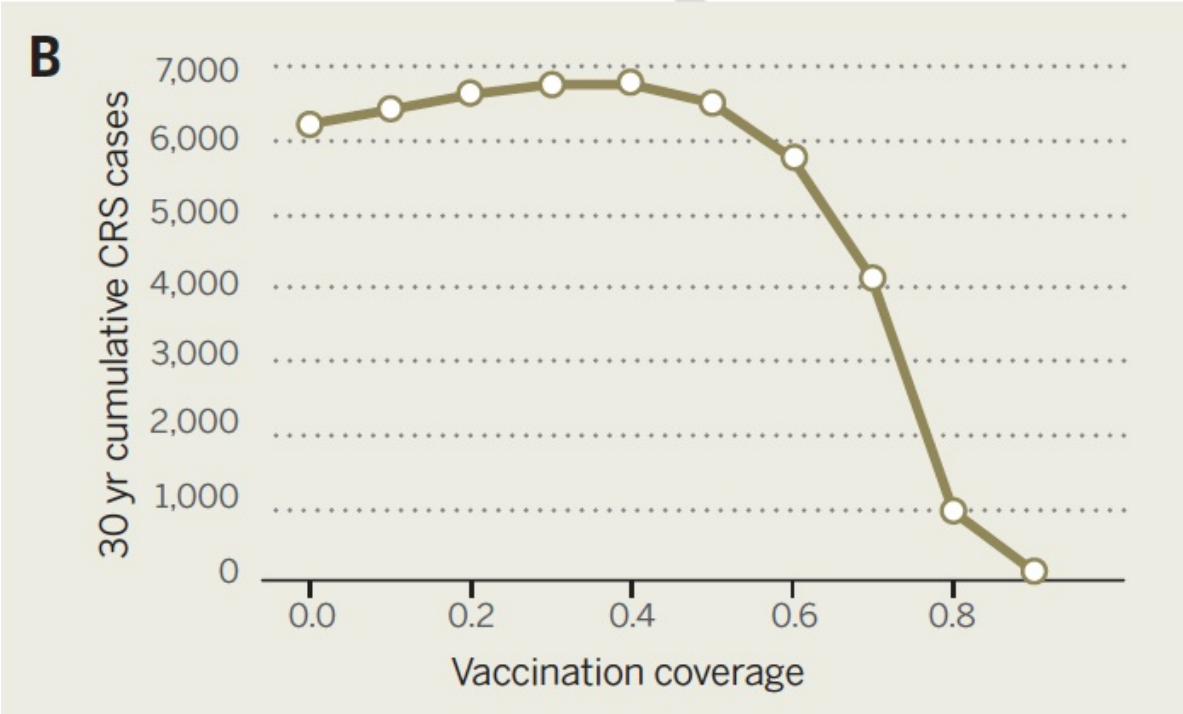
- Treating high-risk groups in the presence of antibiotic resistance may not be the best strategy.

Counterintuitive effects - 4



- Suboptimal levels of vaccine coverage increases congenital rubella syndrome.

Counterintuitive effects - 4



- Suboptimal levels of vaccine coverage increases congenital rubella syndrome.
- All counterintuitive effects from Heesterbeek et al. 2015, Modelling infectious disease dynamics in the complex landscape of global health. Science.

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Eight challenges in modelling disease ecology in multi-host, multi-agent systems

Michael G. Buhnerkempe[a,b,*], Mick G. Roberts[c], Andrew P. Dobson[d,e], Hans Heesterbeek[f], Peter J. Hudson[b,g,h], James O. Lloyd-Smith[a,b]

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REVIEW

EPIDEMIOLOGY

Modeling infectious disease dynamics in the complex landscape of global health

Hans Heesterbeek,[1*†] Roy M. Anderson,[2] Viggo Andreasen,[3] Shweta Bansal,[4] Daniela De Angelis,[5] Chris Dye,[6] Ken T. D. Eames,[7] W. John Edmunds,[7] Simon D. W. Frost,[8] Sebastian Funk,[4] T. Deirdre Hollingsworth,[9,10] Thomas House,[11] Valerie Isham,[12] Petra Klepac,[8] Justin Lessler,[13] James O. Lloyd-Smith,[14] C. Jessica E. Metcalf,[15] Denis Mollison,[16] Lorenzo Pellis,[11] Juliet R. C. Pulliam,[17,18] Mick G. Roberts,[19] Cecile Viboud,[18] Isaac Newton Institute IDD Collaboration[‡§]

nized at least 250 years ago when, in 1766, Daniel Bernoulli published a mathematical analysis of the benefits of smallpox inoculation (then called variolation) (*12*). In the past 50 years, the study of infectious disease dynamics has grown into a rich interdisciplinary field. For example, decision-making for vaccination strategies increasingly depends on model analyses in which infection dynamics are combined with cost data (Box 2, Influenza: prevention and control). In recent decades, responses to major infectious disease outbreaks, including HIV, bovine spongiform encephalopathy (BSE), foot-and-mouth disease (FMD), SARS, and pandemic and avian influenza, have shown both the need for and capabilities of models (Box 3, HIV: Test and treat strategy). Model-based analysis of such outbreaks also continually brings improvements in methodology and data, emerging from the comparison of model prediction with observed patterns.

For infectious agents important to public health,

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