



National Food Institute
Technical University of Denmark



Antibiotic Resistance in the Food Chain

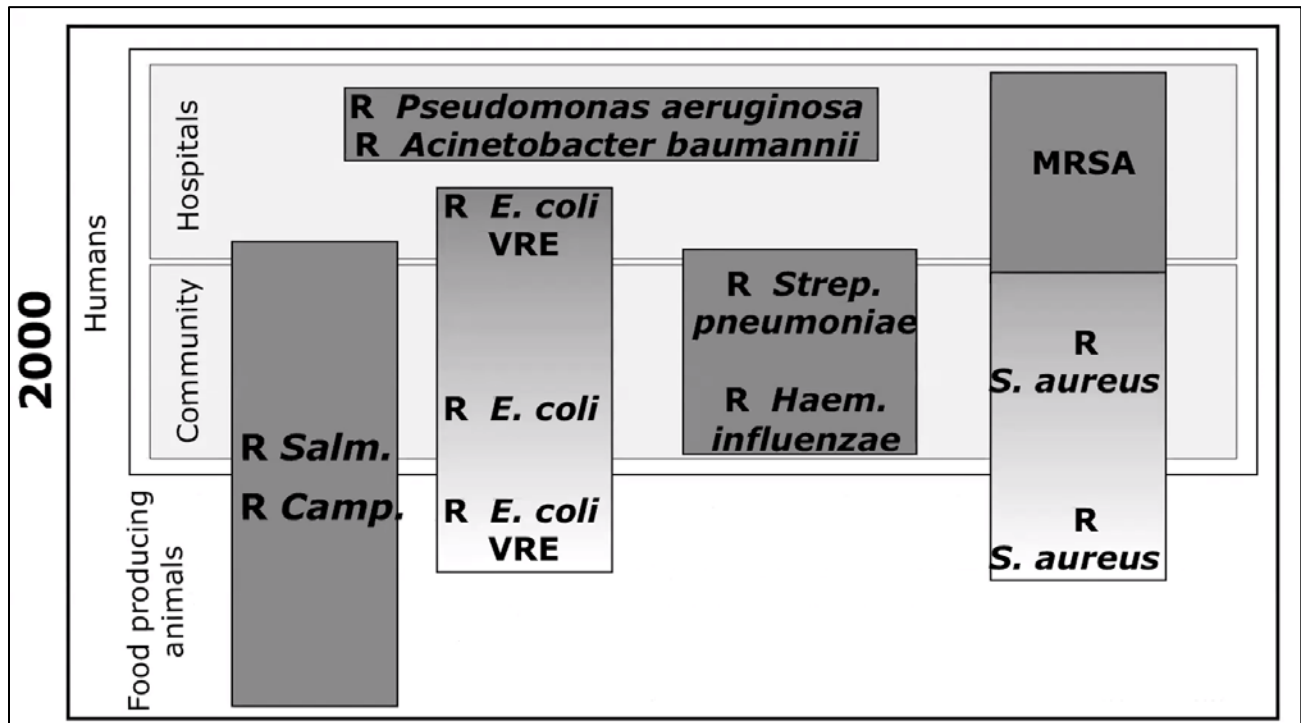
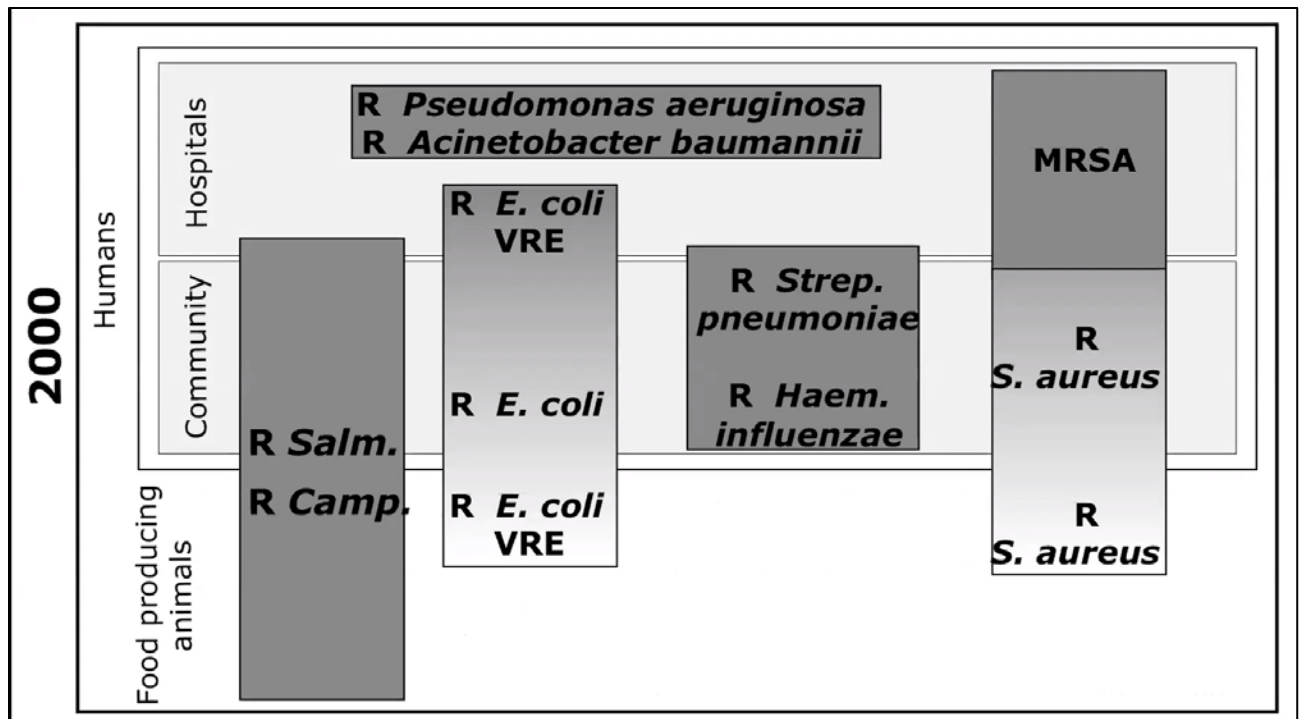
Research and politics, historical and current trends, options and perspectives

Frank M. Aarestrup

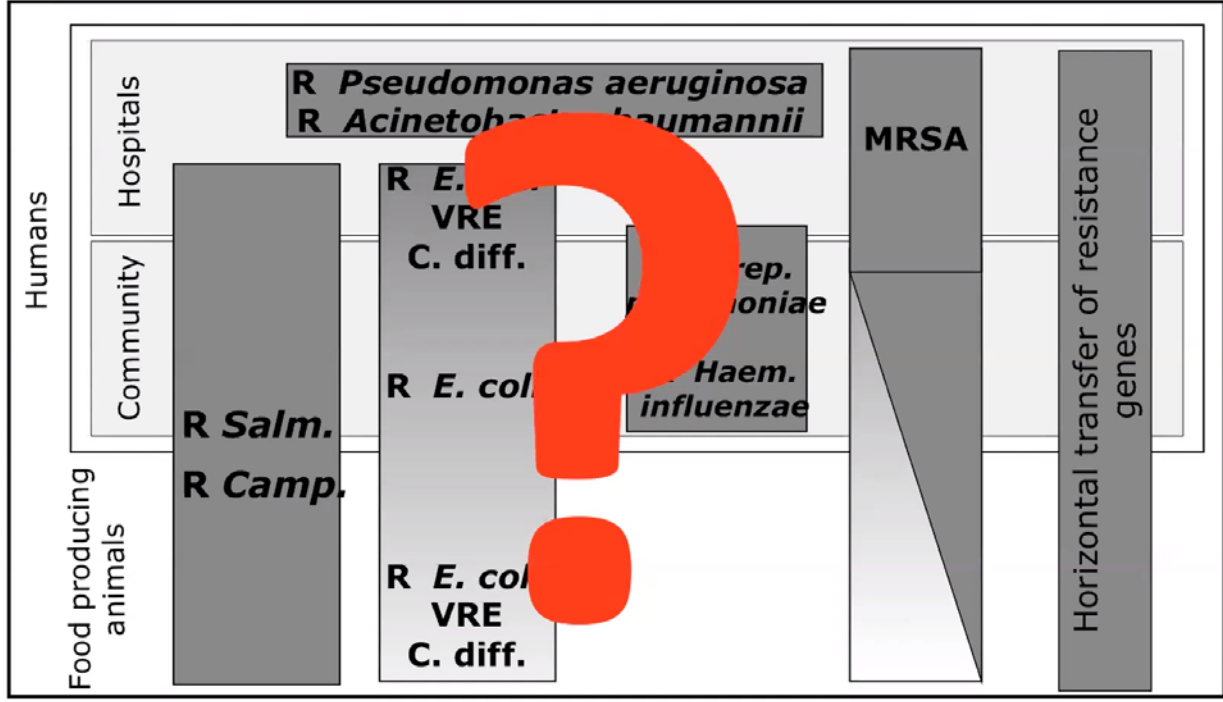
fmaa@food.dtu.dk, www.genomicepidemiology, www.globalsurveillance.eu

Importance of the food animal reservoir for human health

- Different estimates ranging from
 - Almost zero (AHI and IFAH)
 - 1,518 extra deaths and an associated increase of 67,236 days of hospital admissions in Europe as a result of cephalosporin use in chickens alone (Collignon et al. 2013)

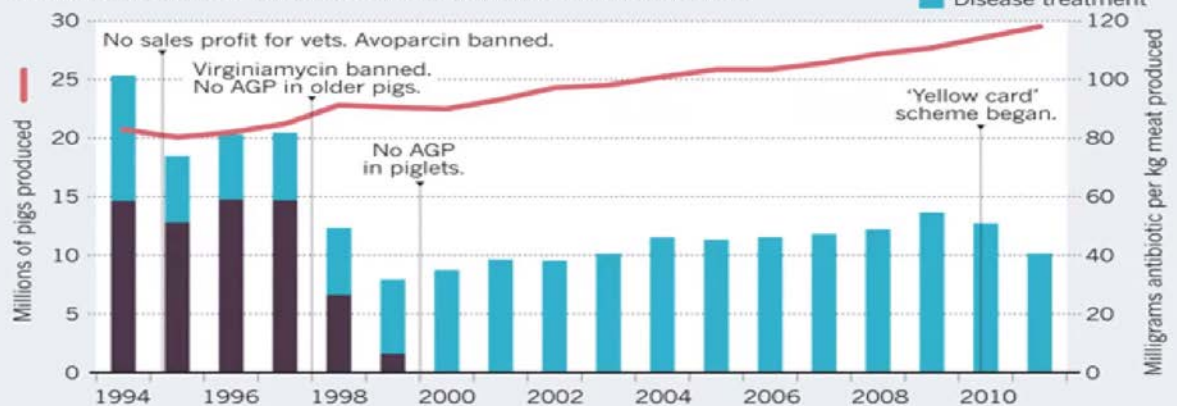


2020

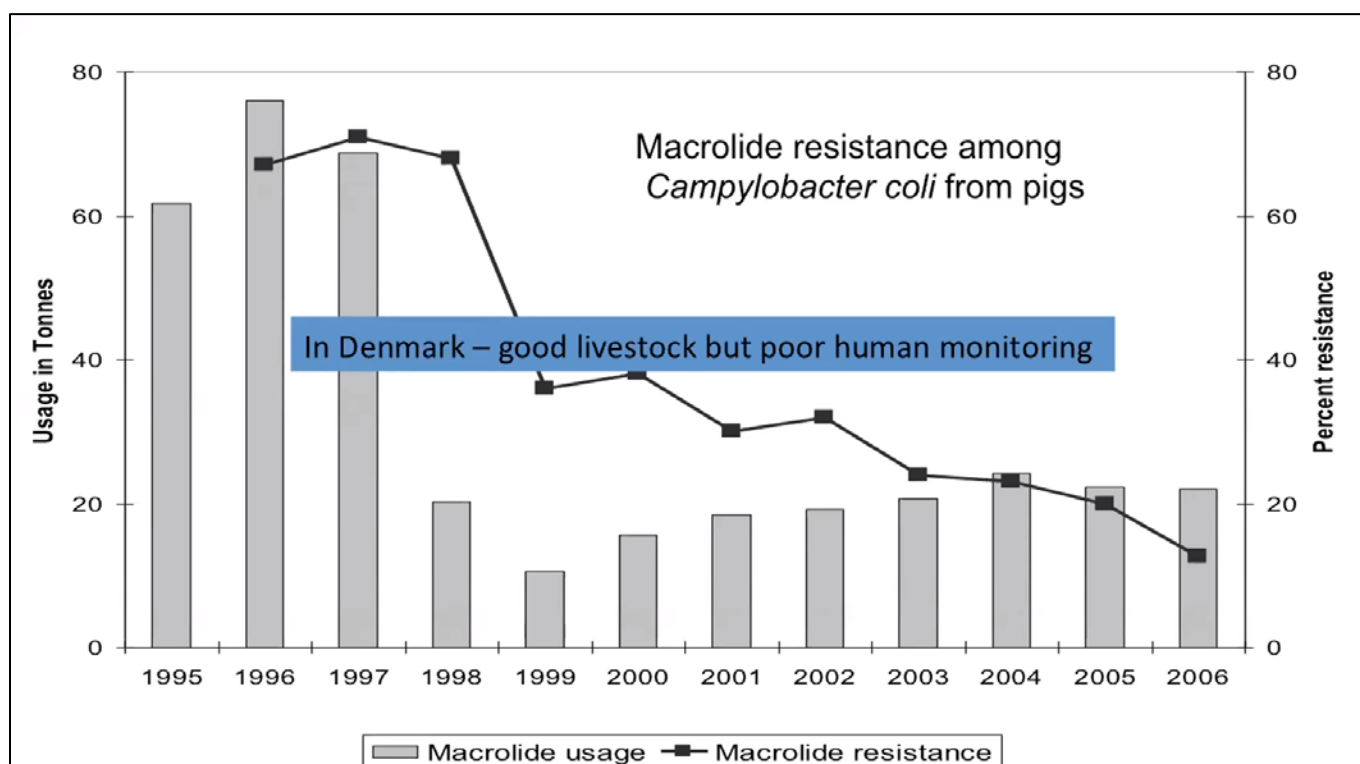
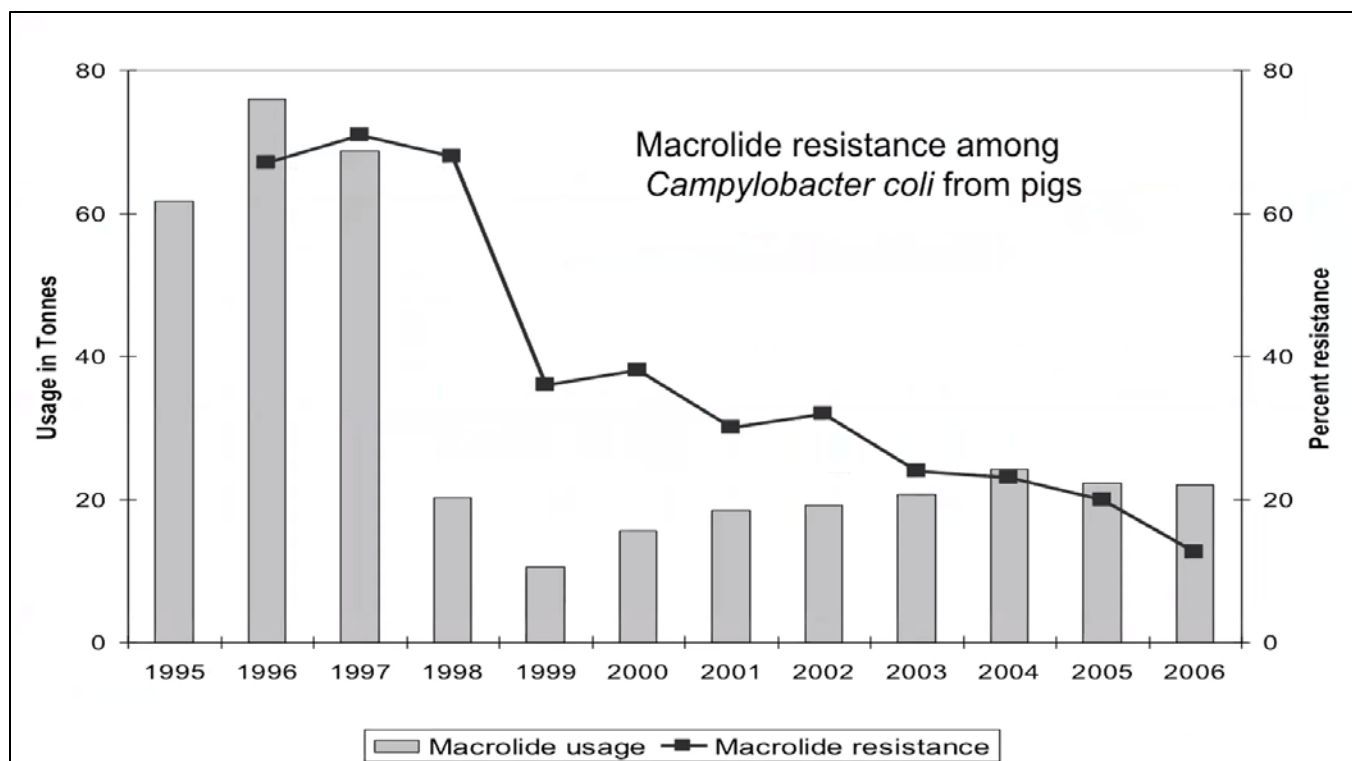


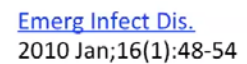
BACON BOOST

Denmark's actions to stop using antibiotics as growth promoters (AGP) in livestock has reduced antibiotic consumption but not pig production.



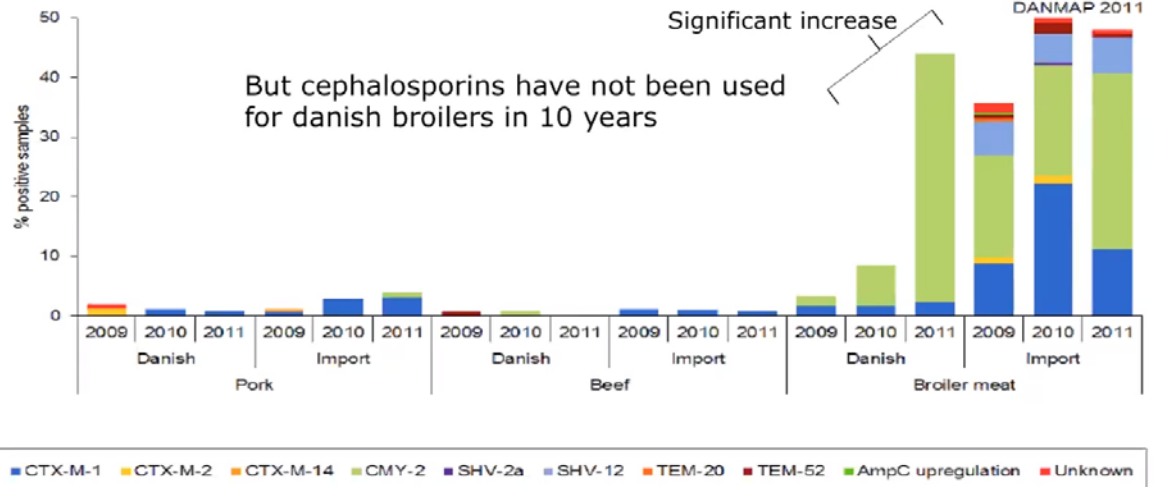
[Nature](#), 2012;486:465-6





a) *E. coli* was isolated after selective enrichment with ceftriaxone (1 µg/ml). The genetic background for ESBL resistance was revealed by use of PCR, micro array and DNA sequencing

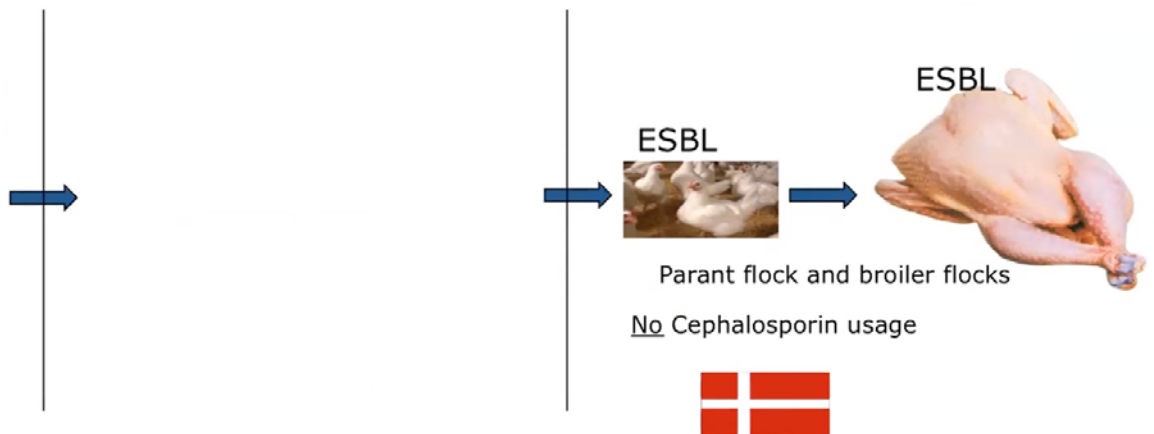
Figure 2. Occurrence (%) of ESBL-producing *Escherichia coli* and genes in meat^(a b), Denmark



a) *E. coli* was isolated after selective enrichment with ceftriaxone (1 µg/ml). The genetic background for ESBL resistance was revealed by use of PCR, micro array and DNA sequencing

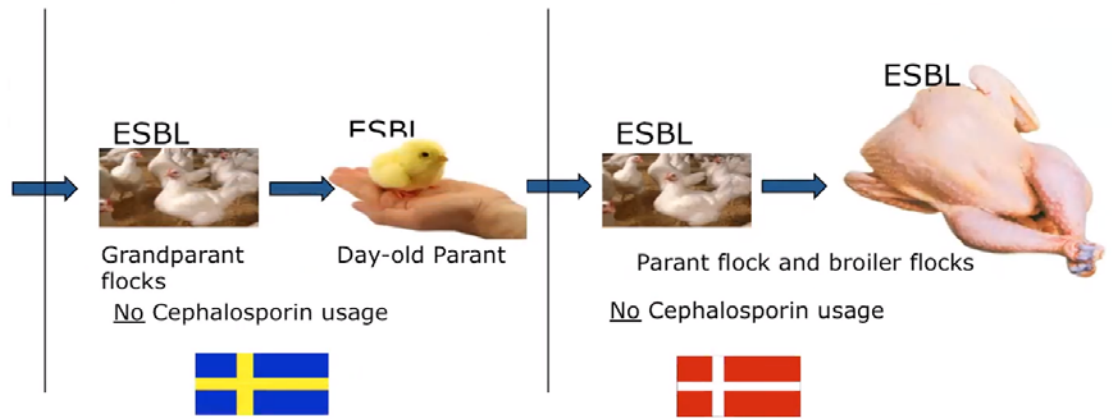
b) Each year approximately 1,000 samples are collected evenly distributed between the six categories of meat

The Danish broiler production



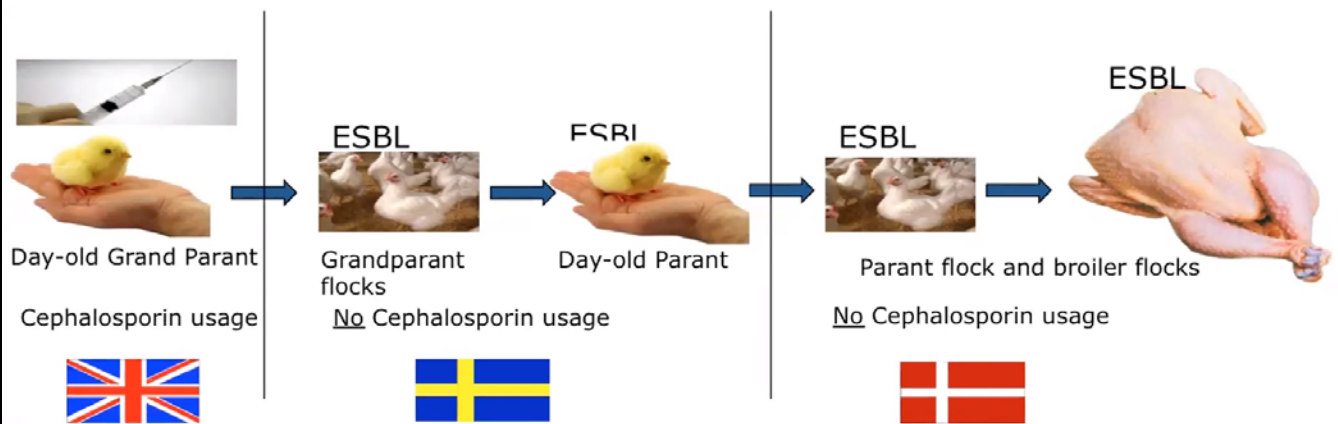
Usage in one country can affect resistance in another country

The Danish broiler production



Usage in one country can affect resistance in another country

The Danish broiler production

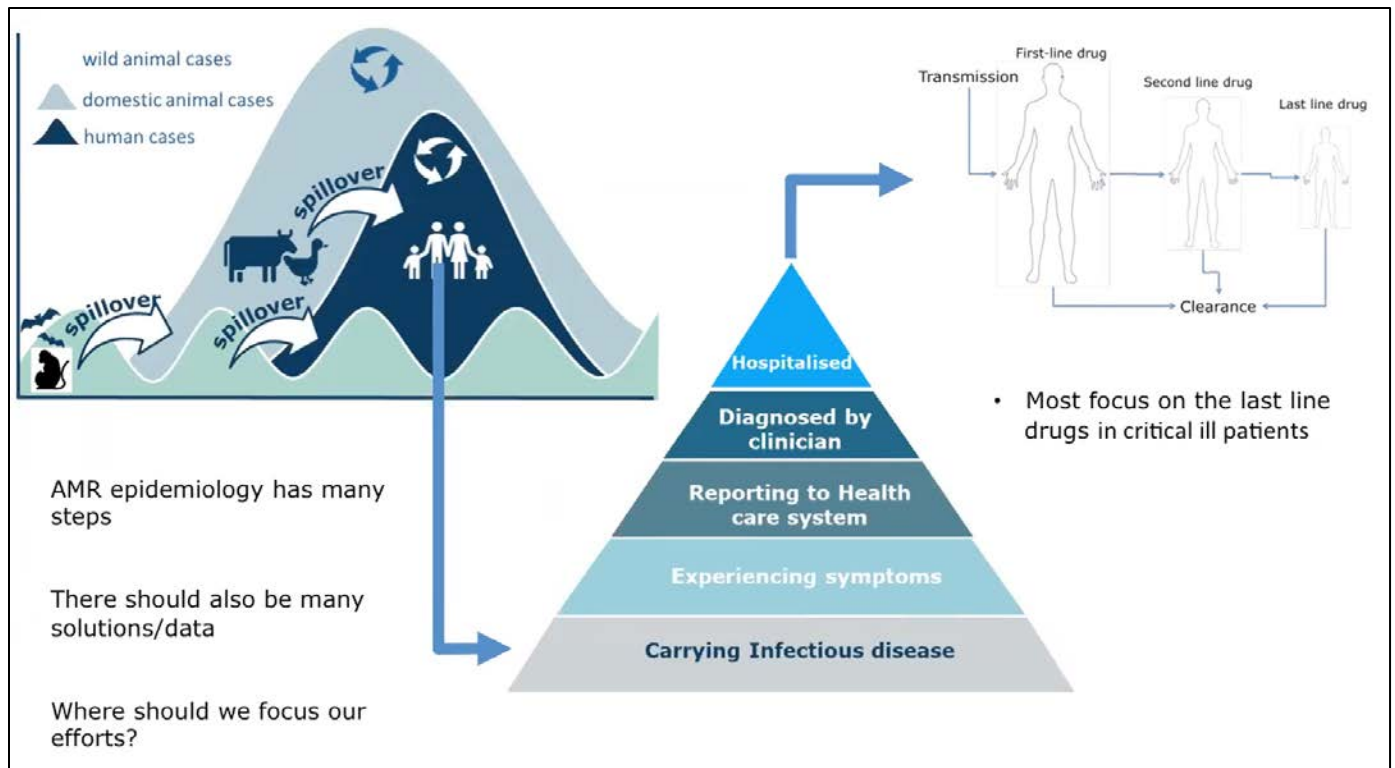


Usage in one country can affect resistance in another country



Why is it so difficult?

- Very few examples of antimicrobial agents exclusively used for animals
- Some human monitoring, but limited animal
- Need for comparable longitudinal surveillance data of all potential reserrovirs



Animal antibiotic use has an early but important impact on the emergence of antibiotic resistance in human commensal bacteria

David L. Smith^{1*}, Anthony D. Harris², Judith A. Johnson³, Ellen K. Silbergeld⁴, and J. Glenn Morris, Jr.⁵

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Research



Cite this article: van Bunnik B.A.D., Woolhouse M.E.J. 2017 Modelling the impact of curtailing antibiotic usage in food animals on antibiotic resistance in humans. *R. Soc. open sci.* **4**: 160367.

Modelling the impact of curtailing antibiotic usage in food animals on antibiotic resistance in humans

B. A. D. van Bunnik and M. E. J. Woolhouse

Centre for Immunity, Infection and Evolution and Usher Institute of Population Health Sciences and Informatics, Edinburgh University, Edinburgh, UK

Once AMR after emergence in livestock has transmitted to and established itself in humans, there is little effect of removing AMR in livestock

Animal antibiotic use has an early but important impact on the emergence of antibiotic resistance in human commensal bacteria

David L. Smith^{1*}, Anthony D. Harris^{2*}, Judith A. Johnson³, Ellen K. Silbergeld⁴, and J. Glenn Morris, Jr.^{5*}

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Research

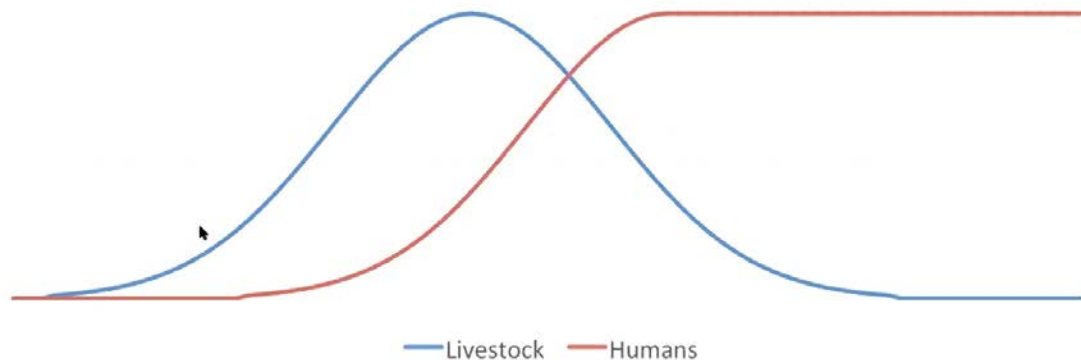


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Modelling the impact of curtailing antibiotic usage in food animals on antibiotic resistance in humans

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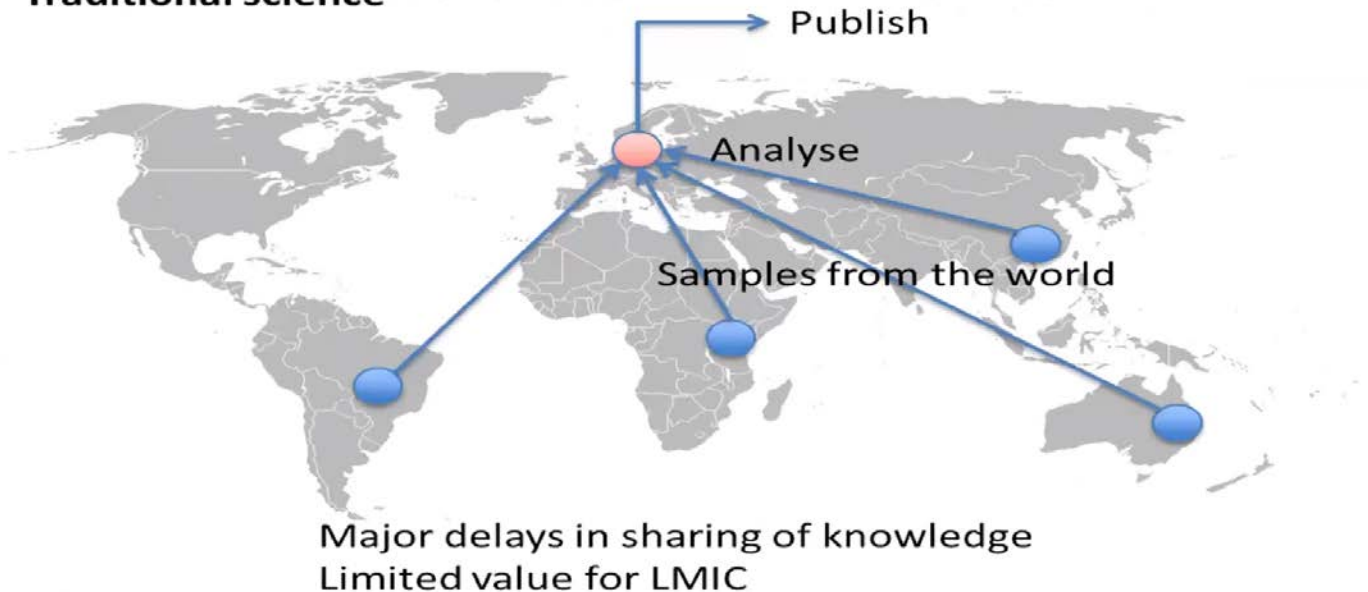
What the world needs

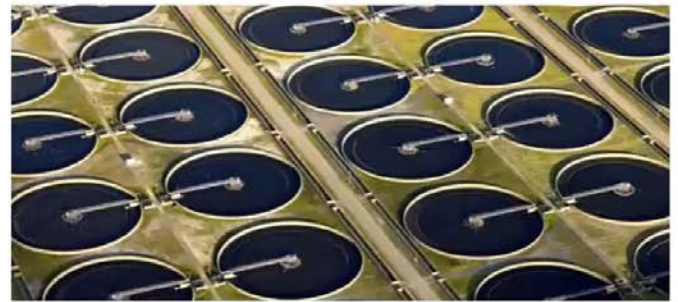
- Real-time data on occurrences of all infectious agents everywhere
 - Geography, reservoir and pathogen independent
 - Observe trends and to rapidly compare between data
 - Transfer of information to those who need to:
 - Take public health response
 - Develop tests and treatments
 - Take clinical decisions
- Issues to solve
 - Data from global sources
 - Data from non-clinical reservoirs
 - Rapid global sharing of data
 - Analysing (BIG & COMPLEX) data in context

Next Generation Sequencing (NGS) Advantages

- DNA/RNA are common across pathogens, therefore, methods to analyse genomes are potentially universal
- NGS provides a universal language
- NGS capacity is developing fast, and costs are becoming competitive
 - Less equipped labs may leapfrog

Traditional science



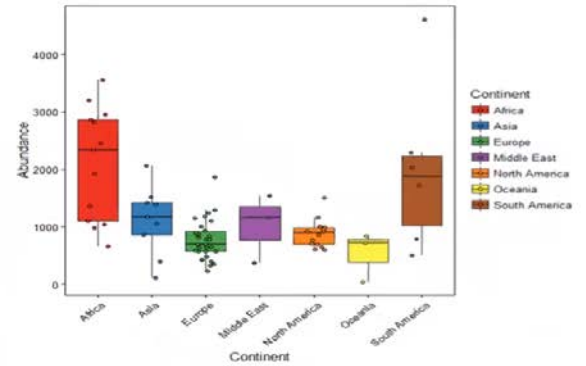
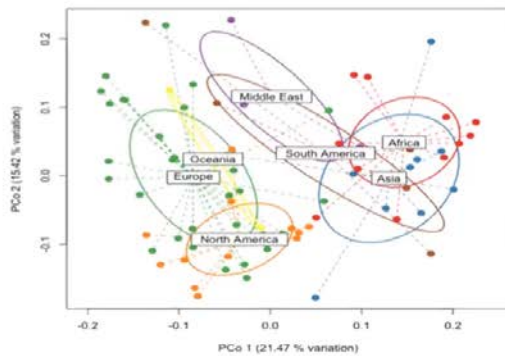
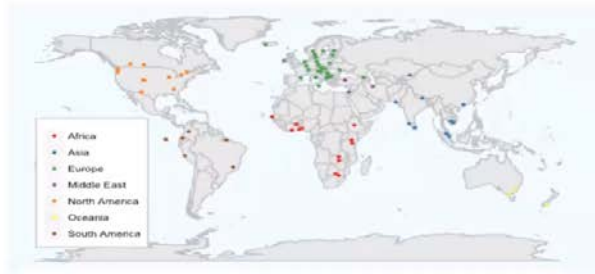


Metagenomics – One technology that takes all

Metagenomics is defined as the **sequencing-based analysis of genomes** contained within an **environmental sample**



Global sewage surveillance - 2016



79 cities – 63 countries

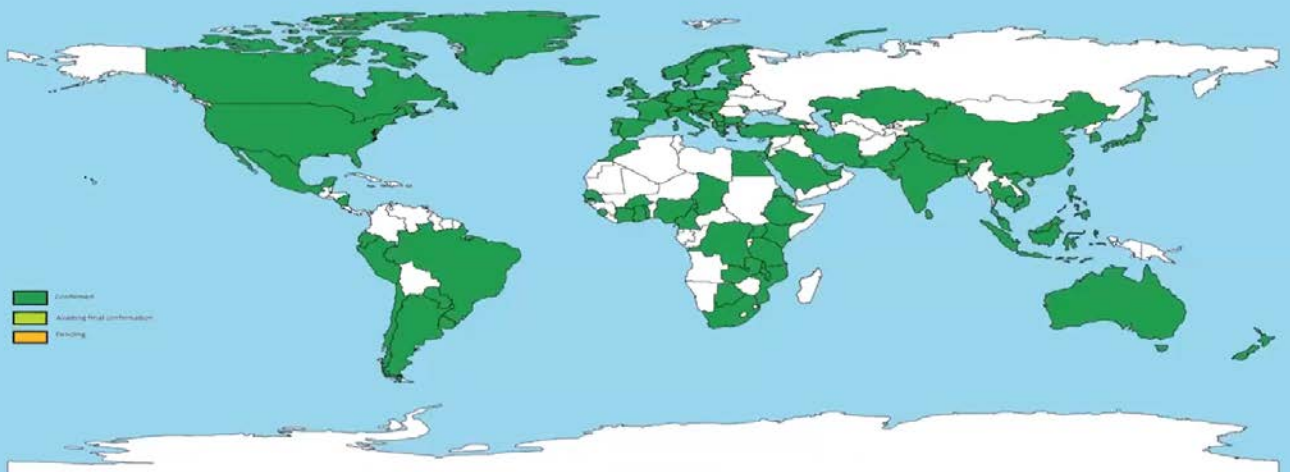
1.500 Gb, large diversity + 30 million genes

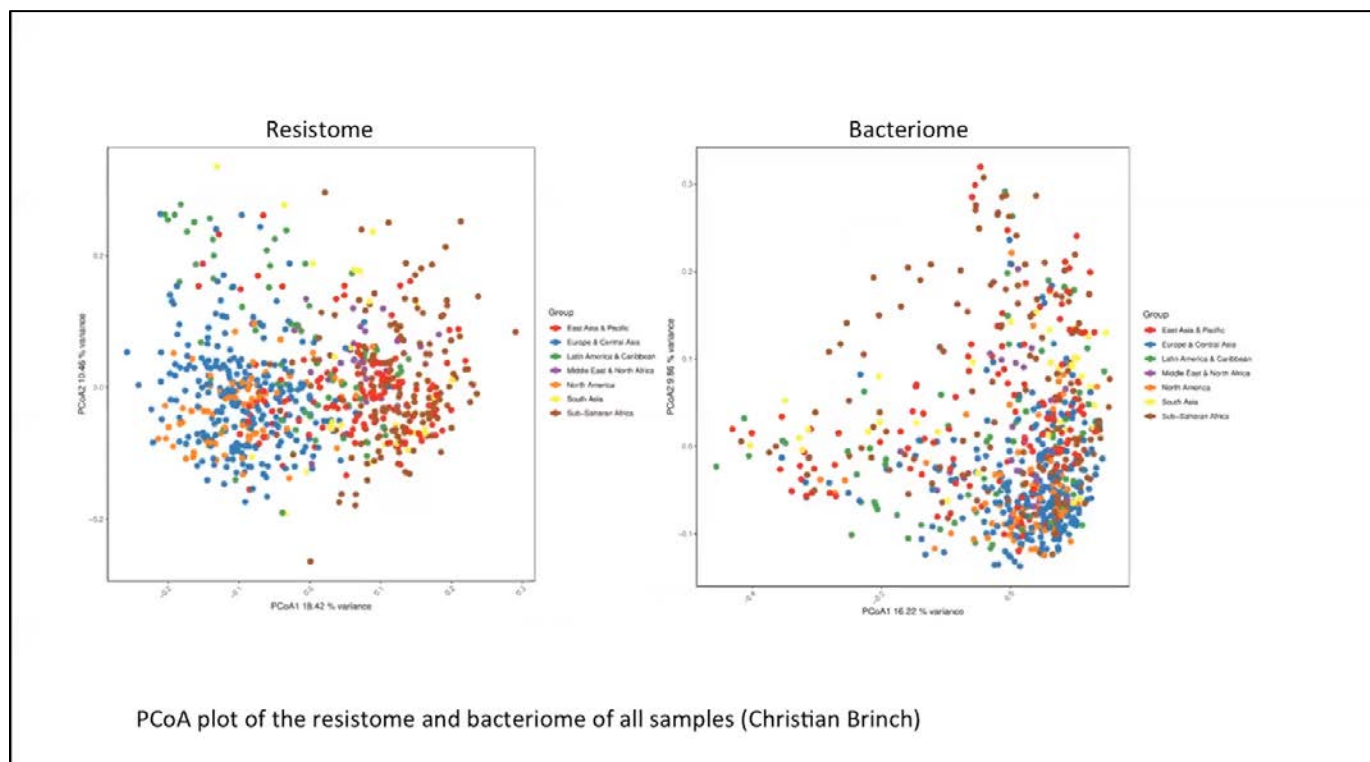
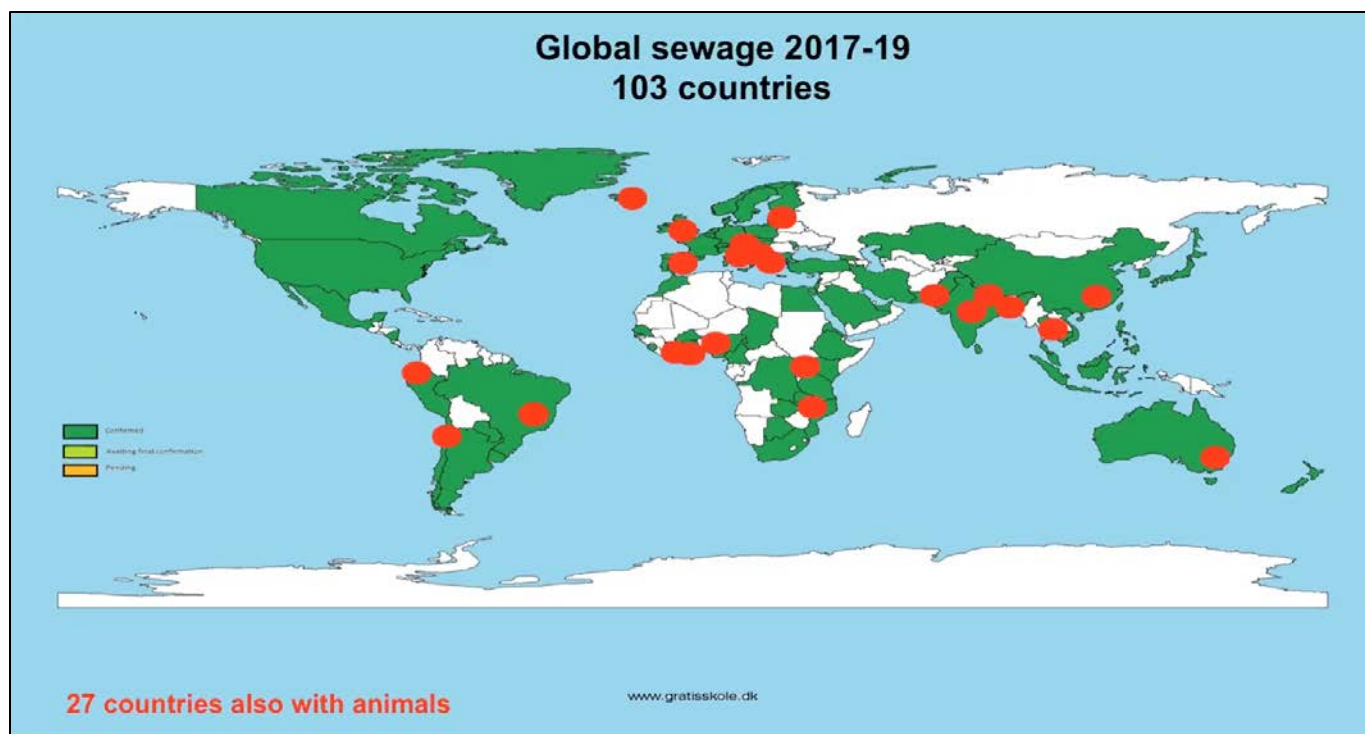
Clear separation into:

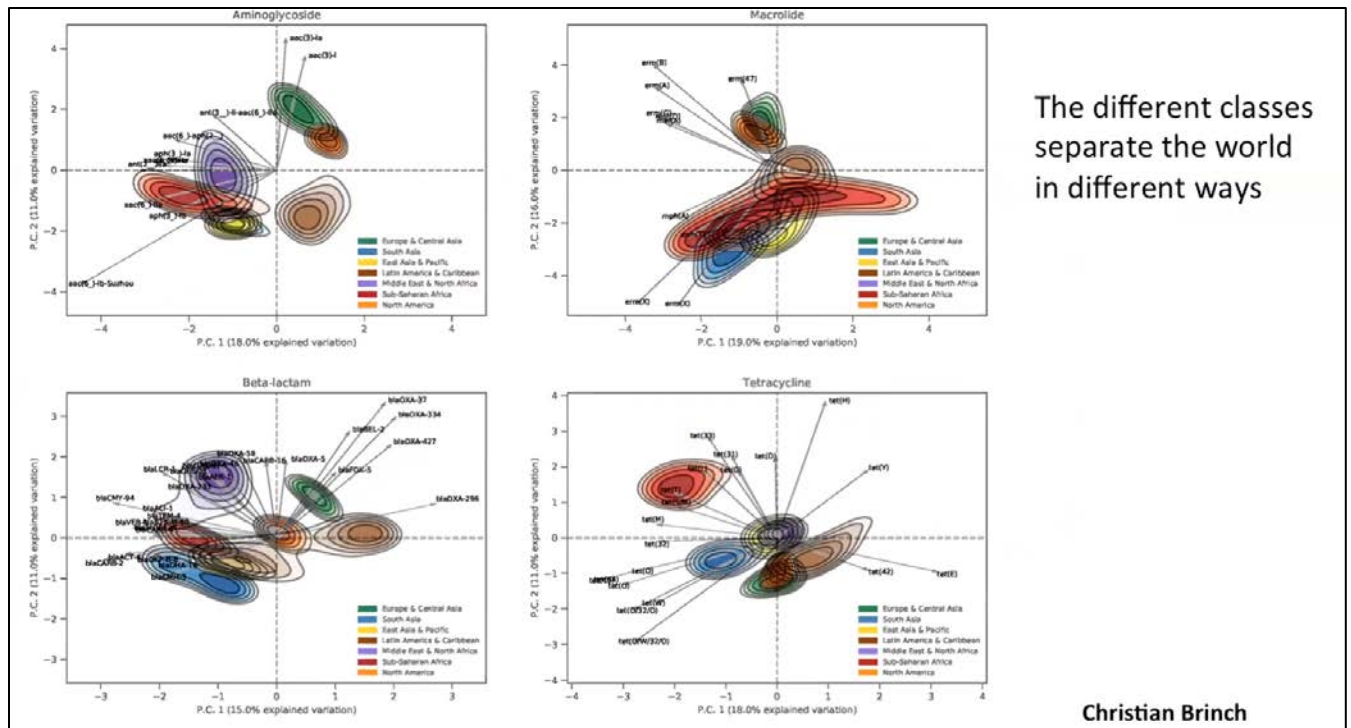
Asia, Africa, Middle east, South Am.
Europe, North Am., Oceania

Nature Comm. 2019

Global sewage 2017-19 103 countries







Download of all available metagenomic data

116,762 runs from 75,932 samples from 780 projects

150 Terabytes

- Download time 1 month

Mapped to all known ARGs

- 2 months on a 40,000 core HPC

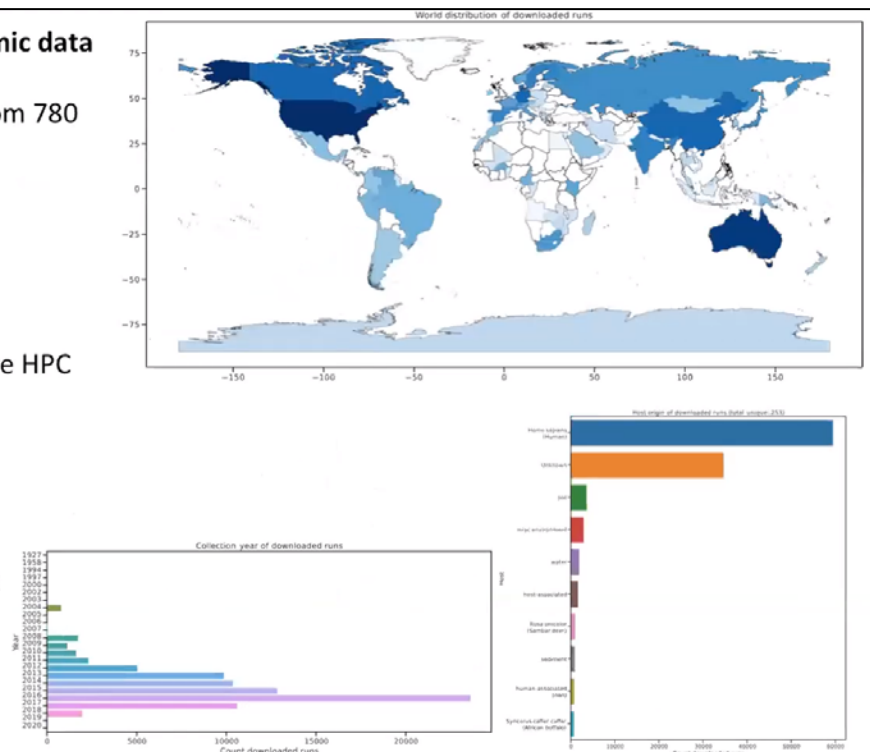
Lack of reservoir data

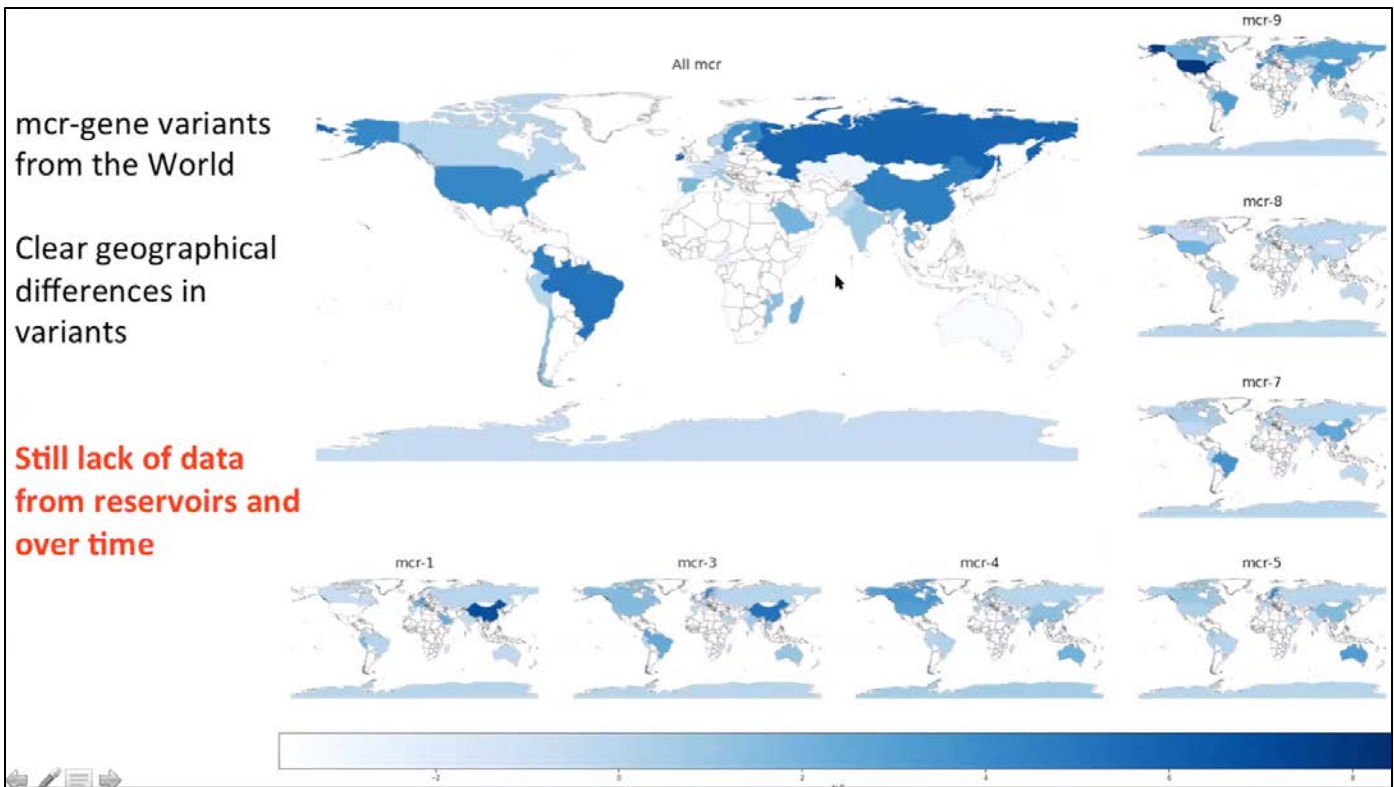
Un-equal distribution

Only few years

Most livestock actually from Denmark

H-M. Martiny





Conclusions

- We need comparable longitudinal global data to identify and quantify the transmission of antimicrobial resistance
- NGs and metagenomics are creating a common language
- But if reservoirs are not sampled and analysed it makes little sense
- Please send more (standardised) data

Our vision: one system serves all



Guiding principles:

- Cross sector, cross domain, open source (not commercial)
- Interaction with the rest of the world (all inclusive)
- Data for action (actionable outputs)
- Central repository (tools to the data) (ENA, DDJ, NCBI)

