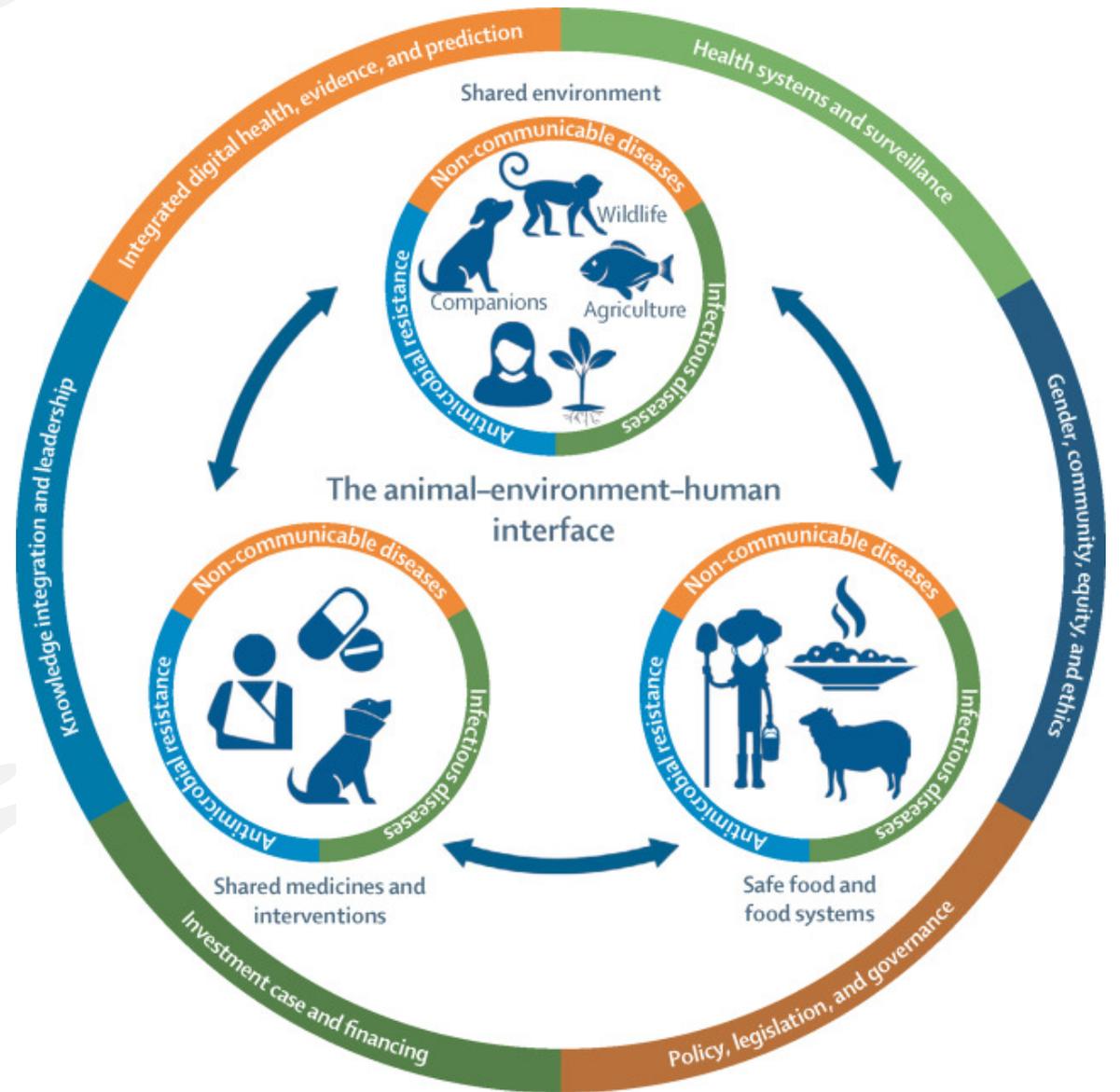


One Health Surveillance

Ramanan Laxminarayan



Surveillance helps understand drivers, reservoirs and pathways for the emergence and spread of resistant pathogens.



Stage 1: Track
resistance/presumed drivers of
resistance in different domains



Resistance has increased nearly three-fold in food animals between 2000 and 2018

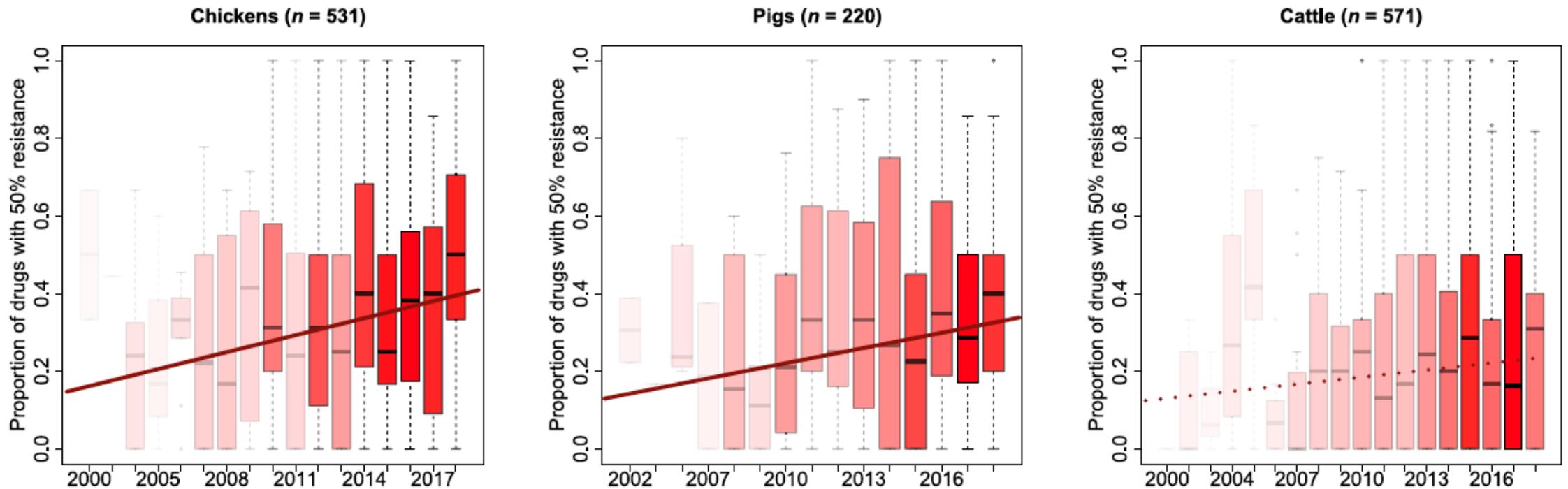
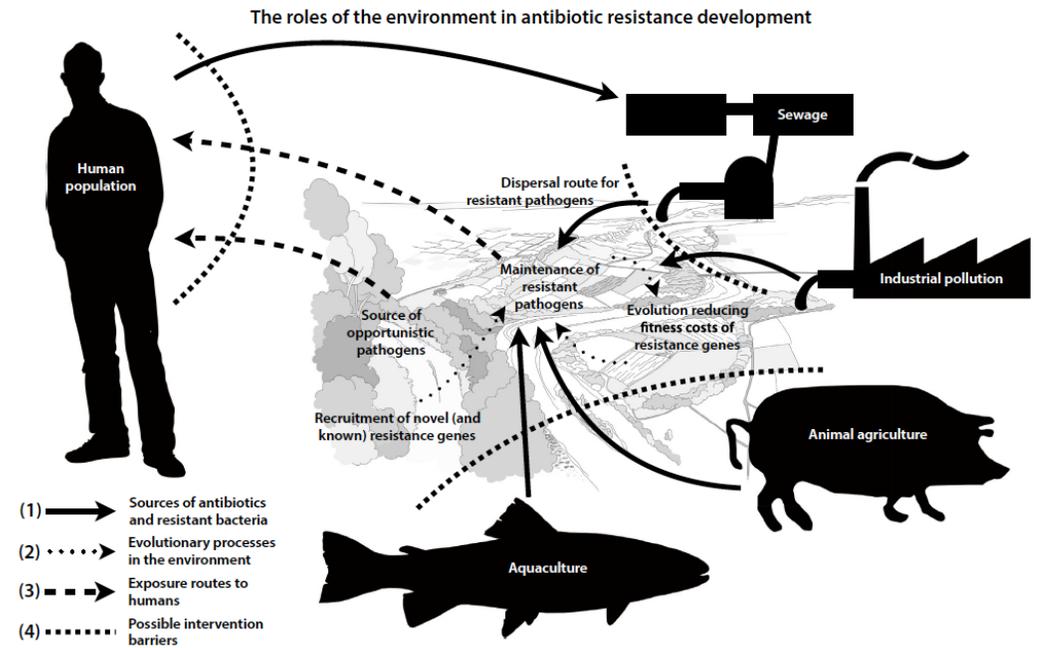
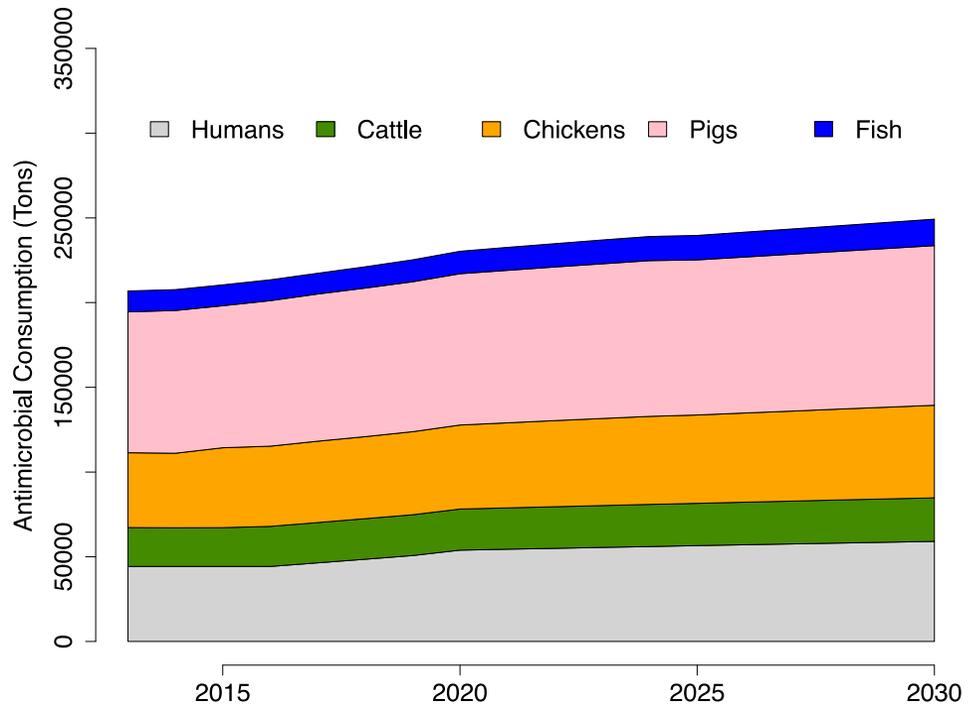


Fig. 2. Increase in antimicrobial resistance in LMICs. Proportion of antimicrobial compounds with resistance higher than 50% (P50) is shown. Solid lines indicate statistically significant (5% level) increases of P50 over time; shading indicates the number of surveys per year relative to total number of surveys per species.

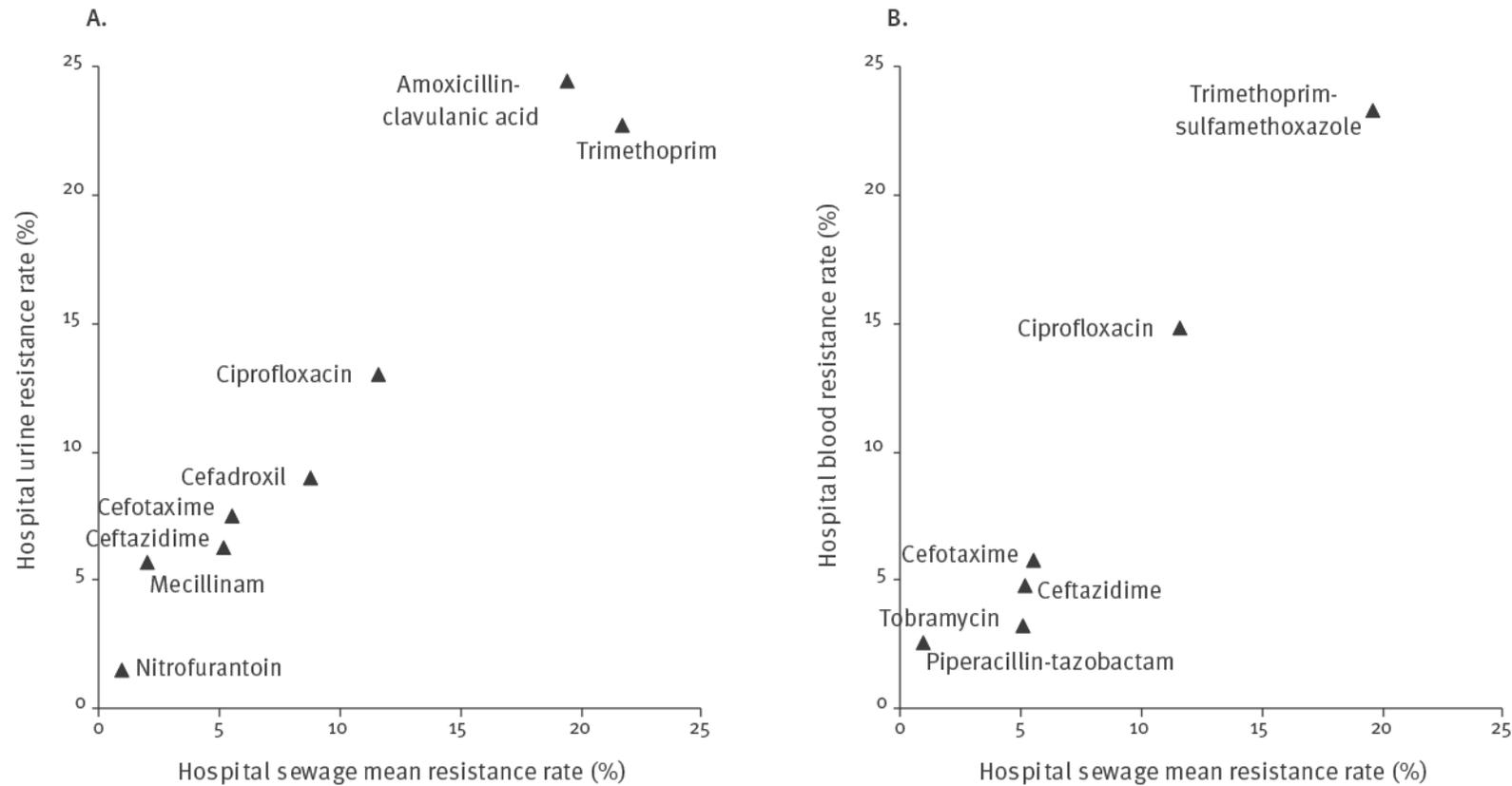


Stage 1: Track resistance/presumed drivers of resistance in different domains

Stage 2: Correlate resistance in different one health domains



Mean resistance rates in *Escherichia coli* isolated from hospital sewage samples compared with those urine and blood samples from the same hospital, Gothenburg, Sweden, 2016 (n=2,007)



Stage 1: Track resistance/presumed drivers of resistance in different domains

Stage 2: Correlate resistance in different one health domains

Stage 3: Build evidence on drivers of resistance between domains (correlation to causality)



Gram-negative bloodstream infections are associated with higher temperature

Table 3. Associations of mean monthly temperature with inpatient BSI frequencies over all seasons and within seasons.*

| Infecting organism | Adjusted percentage change in BSI frequency (95% CI) per 5.6°C (10°F) increase in monthly temperature | | | | |
|--------------------------|---|--|--------------------|--------------------|--------------------|
| | Associations over all seasons [†] | Associations within seasons [‡] | | | |
| | | Winter | Spring | Summer | Fall |
| Gram-negative bacteria | | | | | |
| <i>Acinetobacter</i> spp | 10.8 (6.9 to 14.7) | 9.5 (4.0 to 15.0) | 13.2 (8.2 to 18.3) | 8.0 (3.7 to 12.5) | 11.1 (6.3 to 16.1) |
| <i>E. coli</i> | 3.5 (2.1 to 4.9) | 4.5 (2.7 to 6.3) | 4.6 (3.0 to 6.3) | 1.5 (−0.1 to 3.0) | 3.1 (1.4 to 4.8) |
| <i>K. pneumoniae</i> | 8.0 (6.0 to 10.1) | 9.2 (6.5 to 12.0) | 6.4 (3.9 to 8.9) | 5.4 (3.2 to 7.7) | 8.5 (6.0 to 11.1) |
| <i>P. aeruginosa</i> | 7.5 (5.1 to 10.0) | 6.4 (3.3 to 9.6) | 6.5 (3.4 to 9.6) | 5.0 (2.2 to 7.8) | 9.6 (6.6 to 12.7) |
| Gram-positive bacteria | | | | | |
| <i>Enterococcus</i> spp | 0.3 (−1.1 to 1.7) | 1.2 (−0.7 to 3.0) | 0.5 (−1.3 to 2.4) | −1.5 (−3.2 to 0.1) | −0.7 (−2.5 to 1.1) |
| <i>S. aureus</i> | 2.2 (1.3 to 3.2) | 3.4 (2.1 to 4.6) | 2.2 (1.1 to 3.4) | −0.3 (−1.4 to 0.7) | 2.0 (0.8 to 3.2) |

BSI = bloodstream infection; CI = confidence interval.

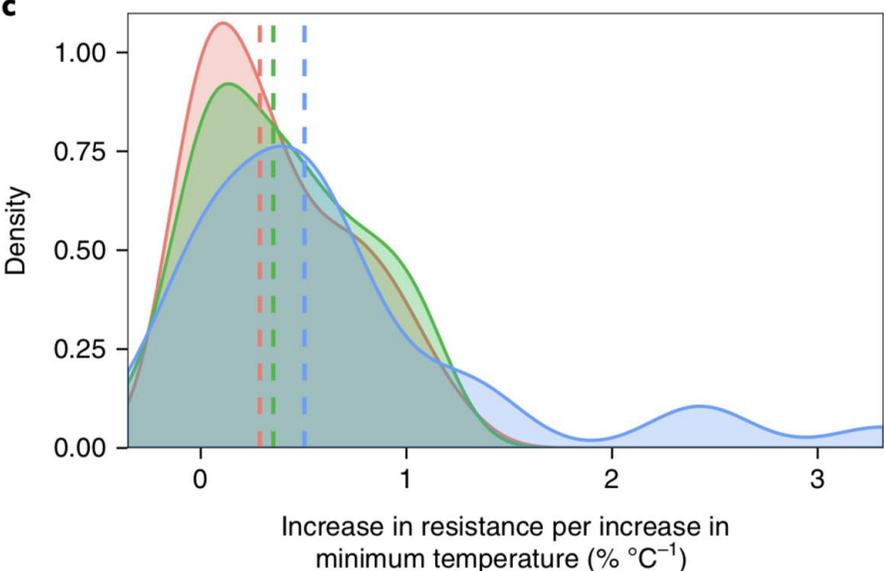
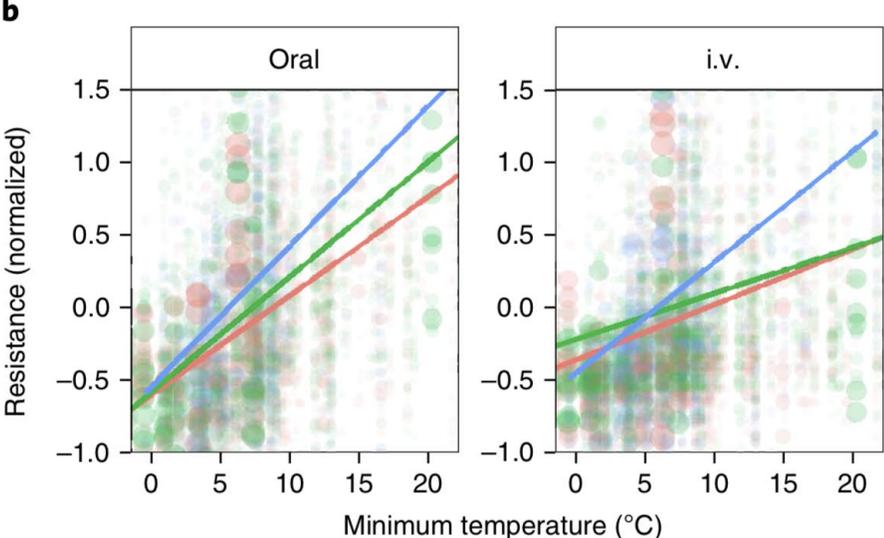
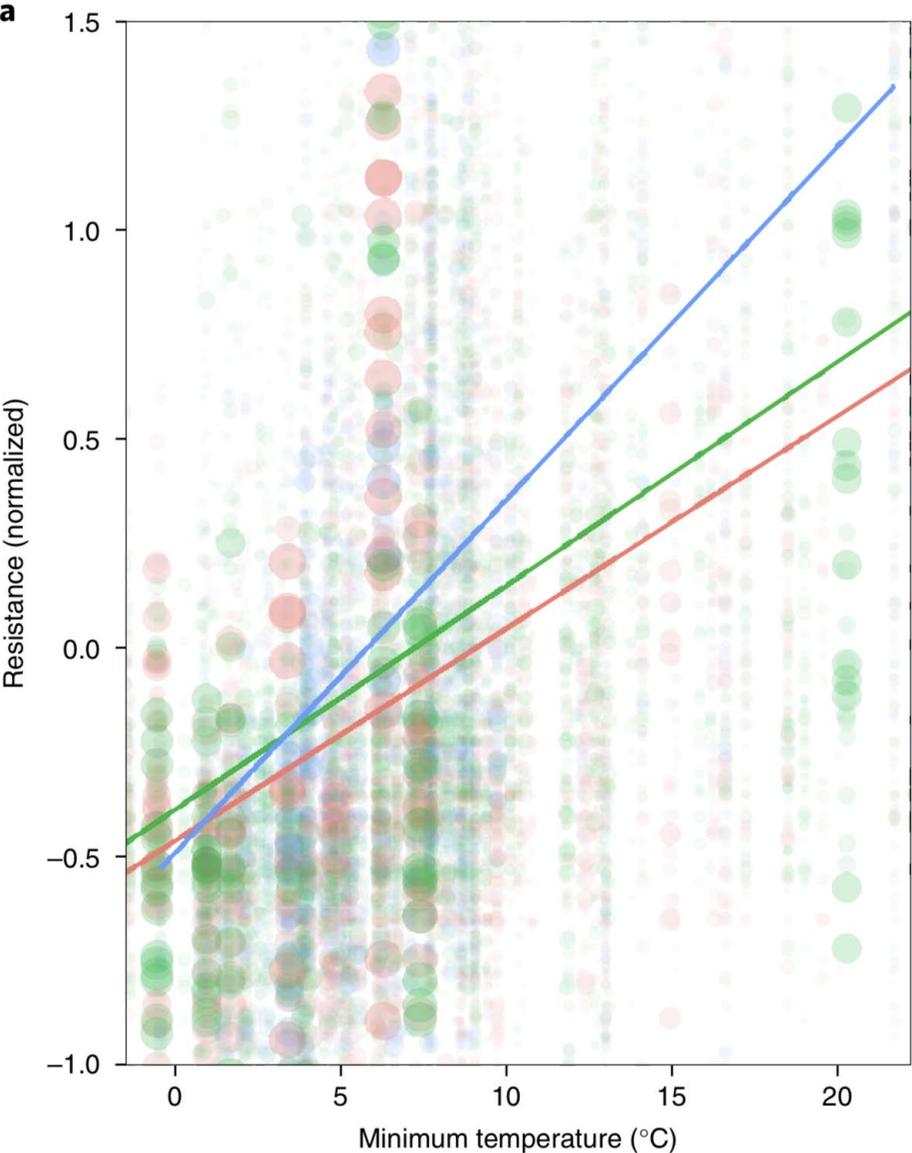
*Estimated using Poisson mixed-effects regression models with random intercepts to account for within-site correlation, natural cubic splines (7 degrees of freedom) to control for long-term trends, and adjustments for census region. Linear terms for both total monthly precipitation and mean relative humidity were included.

[†]Model included controls for season.

[‡]Models included season and weather-by-season interaction term.

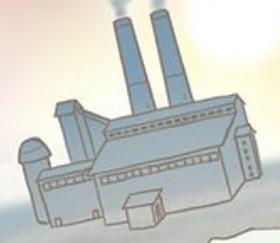
doi:10.1371/journal.pone.0025298.t003

Antibiotic resistance increases with minimum temperature



Climate change may be driving
greater adaptability to higher
temperatures among fungal
pathogens

1 Global warming is responsible for raising the ambient climate temperatures, which selects fungal clades that can reproduce at avian and mammalian basal temperatures.



Wetlands

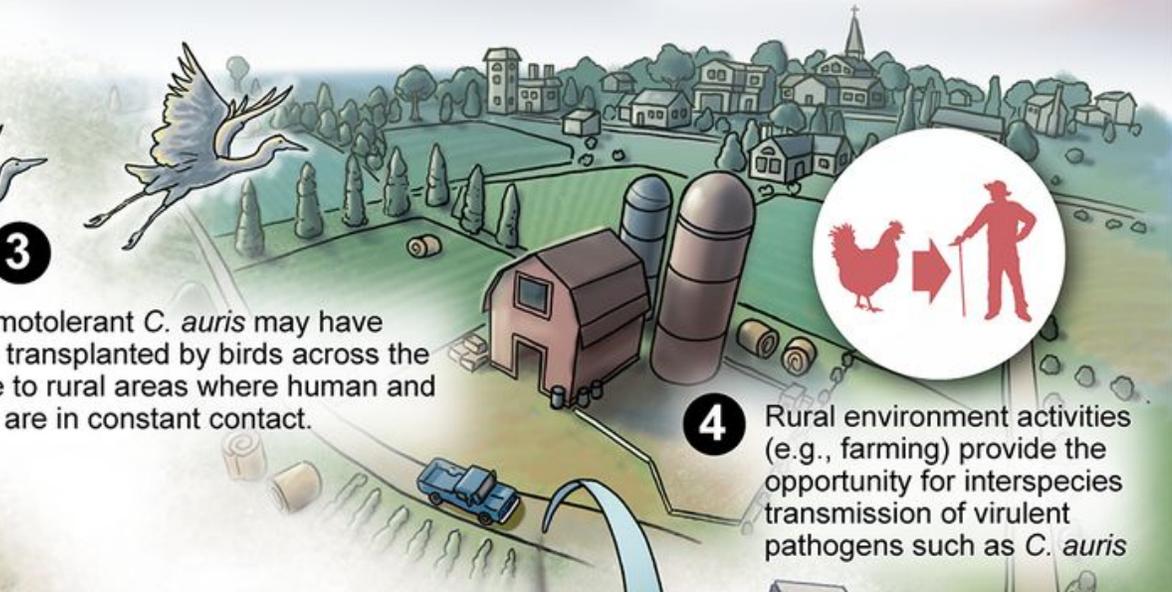


2 *Candida auris* previously existed as a plant saprophyte that gained thermotolerance and salinity tolerance as a result of the effects of climate change on the wetland ecosystem.



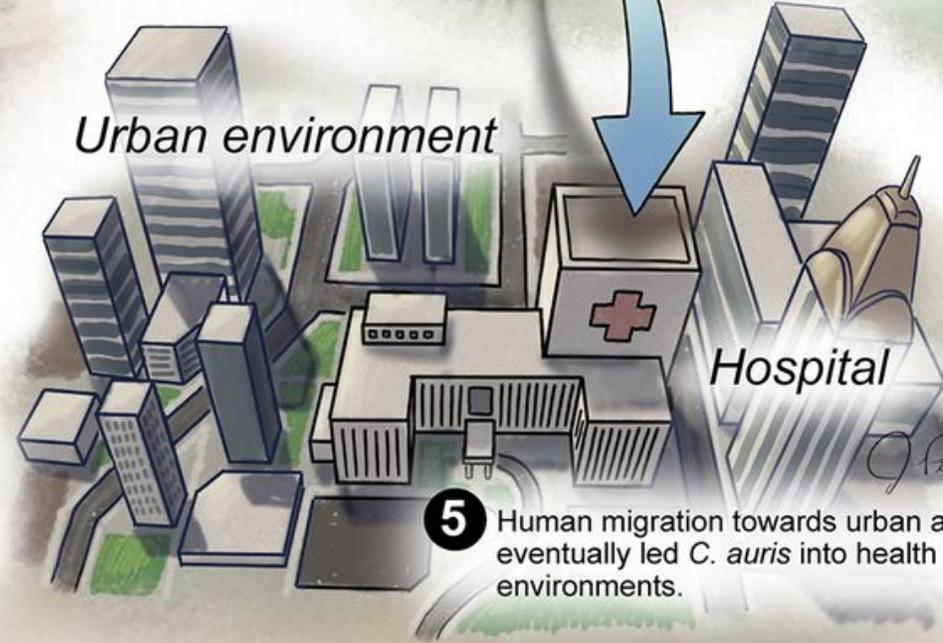
3 Thermotolerant *C. auris* may have been transplanted by birds across the globe to rural areas where human and birds are in constant contact.

Rural environment



4 Rural environment activities (e.g., farming) provide the opportunity for interspecies transmission of virulent pathogens such as *C. auris*

Urban environment



Hospital

5 Human migration towards urban areas eventually led *C. auris* into health care environments.

Stage 1: Track resistance/presumed drivers of resistance in different domains

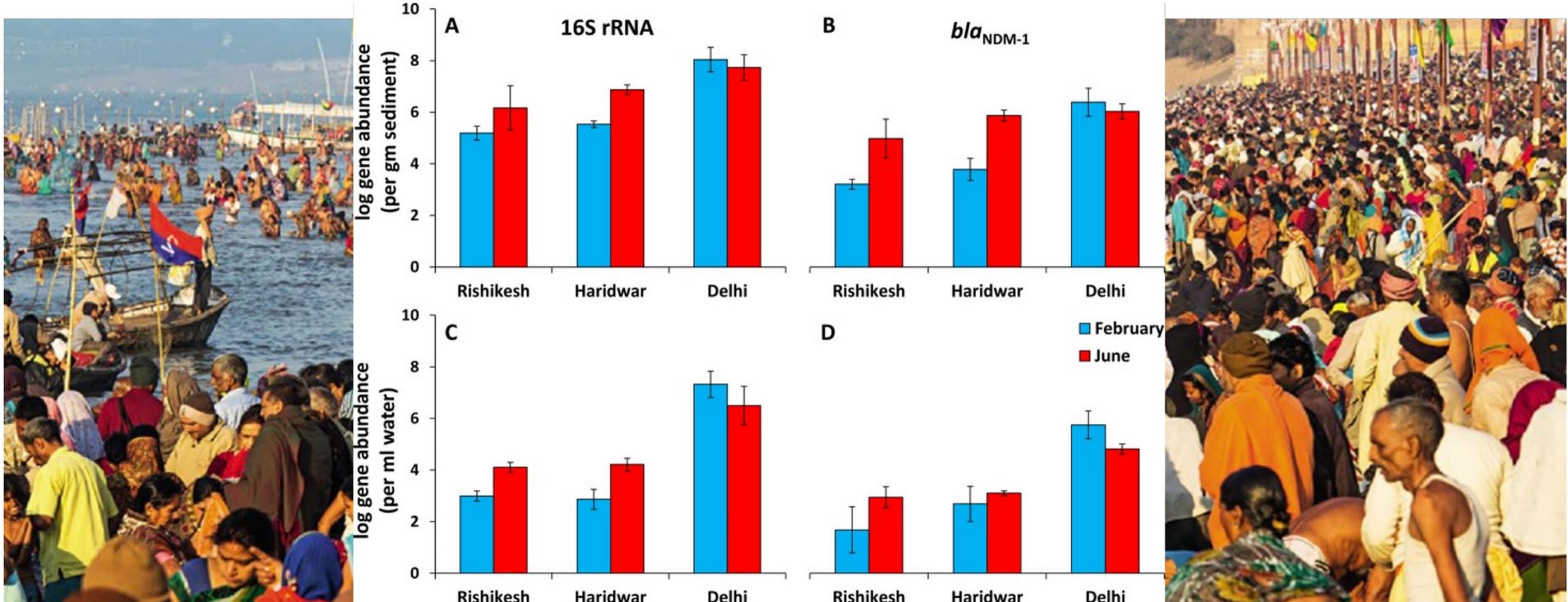
Stage 2: Correlate resistance in different one health domains

Stage 3: Build evidence on drivers of resistance between domains (correlation to causality)

Stage 4: Design and test One Health interventions



*bla*_{NDM-1} was found to be over 20 times greater in the Ganges River during pilgrimage season than at other times of year.

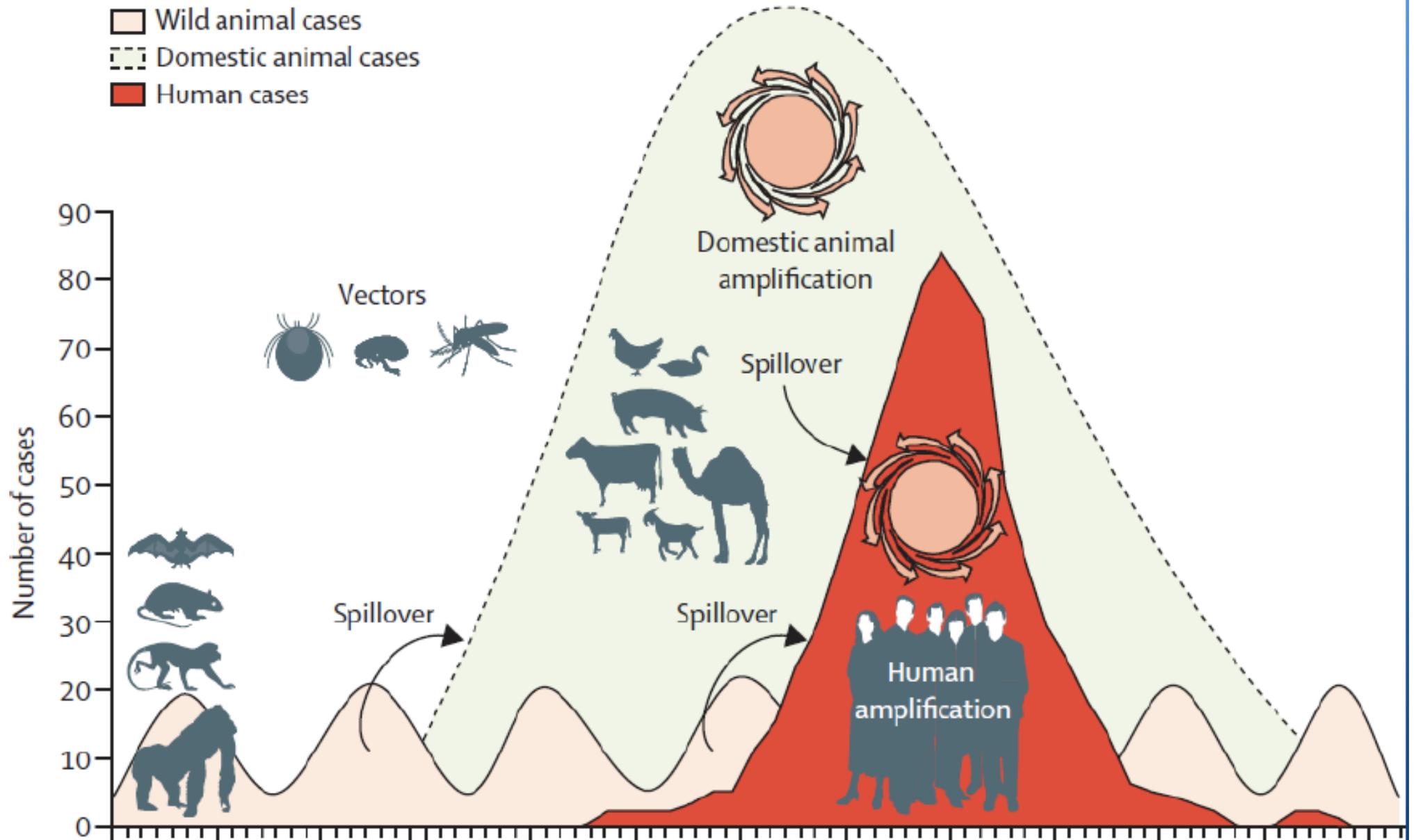


Early detection of NDM-1 and MCR-1 could have helped contain transmission

- When were they reported? When did they likely emerge?
- Novel resistant strains represent entirely new pathogens – since effectively cannot treat them.

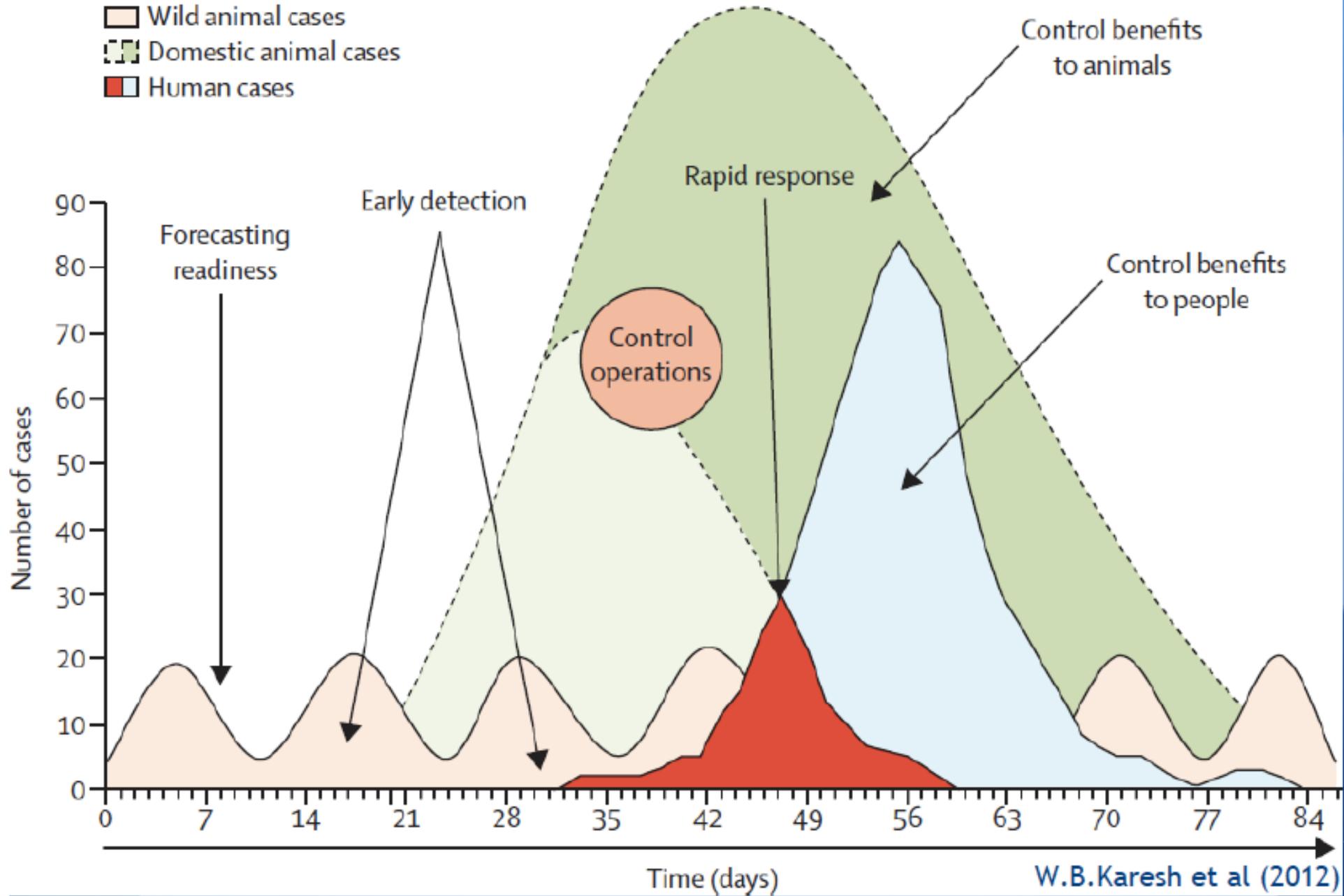
A

- Wild animal cases
- Domestic animal cases
- Human cases



B

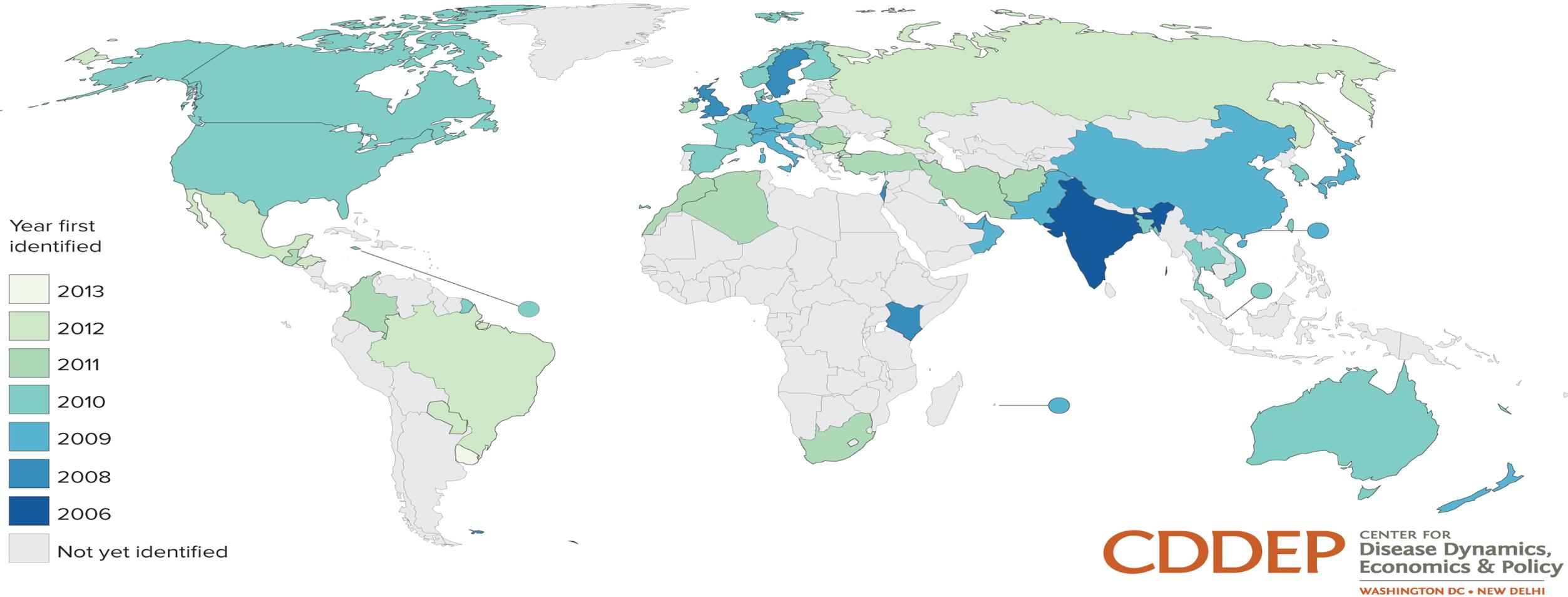
- Wild animal cases
- Domestic animal cases
- Human cases



W.B.Karesh et al (2012)

Trust

Spread of New Delhi metallo beta-lactamase: first detection, by country



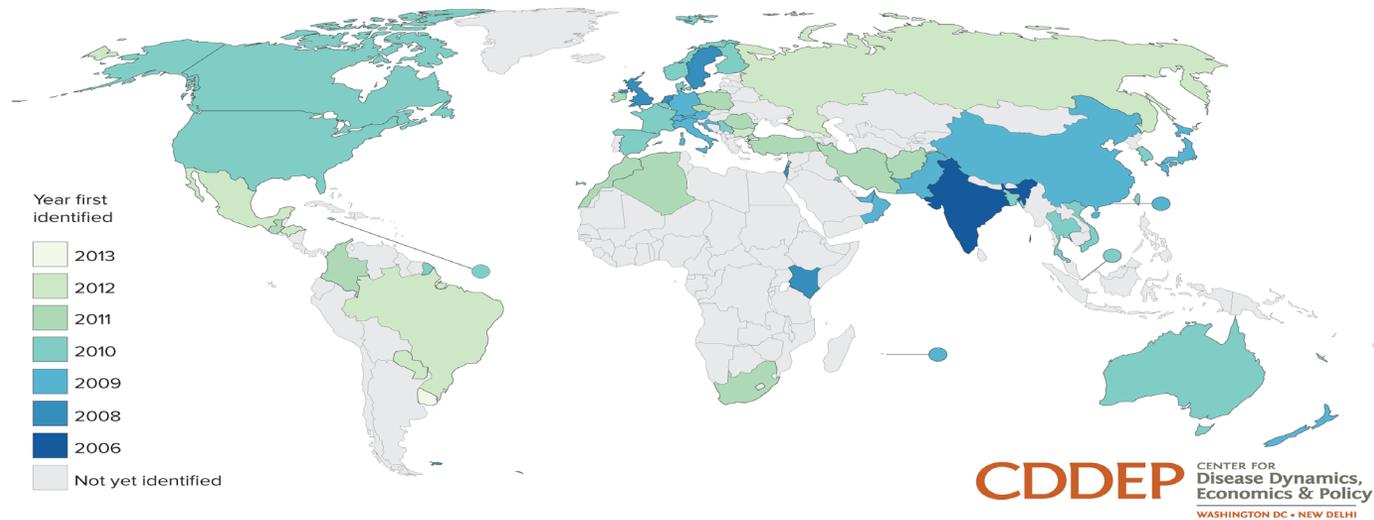
Source: Johnson and Woodford 2013 (adapted)

CDDEP CENTER FOR
Disease Dynamics,
Economics & Policy
WASHINGTON DC • NEW DELHI



New Delhi metallo- β -lactamase (NDM-1) was first detected in a *Klebsiella pneumoniae* isolate in 2008 from a Swedish patient of Indian origin

Spread of New Delhi metallo beta-lactamase: first detection, by country



Source: Johnson and Woodford 2013 (adapted)

Two NDM-1-producing *E. coli* strains from 2006 were retrospectively identified in stored clinical isolates from healthcare facilities in New Delhi, India via the SENTRY Antimicrobial Surveillance Program

Emergence of plasmid-mediated colistin resistance mechanism MCR-1 in animals and human beings in China: a microbiological and molecular biological study



Yi-Yun Liu*, Yang Wang*, Timothy R Walsh, Ling-Xian Yi, Rong Zhang, James Spencer, Yohei Doi, Guobao Tian, Baolei Dong, Xianhui Huang, Lin-Feng Yu, Danxia Gu, Hongwei Ren, Xiaojie Chen, Luchao Lv, Dandan He, Hongwei Zhou, Zisen Liang, Jian-Hua Liu, Jianzhong Shen

Summary

Background Until now, polymyxin resistance has involved chromosomal mutations but has never been reported via horizontal gene transfer. During a routine surveillance project on antimicrobial resistance in commensal *Escherichia coli* from food animals in China, a major increase of colistin resistance was observed. When an *E coli* strain, SHP45, possessing colistin resistance that could be transferred to another strain, was isolated from a pig, we conducted further analysis of possible plasmid-mediated polymyxin resistance. Herein, we report the emergence of the first plasmid-mediated polymyxin resistance mechanism, MCR-1, in Enterobacteriaceae.

Lancet Infect Dis 2015

Published Online

November 18, 2015

[http://dx.doi.org/10.1016/S1473-3099\(15\)00424-7](http://dx.doi.org/10.1016/S1473-3099(15)00424-7)

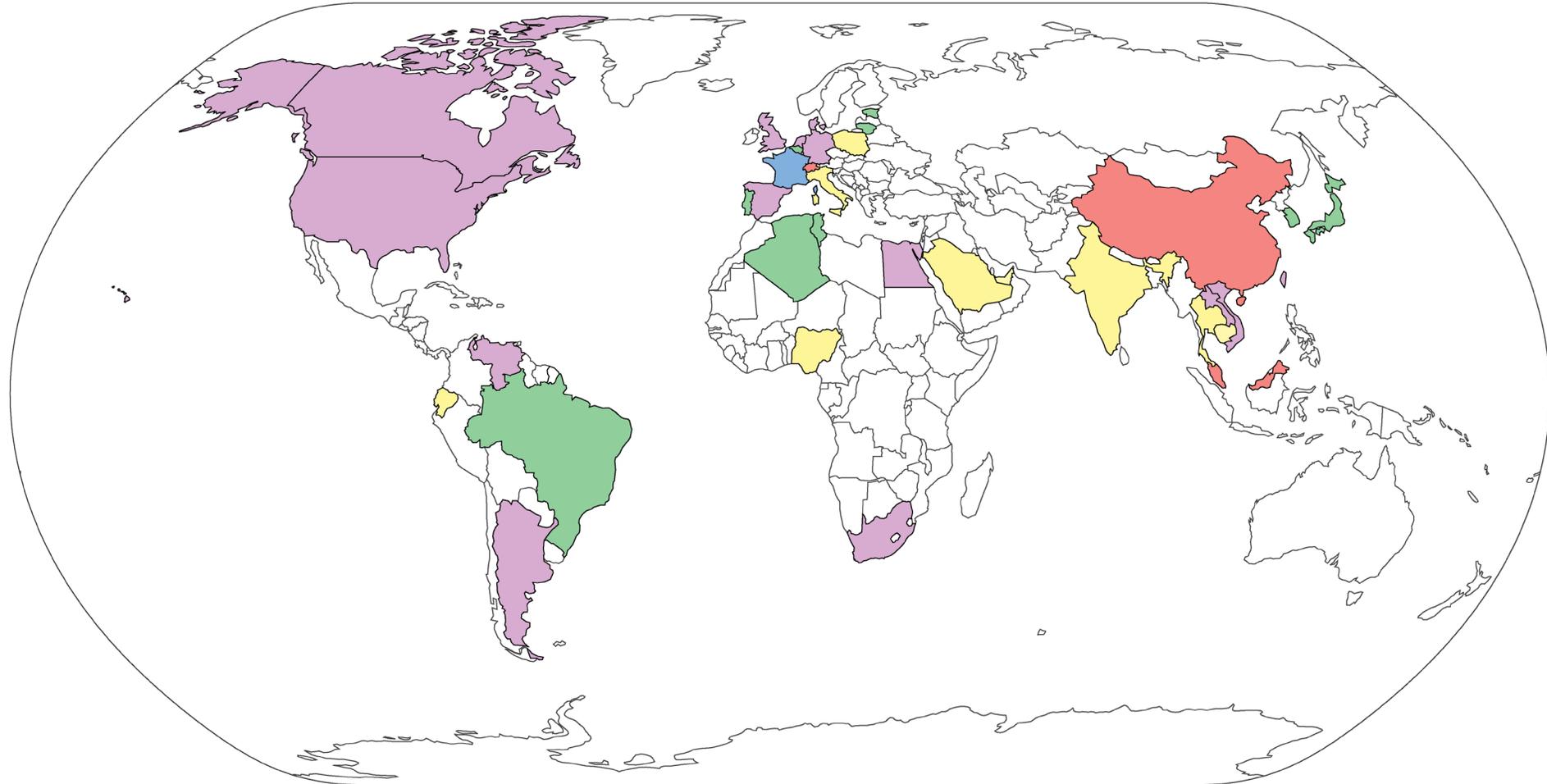
See Online/Articles

[http://dx.doi.org/10.1016/S1473-3099\(15\)00462-6](http://dx.doi.org/10.1016/S1473-3099(15)00462-6)



OneHealthTrust

Countries reporting plasmid-mediated colistin resistance encoded by *mcr-1*



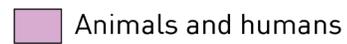
Isolate source(s):



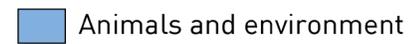
Animals



Humans



Animals and humans



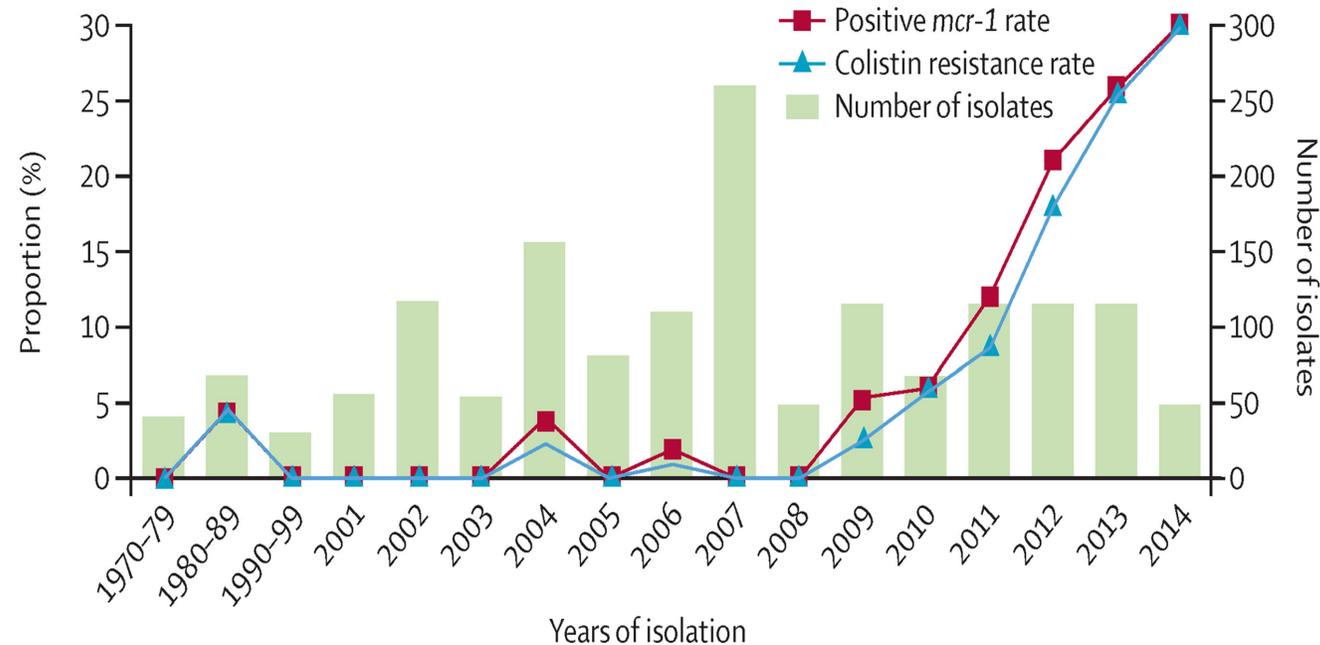
Animals and environment



Animals, humans
and environment

Data source: Al-Tawfiq, J. A., Laxminarayan, R. & Mendelson, M. How should we respond to the emergence of plasmid-mediated colistin resistance in humans and animals? *Int. J. Infect. Dis.* (2016). doi:10.1016/j.ijid.2016.11.415

Presence of *mcr-1* and colistin resistance in *Escherichia coli* of chicken origin during 1970–2014



Indicates that trade of food animals and meat, as well as movement of colonized humans could have played a role in rapid dissemination.

InDepth Network Surveillance Site

Currently 52 HDSSs in 20 countries
39 HDSSs in Africa
11 HDSSs in Asia
2 HDSS in Oceania



But none of these is a One Health Surveillance Site



Over 3,800,000 people under surveillance



One Health Surveillance Site

- Catchment area covering agricultural, forest and urban land
- Catchment human population of 60,000. Domesticated animal and wildlife population being surveyed.
- Survey planned for 20,000 by October 2021
- Longitudinal data on resistant pathogens in humans, animals and the environment along with markers of human, animal and environmental health

Virus detection

- Workforce training and improved lab systems for bio-secure zoonotic disease detection
- Testing animals for zoonotic disease threats
- Detecting known and novel viruses in various ecosystems
- Understanding of disease spillover and transmission dynamics, essential to the design and evaluation of mitigating interventions, and to informing policy by identifying barriers to change and acceptable alternatives.
- We need a new paradigm that is able to quickly identify spillovers as they happen without the need to enhance pathogens. What does early identification of outbreaks look like?