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des maladies animales, 1^{er} juin 2023, Maisons-Alfort

Adaptation de l'approche épidémiologique des maladies animales face aux changements globaux

Changements climatiques et environnementaux

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ANR-10-LAB-2501



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Proposal for a new WOAHA Collaborating Centre

Impacts of global changes on animal infectious diseases

(including animal and zoonotic diseases)

by INRAE, Paris, France,
Department of animal health

Running title: Animal diseases and global changes



travel/
transportation



climate
change



increased utilisation/
exploitation of wildlife



changes in food
value chains

Quelques remarques liminaires

En comparaison de la santé humaine (infectiologique), où une tradition existe essentiellement britannique et qui s'est ensuite exportée, en écologie et évolution des maladies infectieuses, il n'y a **pas ou peu de travaux scientifiques sur ces sujets pour la santé animale**, à l'exception des zoonoses et des maladies à transmission vectorielle.

Très peu de ressources disponibles, et il faudrait en comprendre la ou les raisons, notamment au niveau des formations dispensées

L'importance **des niveaux d'organisation du vivant, des notions d'échelles spatiales et temporelles, des transferts d'échelles et de systèmes complexes** (*versus* systèmes linéaires « une cause et un effet », et l'approche majoritaire dite mécanistique)

Adaptation de nombreux secteurs de la recherche (ex. macroécologie ➡ macroépidémiologie) aux questions environnementales, sociétales... planétaires actuelles

Drivers for emerging issues in animal and plant health

**Jane Richardson¹, Caryl Lockhart², Stefano Pongolini³,
William B. Karesh⁴, Matthew Baylis⁵, Tony Goldberg⁶,
Jan Slingenbergh⁷, Paul Gale⁸, Tommaso Venturini⁹,
Mike Catchpole¹⁰, Katinka de Balogh², Marco Pautasso¹,
Alessandro Broglia¹, Franck Berthe¹, Jan Schans¹¹ and
Guy Poppy¹²**

incorporate this understanding into our approach to emerging risks. For this, we face two major challenges. One is cultural; the second is methodological. We have to look at systems not under the narrow view of specific hazards but with a wider approach to system dynamics, and consider a broad spectrum of potential outcomes in terms of risk. In addition, we have to make sense of the vast amounts of data that are available in the modern age. This paper aims to help in preparing for the cultural and methodological shifts needed in our approach to emerging risks.

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Current drivers and future directions of global livestock disease dynamics

Brian D. Perry^{a,1}, Delia Grace^b, and Keith Sones^c

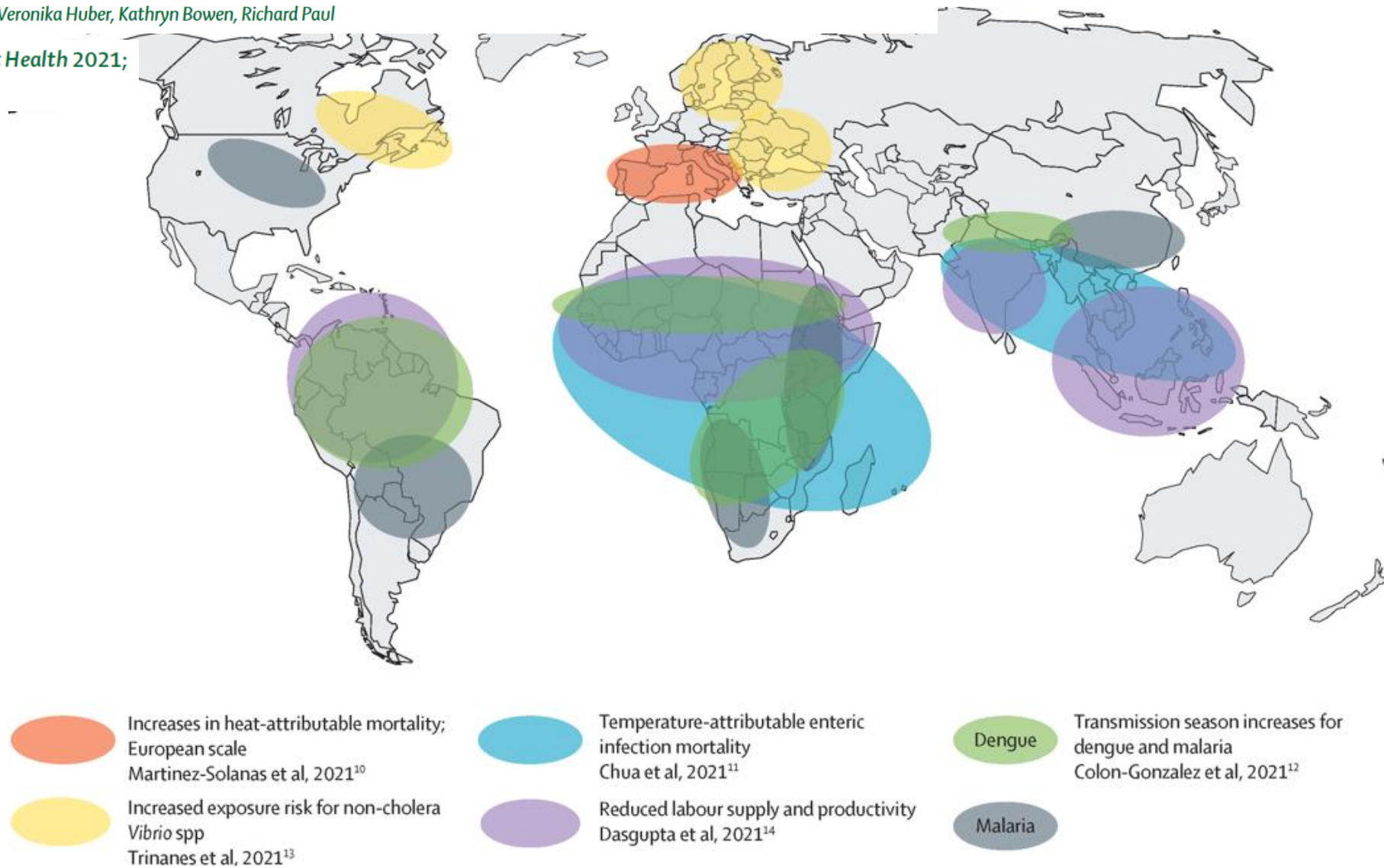
PNAS | December 24, 2013 | vol. 110 | no. 52 | 20871–20877

We review the global dynamics of livestock disease over the last two decades. Our imperfect ability to detect and report disease hinders assessment of trends, but we suggest that, although endemic diseases continue their historic decline in wealthy countries, poor countries experience static or deteriorating animal health and epidemic diseases show both regression and expansion. At a mesolevel, disease is changing in terms of space and host, which is illustrated by bluetongue, Lyme disease, and West Nile virus, and it is also emerging, as illustrated by highly pathogenic avian influenza and others. Major proximate drivers of change in disease dynamics include ecosystem change, ecosystem incursion, and movements of people and animals; underlying these are demographic change and an increasing demand for livestock products. We identify three trajectories of global disease dynamics: *(i)* the worried well in developed countries (demanding less risk while broadening the circle of moral concern), *(ii)* the intensifying and market-orientated systems of many developing countries, where highly complex disease patterns create hot spots for disease shifts, and *(iii)* the neglected cold spots in poor countries, where rapid change in disease dynamics is less likely but smallholders and pastoralists continue to struggle with largely preventable and curable livestock diseases.

Taking globally consistent health impact projections to the next level

Joacim Rocklöv, Veronika Huber, Kathryn Bowen, Richard Paul

Lancet Planet Health 2021;
5: e487–93



Despite intensive research activity within the area of climate change, substantial knowledge gaps still remain regarding the potential future impacts of climate change on human health. A key shortcoming in the scientific understanding of these impacts is the lack of studies that are conducted in a coordinated and consistent fashion, producing directly comparable outputs. This Viewpoint discusses and exemplifies a bottom-up initiative generating new research evidence in a more coordinated and consistent way compared with previous efforts. It describes one of the largest model comparisons of projected health impacts due to climate change, so far. Yet, the included studies constitute only a selection of health impacts in a variety of geographical locations, and are therefore not a comprehensive assessment of all possible impact pathways and potential consequences. The new findings of these studies shed light on the complex and multidirectional impacts of climate change on health, where impacts can be both adverse or beneficial. However, the adverse impacts dominate overall

Taking globally consistent health impact projections to the next level

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Climate tops list of global threats in EU 'strategic foresight' report

By Frédéric Simon | EURACTIV ⌚ Est. 4min

📅 8 sept. 2021 (updated: 📅 10 sept. 2021)



While the focus last year was placed on “resilience” in the aftermath of the global coronavirus pandemic, this year’s report explored “the geopolitical dimension of resilience,” said Maroš Šefčovič, the EU Commissioner in charge of interinstitutional relations and foresight. [European Union, 2021. Source: EC - Audiovisual Service]

📖 EURACTIV is part of the Trust Project >>>



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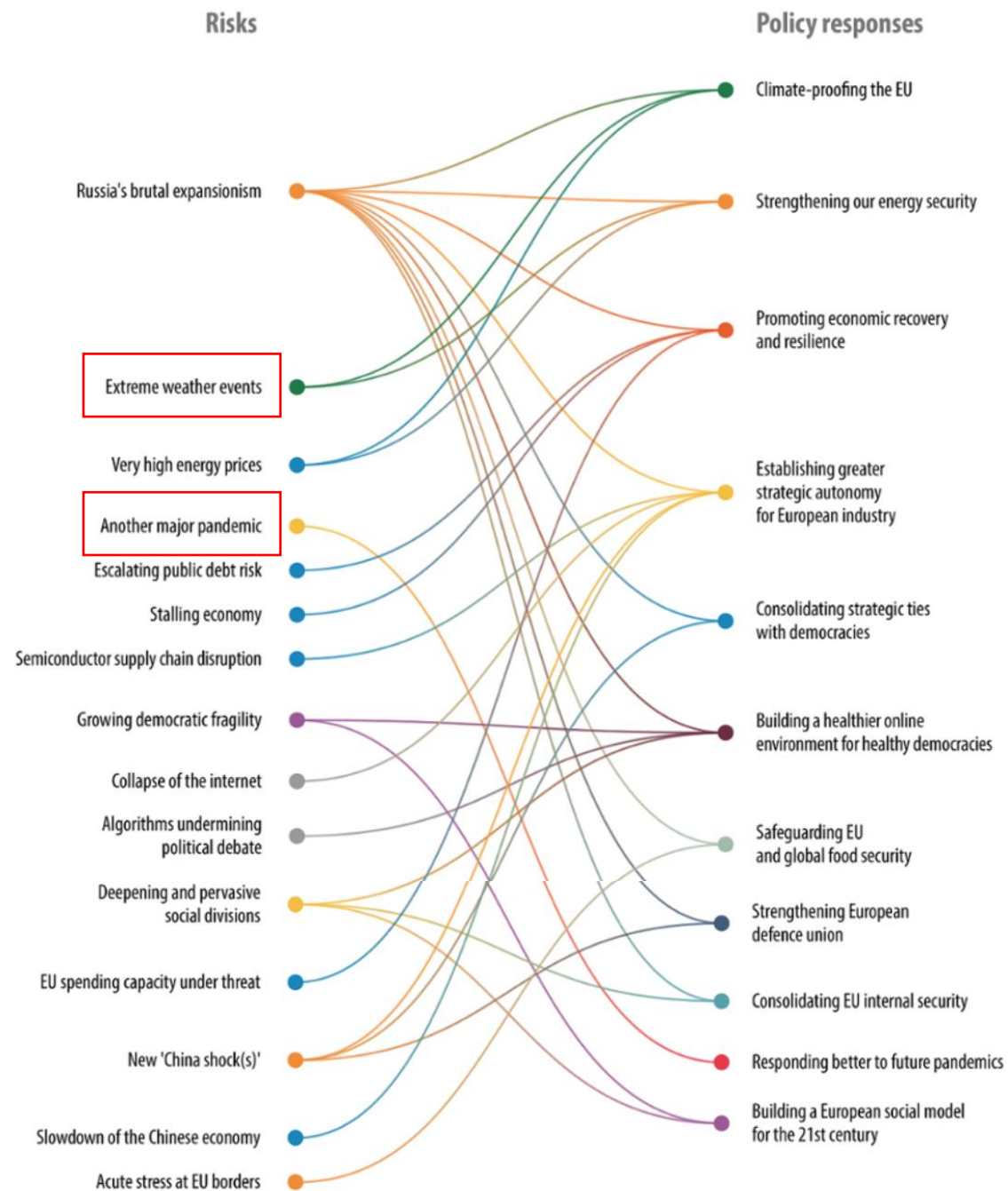


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The effect of global change on mosquito-borne disease

Lydia H V Franklins, Kate E Jones, David W Redding, Ibrahim Abubakar

Lancet Infect Dis 2019;
19: e302-12

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June 18, 2019
[http://dx.doi.org/10.1016/S1473-3099\(19\)30161-6](http://dx.doi.org/10.1016/S1473-3099(19)30161-6)

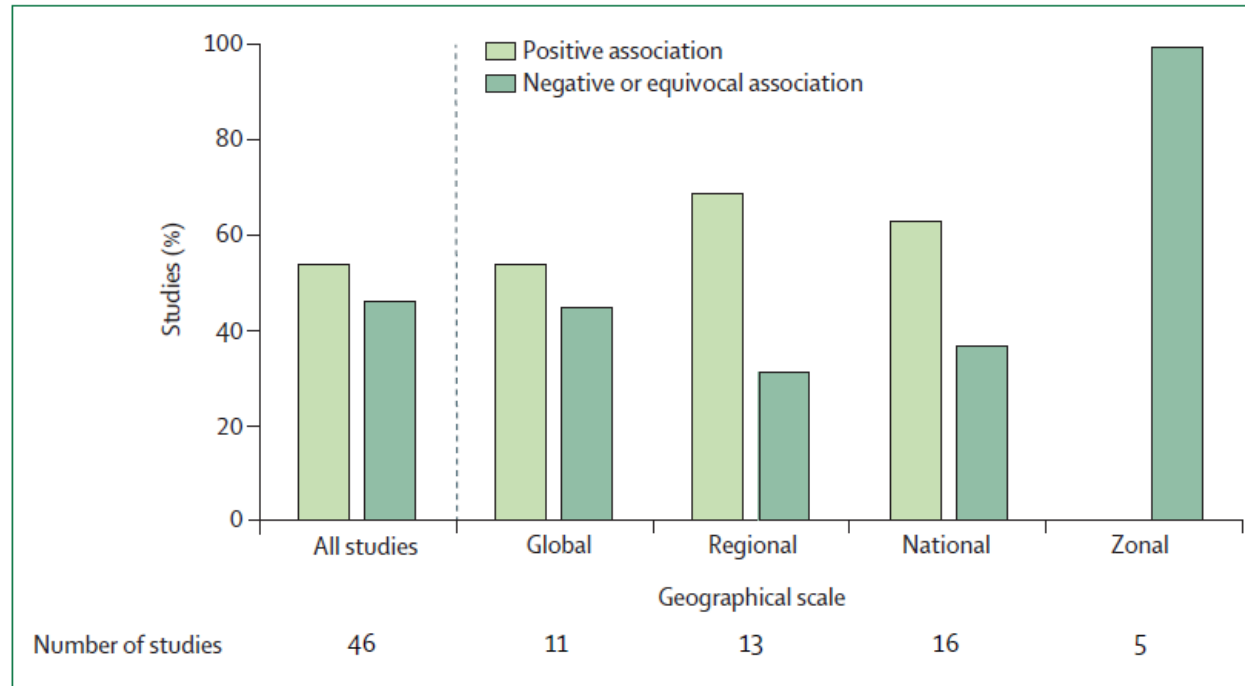


Figure 1: The percentage of studies predicting a positive or a negative or equivocal association between climate change and mosquito-borne disease risk per geographical region following review of the effect of climate change on disease risk

54% + versus 46% - ou ✗
Des 54% +, 97% des études uniquement des
variables biométéorologiques

Biais de communication, responsabilité des institutions et temps de la recherche.

Aiôn ou Khronos !

Climate change and human infectious diseases: A synthesis of research findings from global and spatio-temporal perspectives

Lu Liang^{a,b,*}, Peng Gong^{b,c}

Environment International 103 (2017) 99–108

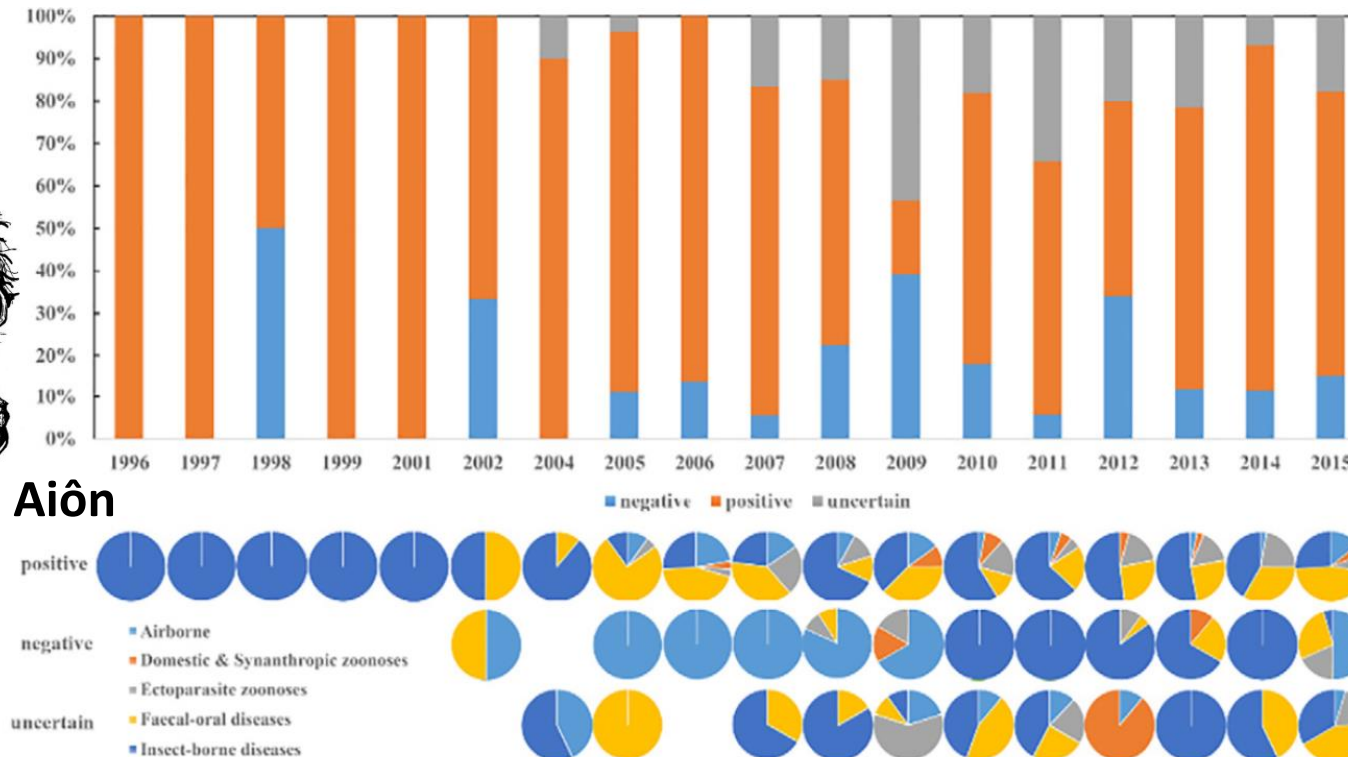
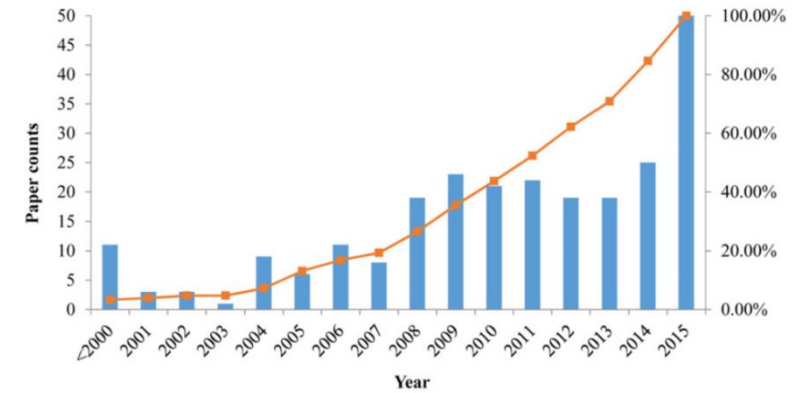


Fig. 3. CC-ID research trend. The bar figure shows the annual total number of related peer-reviewed literature, and the colors indicate the three relation types. The percentage of positive, negative and uncertain responses to climate change is scaled by the total number of cases. The pie charts show the proportion of ID types in each response relation over time.

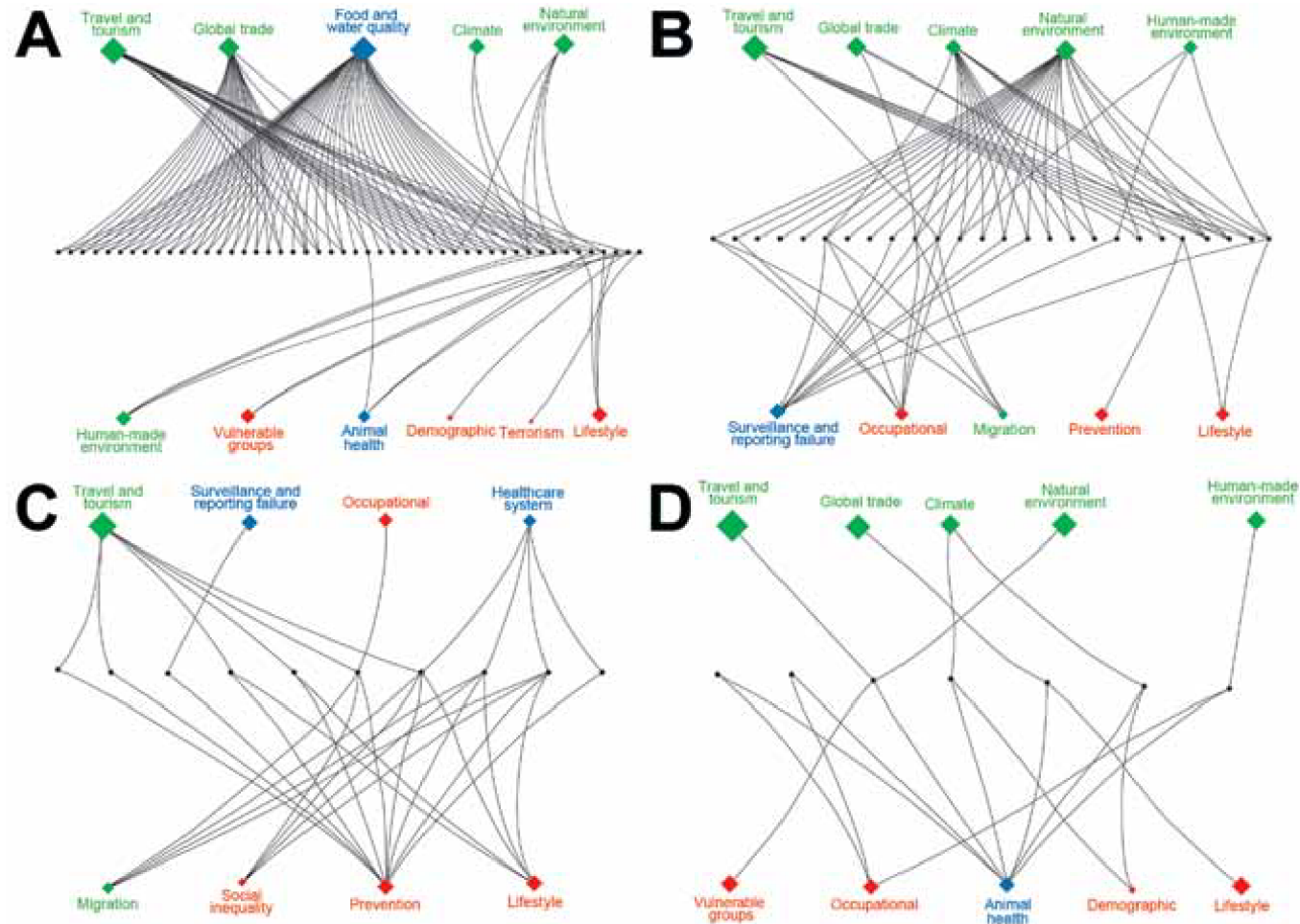


Figure 2. Infectious disease threat events (IDTEs), by contributing drivers, observed in Europe, 2008–2013. The 3 IDTE categories are represented by green (globalization and environment), red (sociodemographic), and blue (public health systems) symbols, the sizes of which are proportional to the overall frequency of the driver. A) Foodborne and waterborne IDTEs. B) Vectorborne and rodentborne IDTEs. C) Other zoonoses IDTEs. D) Vaccine preventable IDTEs.

Determinants and Drivers of Infectious Disease Threat Events in Europe

Jan C. Semenza, Elisabet Lindgren, Laszlo Balkanyi, Laura Espinosa, My S. Almqvist, Pasi Penttinen, Joacim Rocklöv

Emerging Infectious Diseases • www.cdc.gov/eid • Vol. 22, No. 4, April 2016

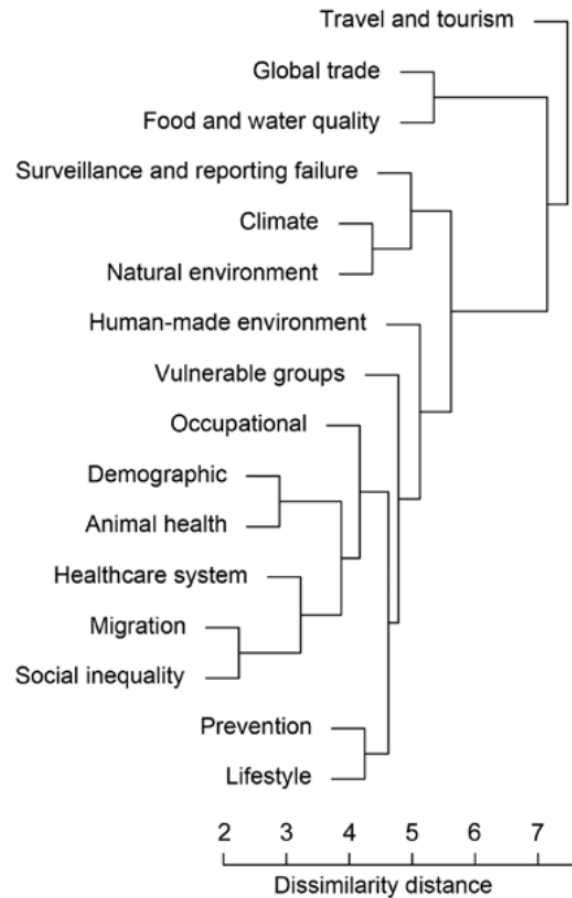


Figure 3. Cluster dendrogram from hierarchical cluster analysis of drivers contributing to observed infectious disease threat events (IDTEs), Europe, 2008–2013. Individual segments (leaves) on the lower part of the tree are more related to each other, as indicated by distances between the branches. Drivers below travel and tourism also occurred less often as underlying drivers of IDTEs and tended to be more contextual in nature. Scale bar indicates dissimilarity distance for drivers, as measured by frequency of pairwise co-occurrence in clusters. Similar drivers (e.g., that co-occurred in outbreaks) are at a close distance, and those that were more independent of other drivers show higher dissimilarity.

We found globalization and environment to be the most noteworthy driver category for IDTEs in Europe. More specifically, travel and tourism, food and water quality, natural environment, global trade, and climate were the top 5 drivers of all IDTEs identified through epidemic intelligence at ECDC. Among these, travel and tourism proved to be significantly distinct in the hierarchical cluster analysis and cluster dendrogram (Figure 3). In this analysis of epidemic intelligence data, travel and tourism was not only the most distinct but also the most recurrent driver

Determinants and Drivers of Infectious Disease Threat Events in Europe

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Emerging Infectious Diseases • www.cdc.gov/eid • Vol. 22, No. 4, April 2016

Disease control tools to secure animal and public health in a densely populated world

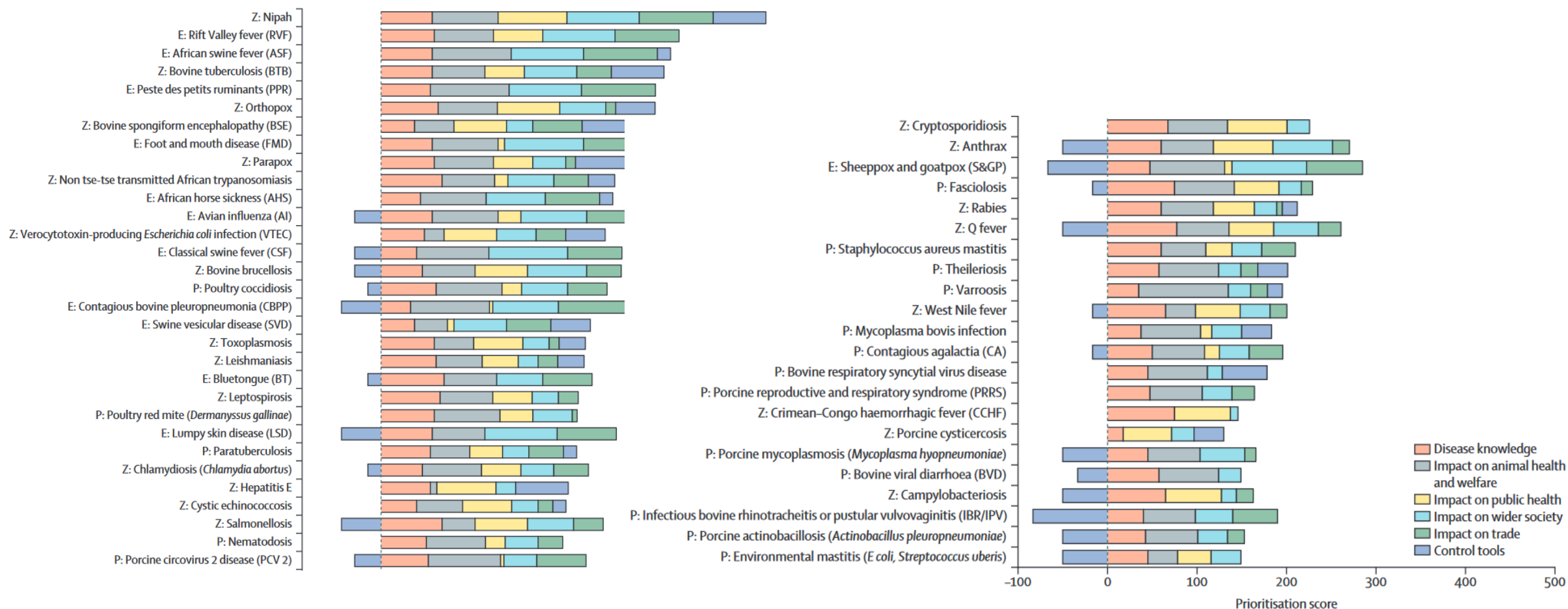
Johannes Charlier, Herman W Barkema, Paul Becher, Paola De Benedictis, Ingrid Hansson, Isabel Hennig-Pauka, Roberto La Ragione, Lars E Larsen, Evelyn Madoroba, Dominiek Maes, Clara M Marín, Franco Mutinelli, Alasdair J Nisbet, Katarzyna Podgórska, Jozef Vercruysse, Fabrizio Vitale, Diana J L Williams, Ruth N Zadoks

Lancet Planet Health 2022;

6: e812–24

DISCONTTOOLS,

Animal health is a prerequisite for global health, economic development, food security, food quality, and poverty reduction, while mitigating against climate change and biodiversity loss. We did a qualitative review of 53 infectious diseases in terrestrial animals with data from DISCONTTOOLS, a specialist database and prioritisation model focusing on research gaps for improving infectious disease control in animals. Many diseases do not have any appropriate control tools, but the prioritisation model suggests that we should focus international efforts on Nipah virus infection, African swine fever, contagious bovine pleuropneumonia, peste des petits ruminants, sheeppox and goatpox, avian influenza, Rift Valley fever, foot and mouth disease, and bovine tuberculosis, for the greatest impact on the UN's Sustainable Development Goals. Easy to use and accurate diagnostics are available for many animal diseases.



Disease control tools to secure animal and public health in a densely populated world

Johannes Charlier, Herman W Barkema, Paul Becher, Paola De Benedictis, Ingrid Hansson, Isabel Hennig-Pauka, Roberto La Ragione, Lars E Larsen, Evelyn Madoroba, Dominiek Maes, Clara M Marín, Franco Mutinelli, Alasdair J Nisbet, Katarzyna Podgórska, Jozef Vercruysse, Fabrizio Vitale, Diana J L Williams, Ruth N Zadoks

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DISCONTOLS,

Key messages

- We did a qualitative review on the research gaps around 53 infectious diseases in animals
- We identified animal diseases with greatest potential for impact on UN Sustainable Development Goals
- There is a pressing need to increase and sustain fundamental and applied research into diagnostic development, vaccinology, digital health, therapeutics, and control strategies
- Increased research on animal health is a prerequisite to address global issues, such as food security, climate change, antimicrobial and antiparasitic resistance, and epidemic preparedness



Impacts of biodiversity on the emergence and transmission of infectious diseases

Felicia Keesing¹, Lisa K. Belden², Peter Daszak³, Andrew Dobson⁴, C. Drew Harvell⁵, Robert D. Holt⁶, Peter Hudson⁷, Anna Jolles⁸, Kate E. Jones⁹, Charles E. Mitchell¹⁰, Samuel S. Myers¹¹, Tiffany Bogich³ & Richard S. Ostfeld¹²

2 DECEMBER 2010 | VOL 468 | NATURE

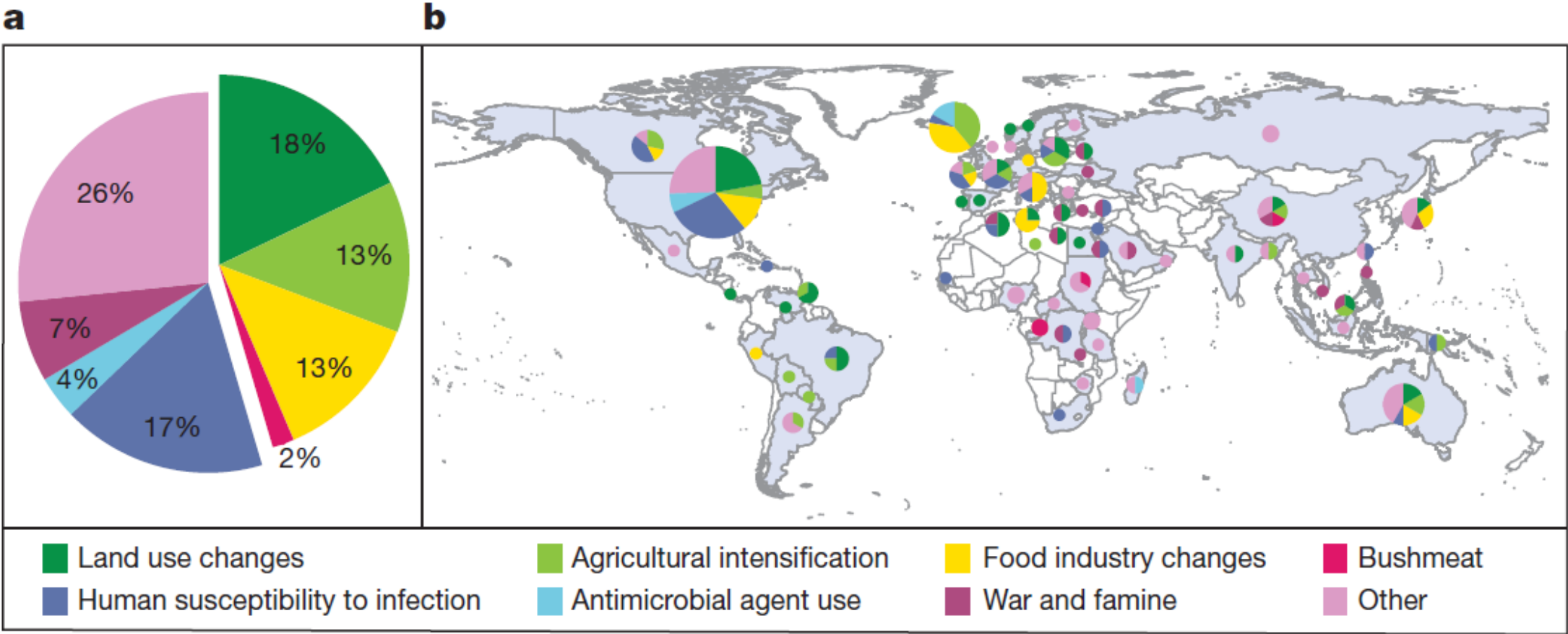


Figure 2 | Drivers and locations of emergence events for zoonotic infectious diseases in humans from 1940–2005. **a**, Worldwide percentage of emergence events caused by each driver; **b**, Countries in which the emergence events took place, and the drivers of emergence. The size of the circle represents the number of emergence events: for scale, the number of events in the United States was 59. Globally, almost half of these diseases resulted from changes in land use, changes

in agricultural and other food production practices, or through wildlife hunting, which suggests that contact rates between humans and other animals are an important underlying cause of zoonotic disease emergence. ‘Other’ includes international travel and commerce, changes in human demographics and behaviour, changes in the medical industry, climate and weather, breakdown of public health measures, and unspecified causes. Analysed from data in ref. 40.

Emerging human infectious diseases and the links to global food production

Jason R. Rohr^{1,2*}, Christopher B. Barrett³, David J. Civitello⁴, Meggan E. Craft⁵, Bryan Delius², Giulio A. DeLeo⁶, Peter J. Hudson⁷, Nicolas Jouanard⁸, Karena H. Nguyen², Richard S. Ostfeld⁹, Justin V. Remais¹⁰, Gilles Riveau⁸, Susanne H. Sokolow^{6,11} and David Tilman¹²

nature
sustainability

NATURE SUSTAINABILITY | VOL 2 | JUNE 2019 | 445–456

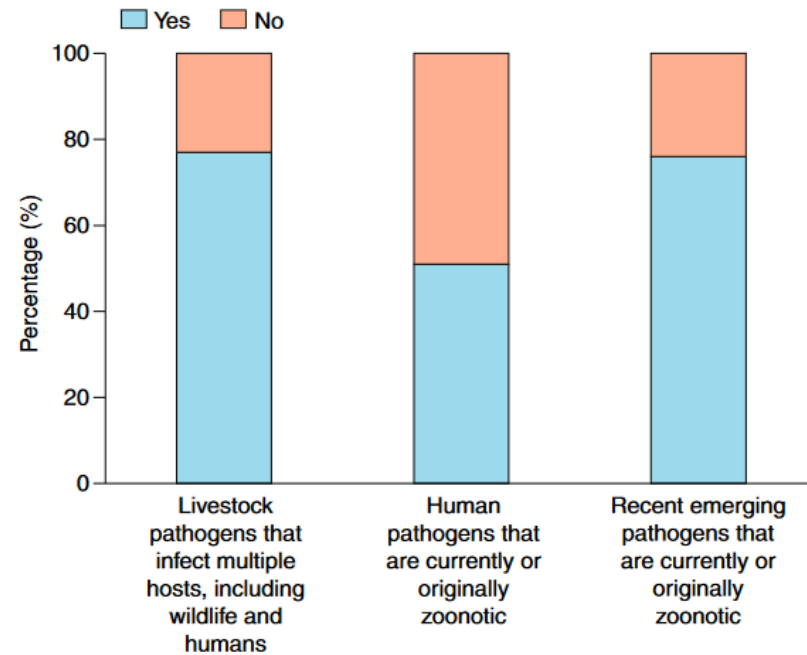


Fig. 4 | Livestock pathogens and zoonoses. Percentage of livestock pathogens that infect multiple host species¹¹⁵, human pathogens that are currently or originally zoonotic^{29,116}, and recent emerging pathogens that are zoonotic^{1,29}.

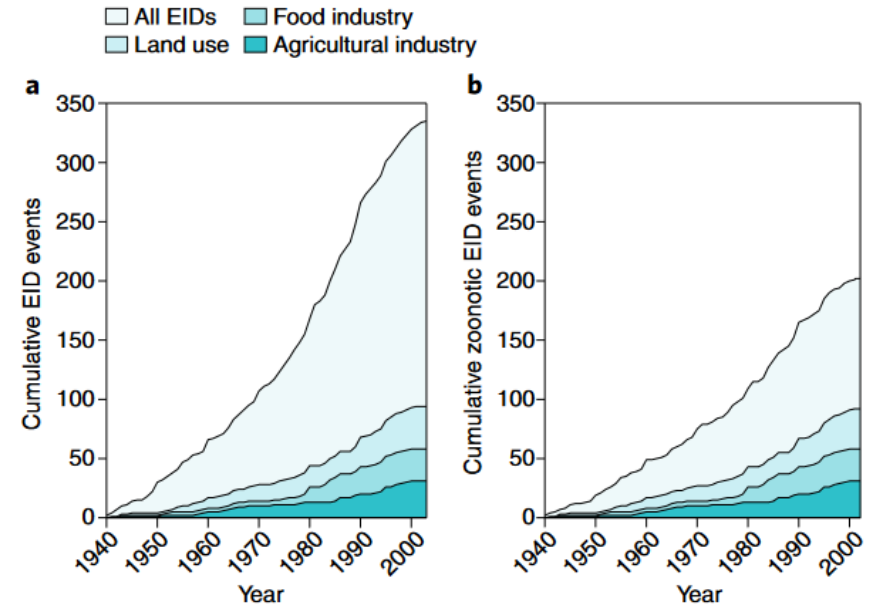
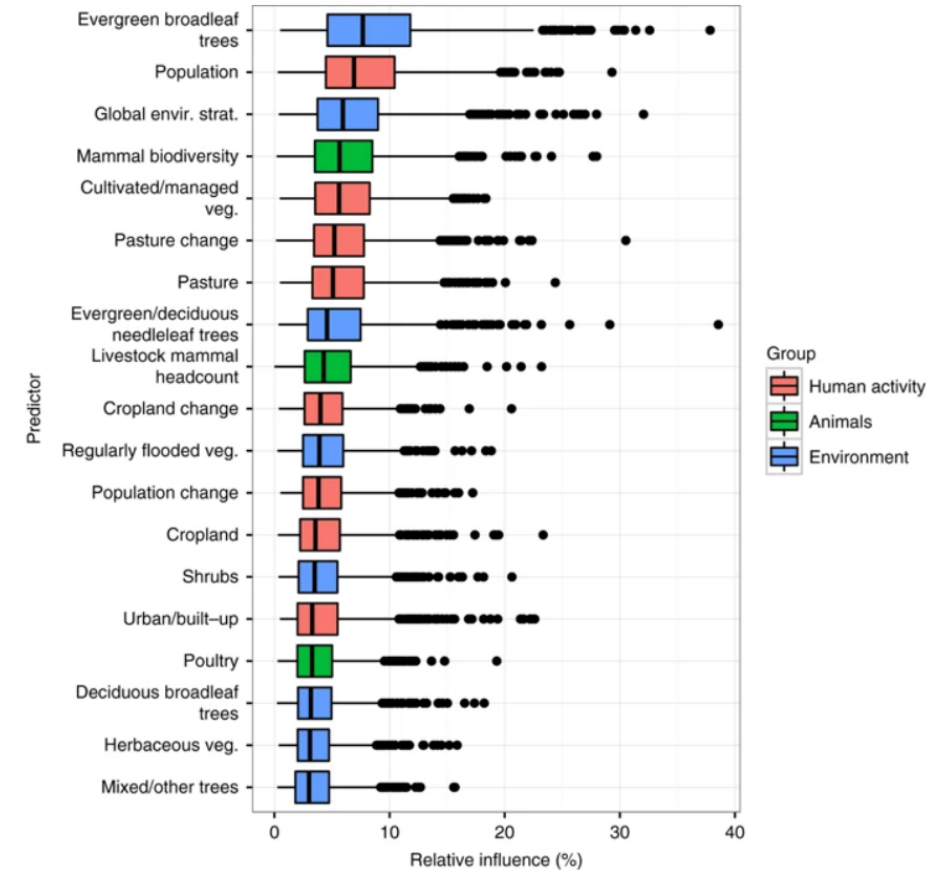


Fig. 5 | Effects of agricultural drivers on emerging infectious diseases (EIDs) and zoonotic EIDs of humans since 1940. a,b, Agricultural drivers were associated with 25% of all (a) and nearly 50% of zoonotic (b) diseases that emerged in humans. For these figures, we use the definition of a zoonotic EID provided by Jones et al.¹, which is a disease that emerged via non-human to human transmission, not including vectors. See Supplementary Methods for the methods used to develop this figure.

Fig. 1



The relative influence of predictors on EID event occurrence probability. The box plots show the spread of relative influence across 1000 replicate model runs to account for uncertainty in EID event location (see above). Whiskers represent the minimum or maximum datum up to 1.5 times the inter-quartile range beyond the lower or upper quartile. BRTs do not provide p -values or coefficients, but rank variables by their relative influence in explaining variation in the outcome²⁶

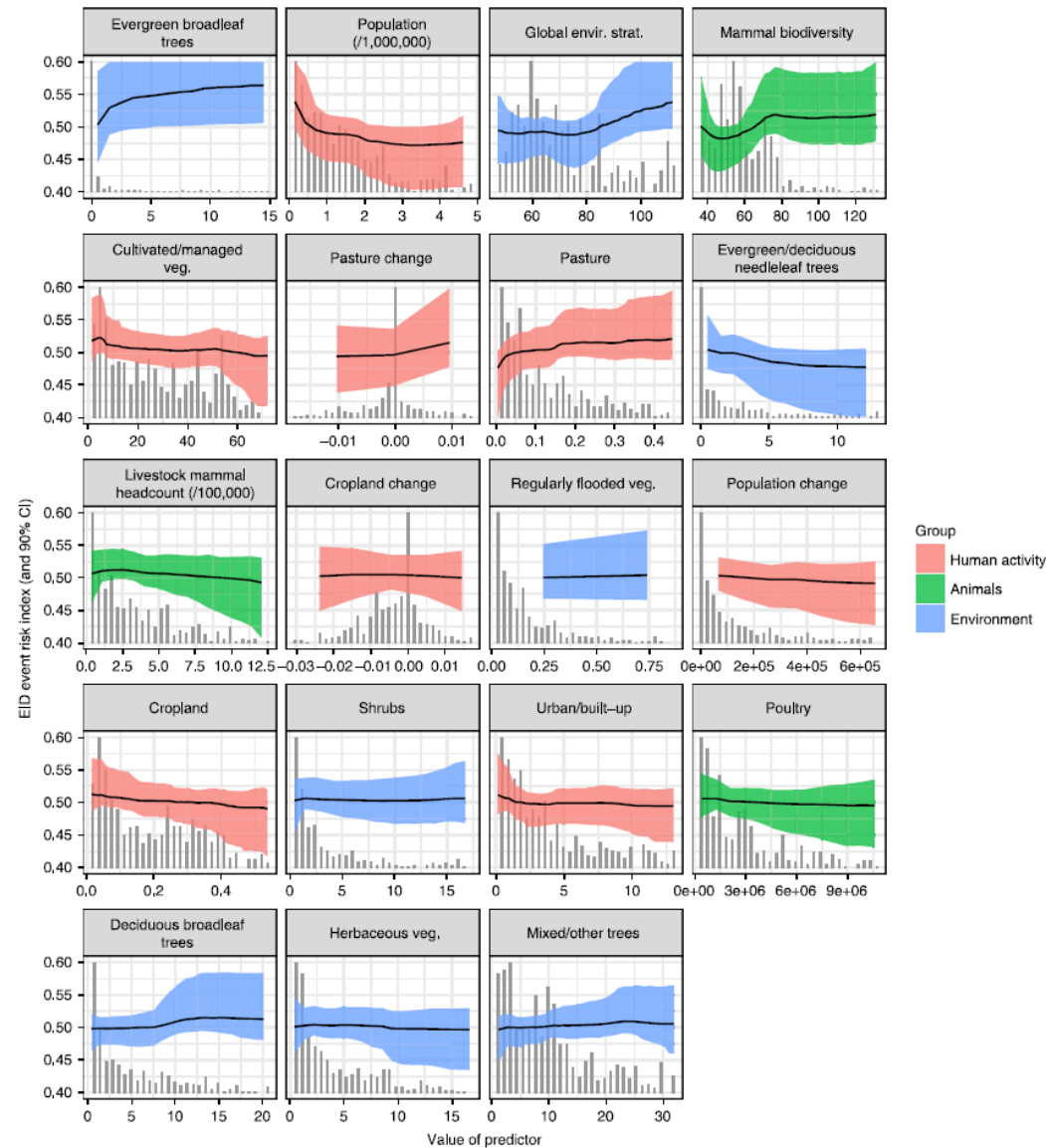


Fig. 2 Partial dependence plots showing the influence on zoonotic EID events for all predictors in the weighted boosted regression tree model, ordered by relative influence. X axes show the range from the 10th to 90th percentiles of sampled values of predictors (e.g., number of mammal species per grid square for mammalian richness, or proportion of grid cell for a land cover type). Y axes show the effect on the EID event risk index from that variable. Black lines show the median and colored areas show the 90% confidence intervals, computed using a bootstrap resampling regime incorporating uncertainty in EID event locations. The overall prevalence of our outcome, which indexes EID event risk, is fixed by the resampling regime between 0 and 1, with a mean at 0.5. Y axes are centered around the mean and scaled to 0.1 above and below. Partial dependence plots display the response for an individual variable in the model while holding all other variables constant^{26, 61}. They allow a visualization of what are mostly non-linear relationships between drivers and the EID event risk index (in this case, after reporting effort is factored out.). See Supplementary Note 3 for results of the model unweighted by reporting effort

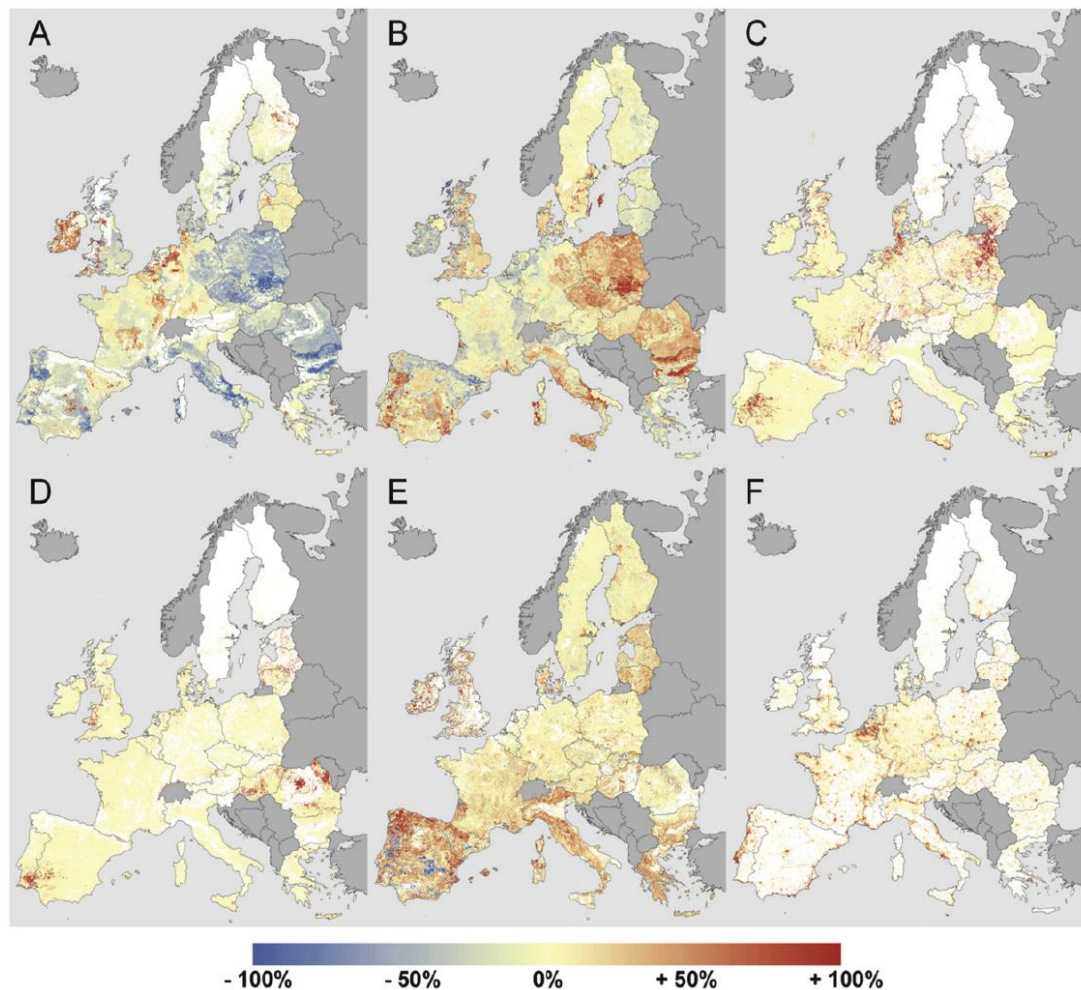


Figure 2. Spatial patterns of changes in the area of broad land-use categories in Europe ((A): cropland extent; (B): pasture extent; (C): agricultural abandonment; (D): agricultural recultivation; (E): forestland extent; (F): urban extent). Changes refer to the period 1990–2006 (A), (B), (E), (F)) and 2001–2012 (C), (D). Scale refers to relative area changes within a $3 \times 3 \text{ km}^2$ gridcell.

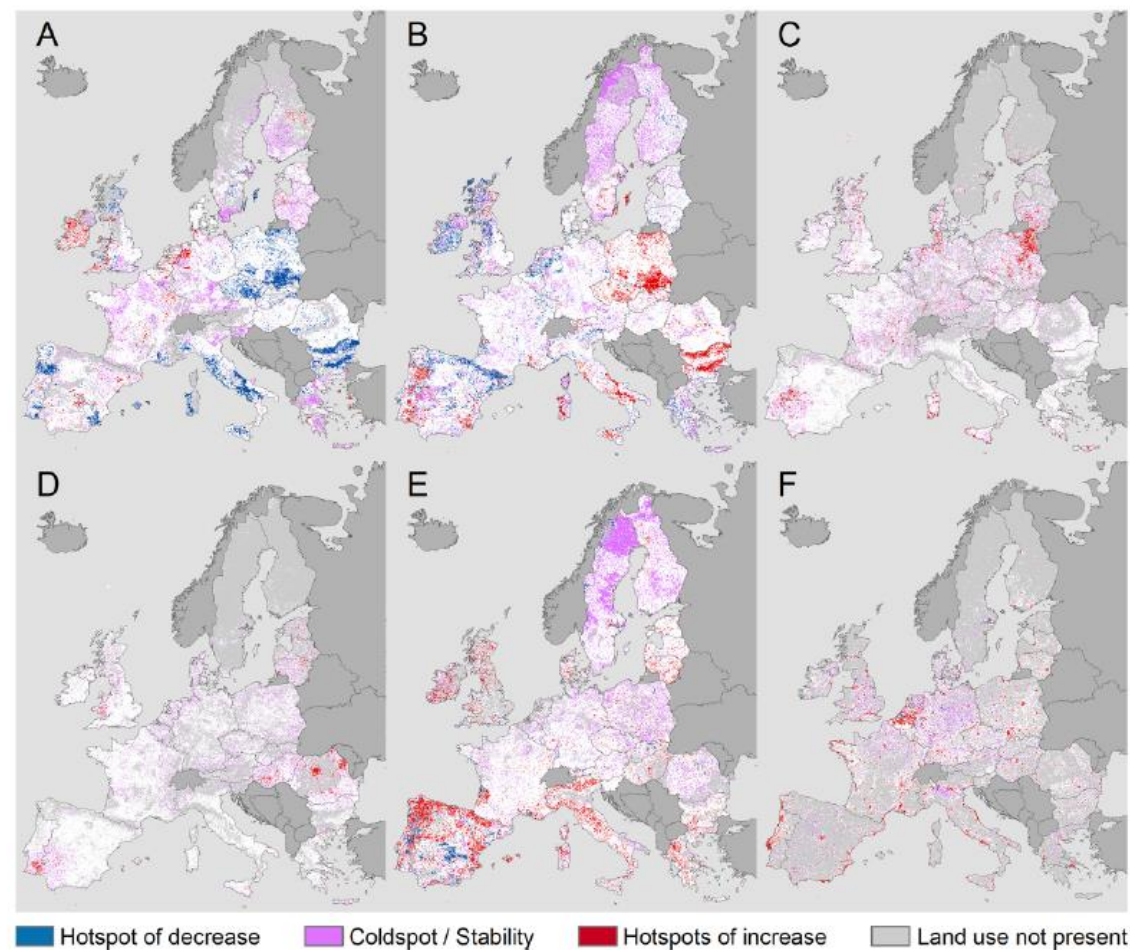


Figure 3. Hotspots of area changes among broad land-use categories between 1990 and 2006 (2000–2012 for (C) and (D)). Europe ((A): cropland extent; (B): pasture extent; (C): agricultural abandonment; (D): agricultural recultivation; (E): forestland extent; (F): urban extent). Hotspots include the 10% largest change values (in positive and negative direction). Coldspots/stability areas entail the 10% smallest change values (both positive and negative) as well as all unchanged areas. Areas outside hotspots and coldspots are in white (for hotspots based on alternative thresholds see supporting information).

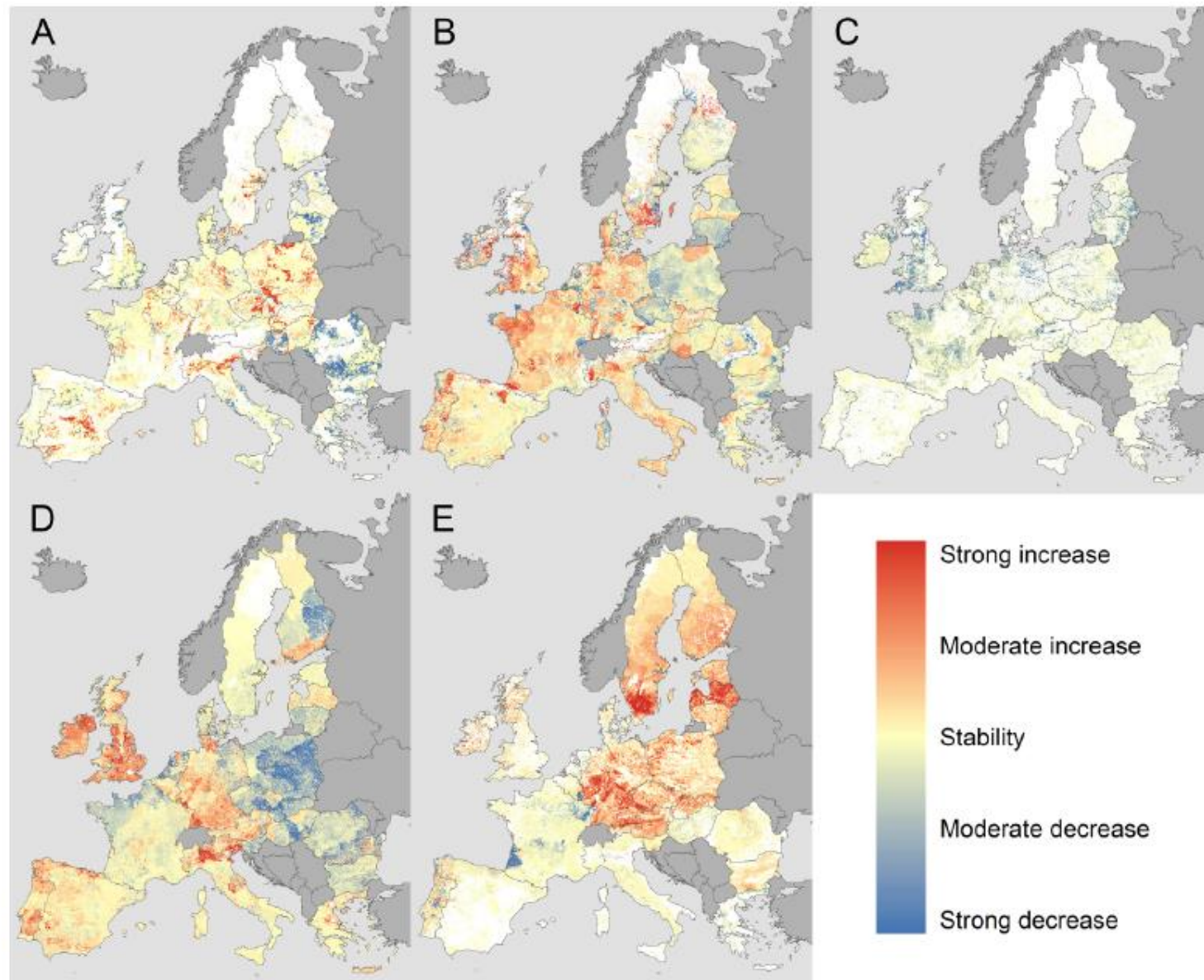


Figure 4. Spatial patterns of changes in the intensity within broad land-use classes in Europe between 1990 and 2006 ((A): fertilizer use on cropland [scaled between -120 and $+150 \text{ kg ha}^{-1}$]; (B): crop yields [$\pm 1 \text{ kg C m}^{-2}$]; (C): livestock density [-90 ; $+25$ livestock units]; (D): biomass removal from grazing land [$\pm 1 \text{ kg C m}^{-2}$]; (E): roundwood production [-14.2 ; $+7.6 \text{ m}^{-3} \text{ ha}^{-1} \text{ yr}^{-1}$]).

La notion de « spillover » ou de « débordement » et rôle des communautés d'espèces animales

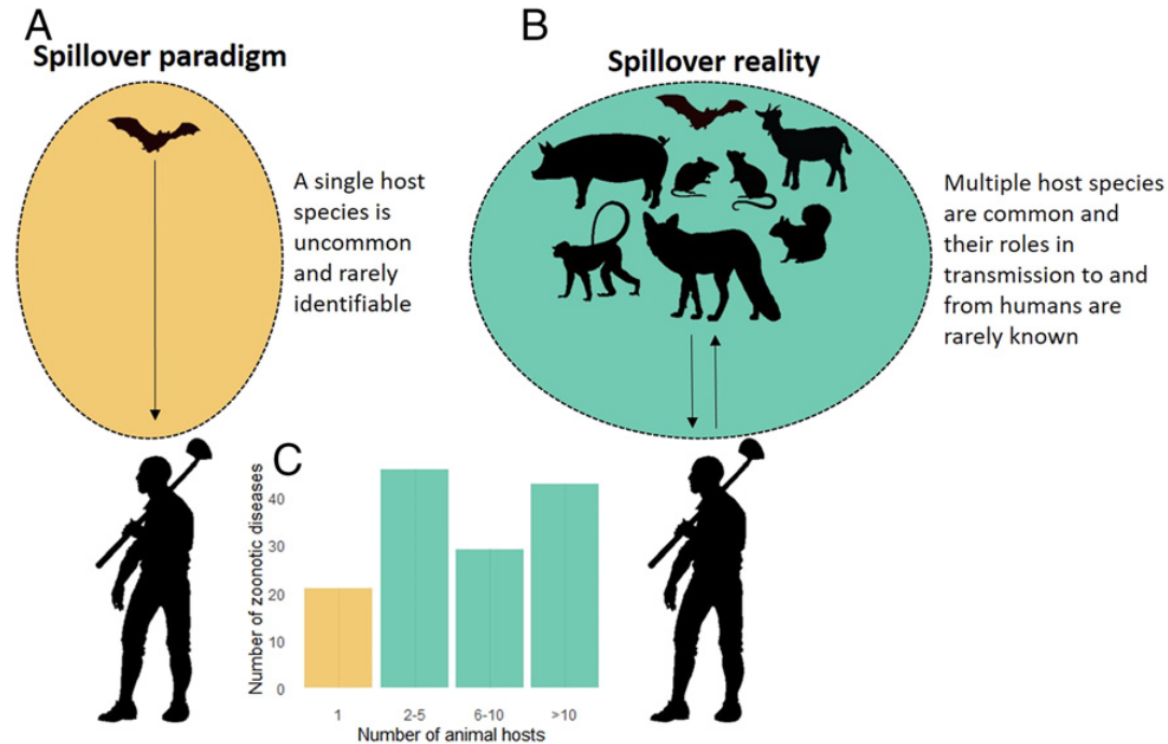


Fig. 4. The paradigm and the reality for research on spillover of zoonotic pathogens into humans. (A) The paradigm emphasizes a single animal host species for a zoonotic pathogen and an original spillover event, though the event and the species are rarely identified. (B) In reality, most zoonotic pathogens have multiple host species whose specific roles in transmission to and from humans are rarely known. (C) The number of viral zoonotic diseases that have 1, 2 to 5, 6 to 10, or 11+ known animal host species other than humans. Plotted from data made available in supplementary materials from Johnson et al. (21); see caveats about these and similar data in [SI Appendix](#).

Impacts of biodiversity and biodiversity loss on
zoonotic diseases

Averting wildlife-borne infectious disease epidemics requires a focus on socio-ecological drivers and a redesign of the global food system

Giulia I. Wegner,^{a*} Kris A. Murray,^{b,c} Marco Springmann,^d Adrian Muller,^{e,f} Susanne H. Sokolow,^{a,h} Karen Saylors,ⁱ and David M. Morens^j

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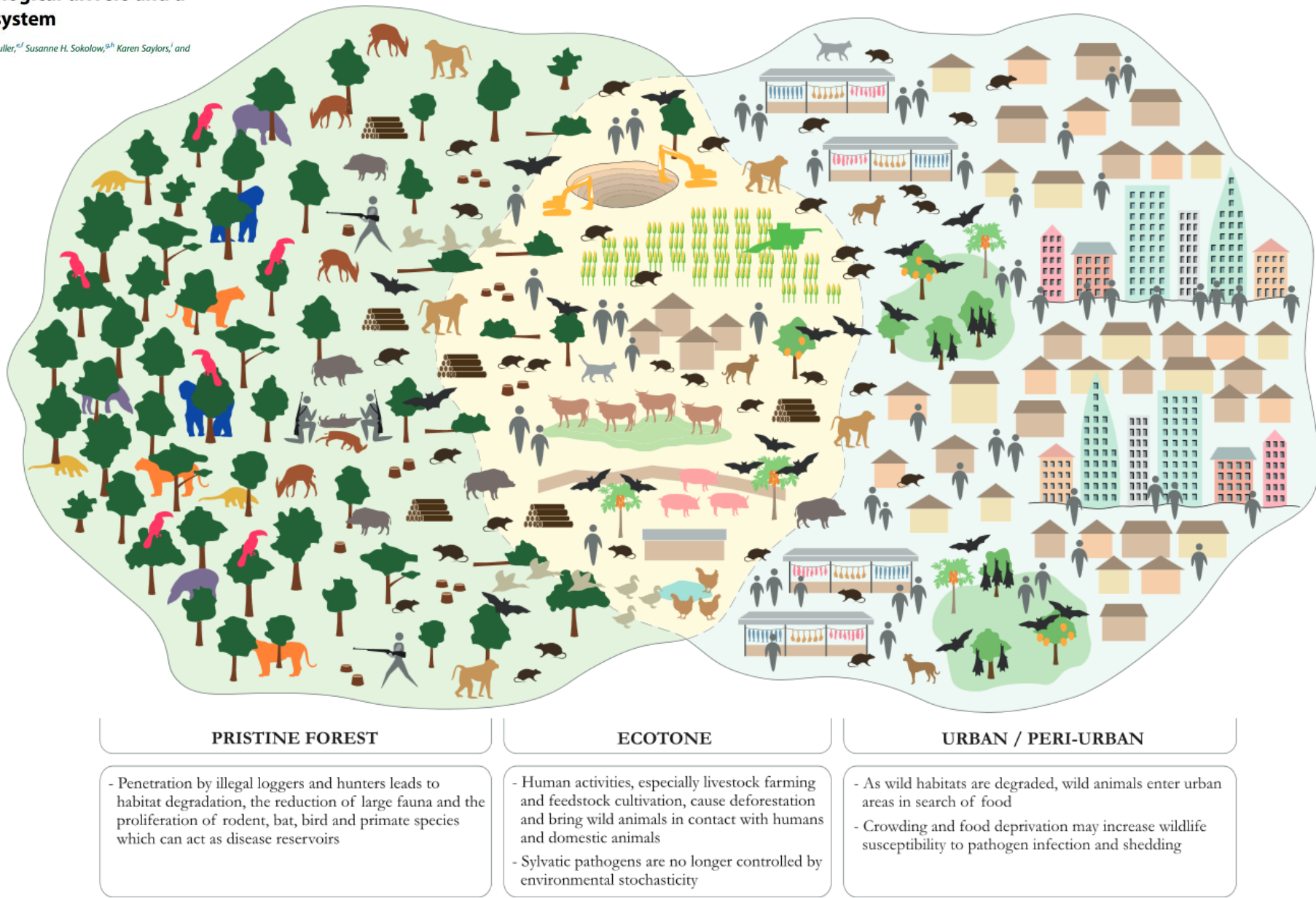


Figure 2. Tropical deforestation and overhunting as drivers of wildlife-origin zoonotic disease transmission



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National Science Foundation, National Institutes of Health, LabEx CEBA

Vous-mêmes pour votre attention

Award #1911457



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Hand, Foot, and Mouth Disease in China: Critical Community Size and Spatial Vaccination Strategies

Received: 30 October 2015

Accepted: 13 April 2016

Published: 29 April 2016

Thomas P. Van Boeckel^{1,2}, Saki Takahashi¹, Qiaohong Liao³, Weijia Xing^{3,4}, Shengjie Lai^{3,5}, Victor Hsiao¹, Fengfeng Liu³, Yaming Zheng³, Zhaorui Chang³, Chen Yuan³, C. Jessica E. Metcalf^{1,6}, Hongjie Yu³ & Bryan T. Grenfell^{1,7}

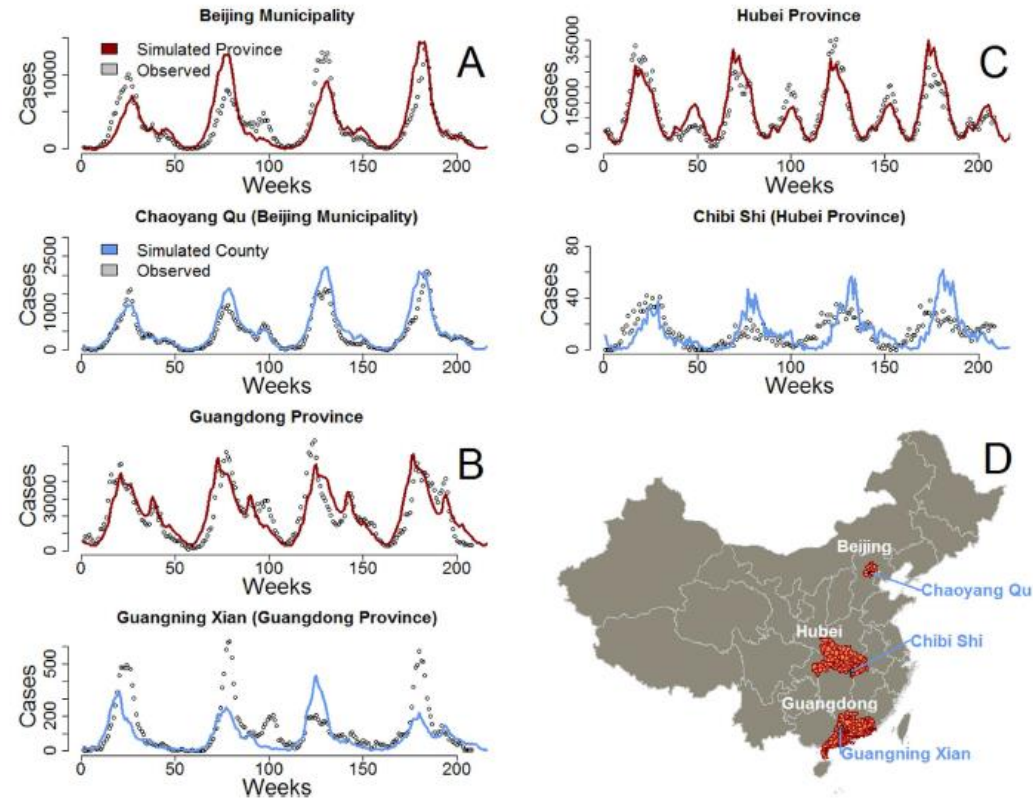


Figure 1. Scaling of the transmission parameters for the TSIR model between the province and county scale in Beijing municipality. (A) Guangdong Province (B) and Hubei Province (C). In each location the average transmission rate β_t was respectively scaled by a factor of 1.10, 2.42 and 0.05 for A, B and C after re-fitting. This figure was generated using the open source statistical software R (cran.r-project.org), version number 3.0.3, including packages maptools and foreign.

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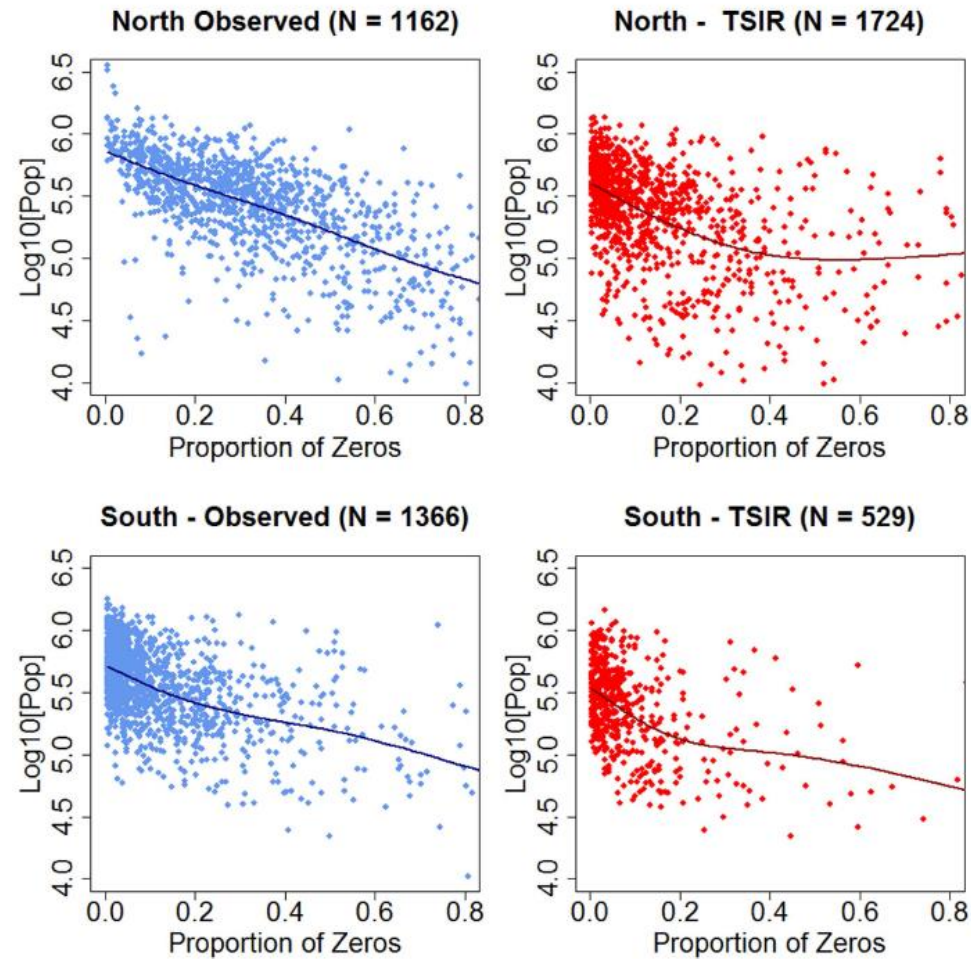


Figure 2. Critical Community size of EV-A71. Population per county as a function of the proportion of zeros in weekly incidence for observed and predicted time series. The intersection of the fitted function with the y-axis indicated the estimate of the critical community size for EV-A71. N is the number of counties with at least

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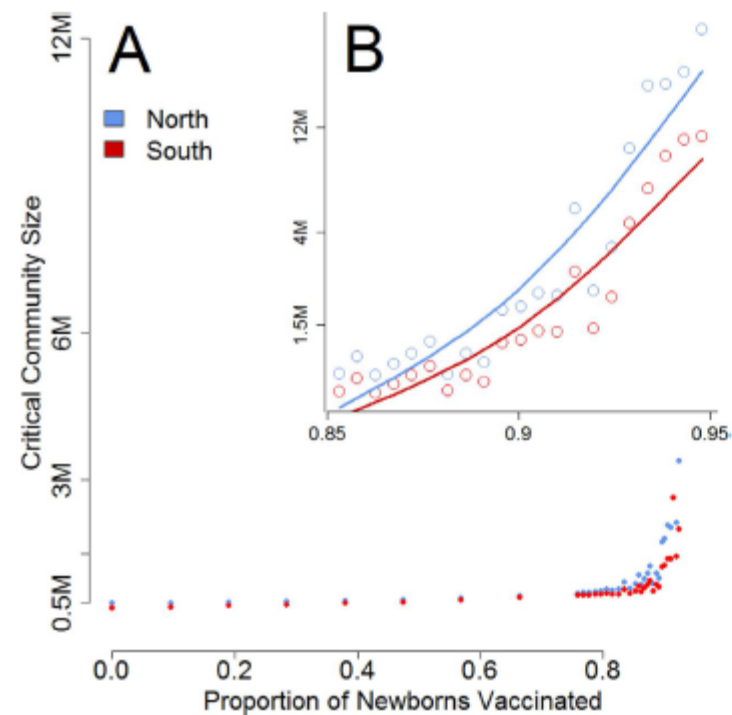


Figure 4. Routine vaccination. Effect of routine vaccination at birth on the critical community size of HFMD in the Northern (blue) and Southern (red) regions of China.

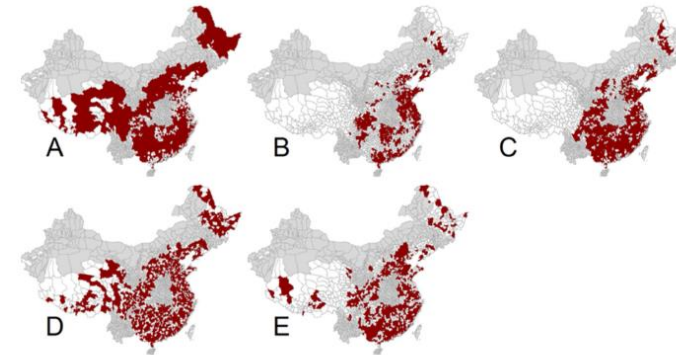


Figure 5. Spatial vaccination strategies. (A) Vaccination targeted in counties with the lowest population, (B) vaccination in the highly populated counties, (C) Vaccination in the counties where population is close to the regional CCS, and (D) vaccination in randomly selected counties. (E) Vaccination in high prevalence counties. Red indicates vaccinated areas, white indicates unvaccinated areas, grey indicates areas excluded from the analysis. This figure was generated using the open source statistical software R (cran.r-project.org), version number 3.0.3, including packages maptools and foreign.