

# Past, present and future in the Danish antimicrobial resistance monitoring programme (DANMAP)

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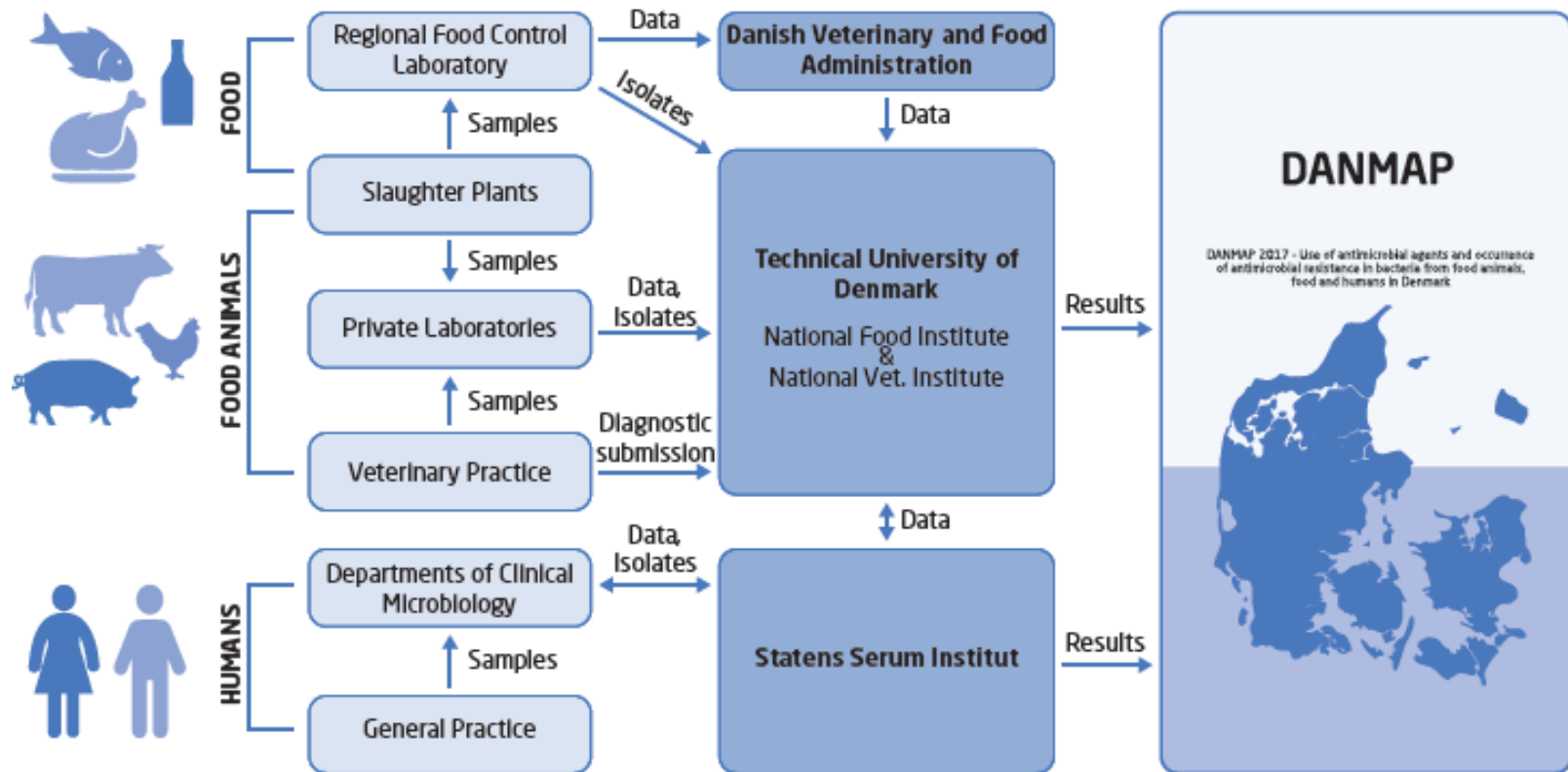
Research Group for Genomic Epidemiology

National Food Institute

Technical University of Denmark

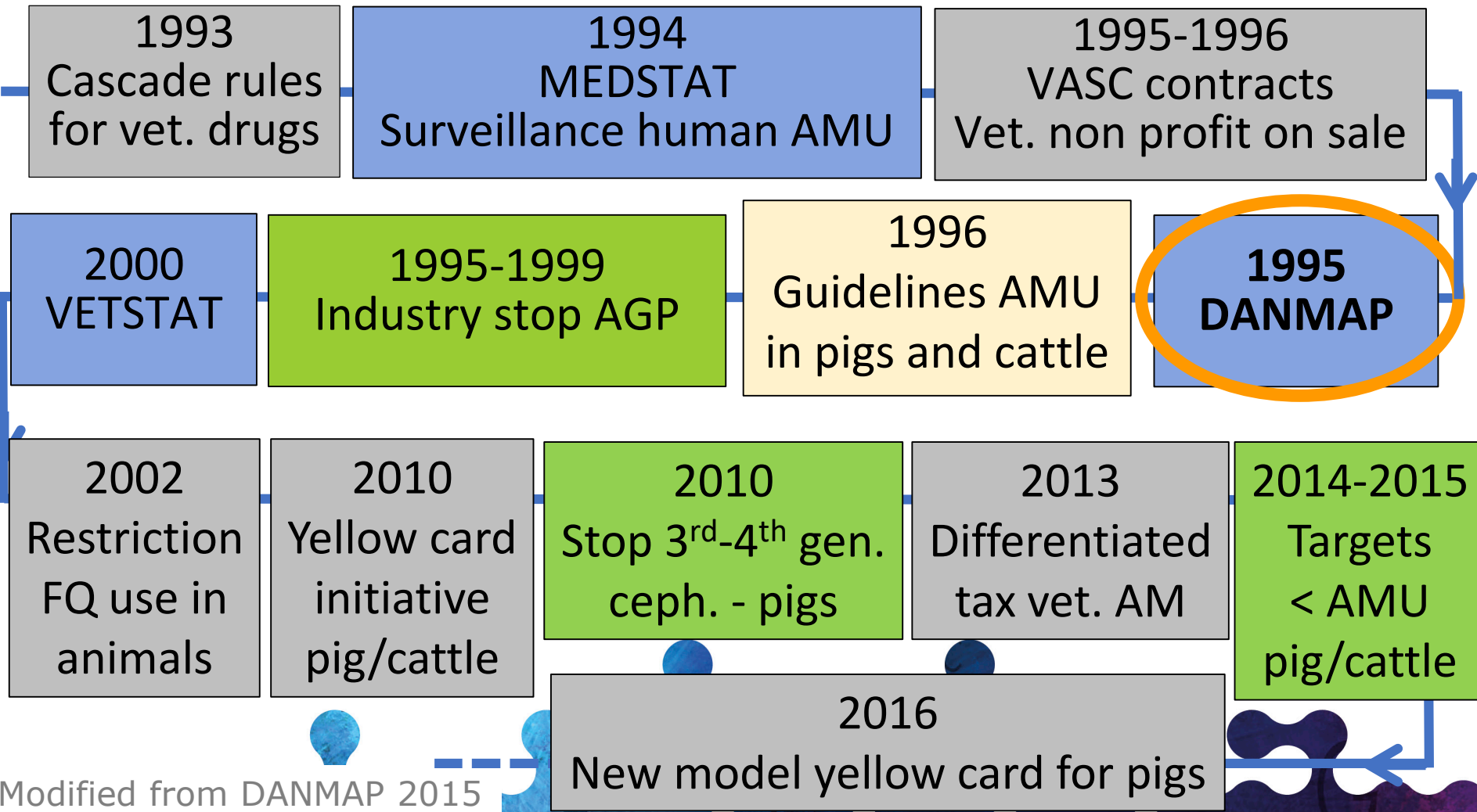


# Organisation of DANMAP

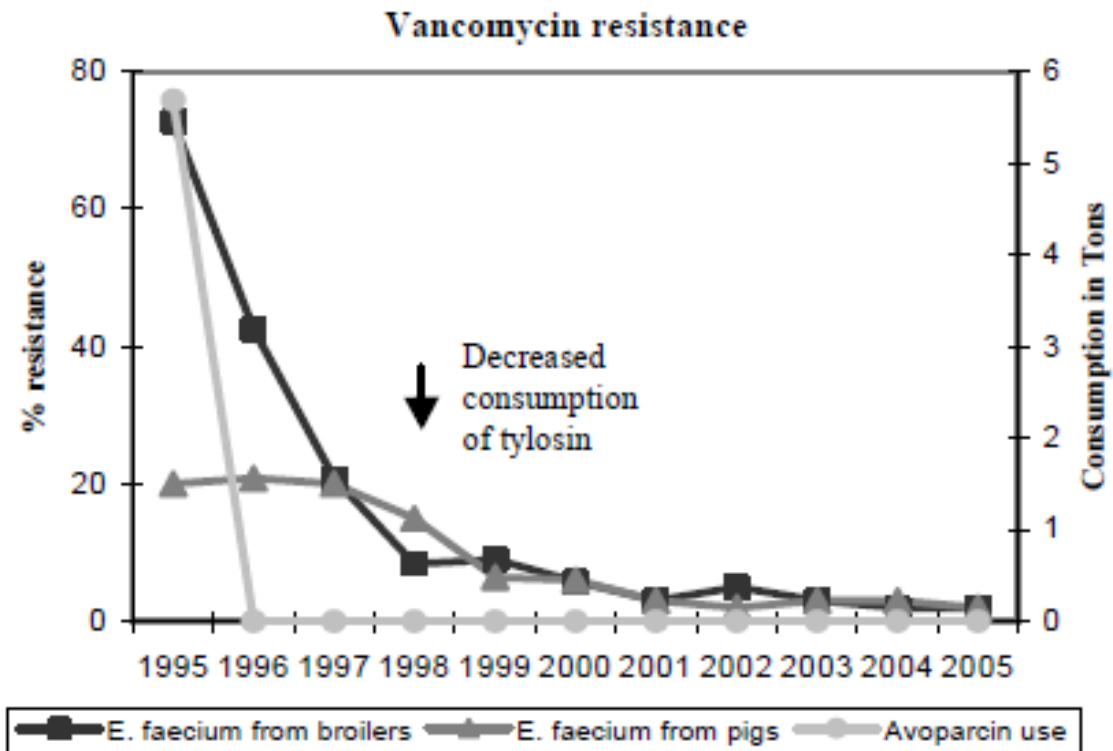


Source: DANMAP 2017

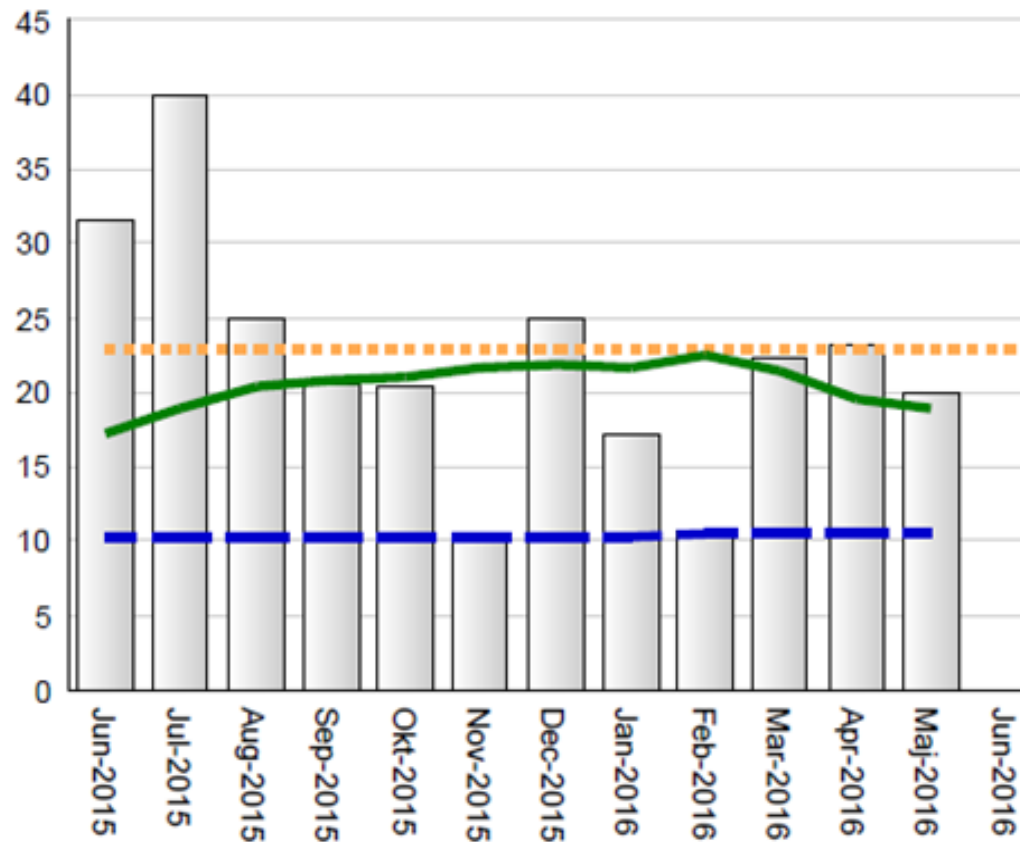
# DANMAP as a milestone to tackle AMU & AMR in humans and food-producing animals



# Termination of AGPs & AMR occurrence



# The yellow card initiative



# DANMAP in the One Health strategy

**Enhanced knowledge  
to improve targeted measures**



# Zoonotic (broiler) origin a ST4292 CMY-2-producing *E. coli* from a Danish patient...

CMY-2 producing *E. coli* isolate causing a bloodstream infection was observed. Investigation of the clonal relationship of ST4292 CMY-2 producing *E. coli* from human and animal origin suggested a close zoonotic link, with only six SNP differences between the human isolate (O) and the closest broiler (animal) isolate (G). Additionally, among nine of the isolates of animal origin (including isolate G) 33 or less SNPs were detected, indicating high clonality between the isolates.

## ...no animal/meat & human link for other ESBL-producing *E. coli*

For the combinations ST69 with CTX-M-1, ST88 with CTX-M-1, ST117 with CTX-M-1, ST224 with CTX-M-15, and ST362 with CTX-M-1, more than 100 SNPs were observed between the isolates of animal and human origin. These five combinations were not investigated further.



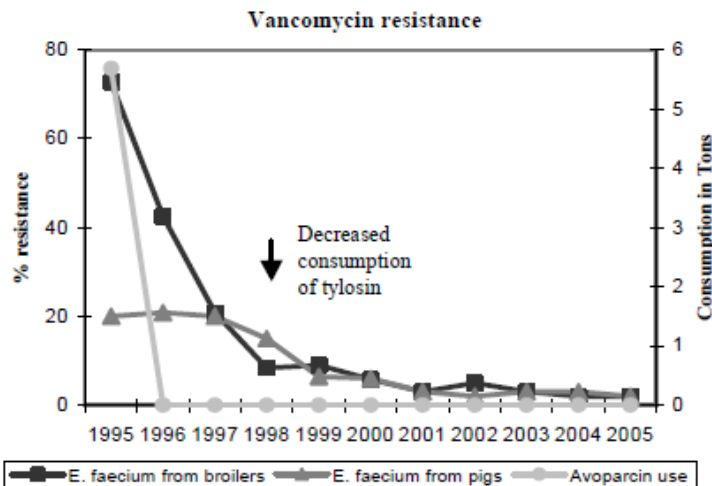
# Rapid detection of emerging resistance...

RAPID COMMUNICATIONS Eurosurveillance 2015

Detection of *mcr-1* encoding plasmid-mediated colistin-resistant *Escherichia coli* isolates from human bloodstream infection and imported chicken meat,

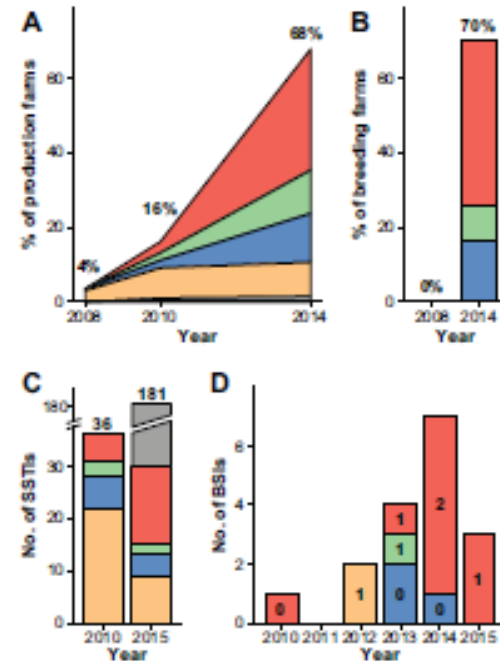
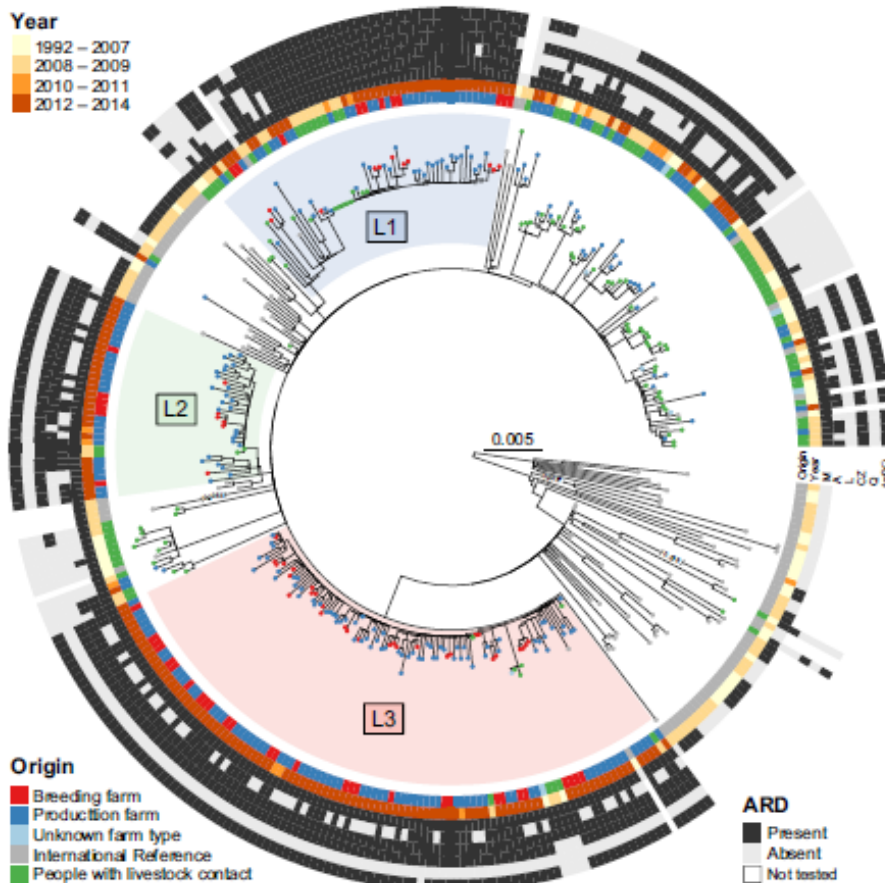
Availability of WGS data allowed detection of *mcr-1* in DK (2012-2015 isolates) within 2 weeks since the first *mcr-1* description

# ...surprising findings of persistent resistance



*E. faecium*, pigs, DANMAP 2012  
*vanR, vanS, vanY, vanZ*: 100% id  
*vanA*: 99.9% id  
*vanX*: 99.8% id

# Dynamics of MRSA CC398 in pigs and humans, DK



# ResFinder 4.0 for *in silico* antibiograms

Gene_accession no.	Class	Phenotype	PMID	Mechanism of resistance	Notes
fosX_1_AP010904	Fosfomycin	Fosfomycin	19675025	Enzymatic inactivation	
fos_1_ACCV01000052	Fosfomycin	Fosfomycin	unpublished	Enzymatic inactivation	
tetA(46)_1_HQ652506	Tetracycline	Doxycycline, Tetracycline, Tigecycline, see Notes	22941900	Increased efflux	both tetA(46) and tetB(46) must be present to confer
tetB(46)_1_HQ652506	Tetracycline	Doxycycline, Tetracycline, Tigecycline, see Notes			
tet(57)_1_KP137702	Tetracycline	Doxycycline, Tetracycline			

- Based on ECOFFs
- Experts' opinion & literature searches

## ResFinder 4.0 performance: *Salmonella* sp.

- 1,095 isolates from NARMS
- 7 antimicrobials (AMP, FOX, CHL, CIP, GEN, NAL, TET)
- 7,657 antimicrobial-isolate combinations

98.5 % genotype-phenotype concordance

AMP	98 %	No gene but pheno <sup>R</sup>	<i>bla</i> <sub>TEM-1</sub> but pheno <sup>S</sup>
FOX	99 %	No gene but <a href="#">pheno<sup>R</sup></a>	
CHL	99 %	No gene but <a href="#">pheno<sup>R</sup></a>	<i>floR</i> but <a href="#">pheno<sup>S</sup></a>
CIP	97 %	<i>qnrB19, qnrS2, or aac(6')-Ib-cr</i> but pheno <sup>S</sup>	
GEN	99 %	No gene but pheno <sup>R</sup>	<i>ant(2'')-Ia</i> but <a href="#">pheno<sup>S</sup></a>
NAL	99 %	No gene/mut. (only <i>qnr</i> ) but pheno <sup>R</sup>	
TET	98 %	No gene but pheno <sup>R</sup>	<i>tetA, B, or C</i> but <a href="#">pheno<sup>S</sup></a>

# ResFinder 4.0 performance: *C. jejuni*

- 223 poultry isolates from five EU countries
- 6 antimicrobials (CIP, ERY, GEN, NAL, STR, TET)
- 1,286 antimicrobial-isolate combinations

98.5 % genotype-phenotype concordance

CIP	98 %	No mut. but pheno <sup>R</sup>	
ERY	99 %	No gene/mut. but pheno <sup>R</sup>	
GEN	100 %	No R isolates in dataset	
NAL	96 %	No gene but pheno <sup>R</sup>	Mut. but <a href="#">pheno<sup>S</sup></a>
STR	100 %	No R isolates in dataset	
TET	98 %	No gene but pheno <sup>R</sup>	<i>tetO</i> but <a href="#">pheno<sup>S</sup></a>

# Take-home messages

- DANMAP was created as part of a strategy to control AMU & AMR in humans and food animals in DK (e.g. to monitor effect of interventions, to set targets, etc.)
- WGS is already becoming more integrated in DANMAP
  - WGS-based prediction of AMR is realistic for some of the most important foodborne pathogens (*Salmonella* sp. and *C. jejuni* - 98.5 % geno-pheno concordance)
  - Cross-sector and interdisciplinary cooperation including integration of WGS data with other data sources can allow us to answer long-standing questions about AMR evolution and transmission

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**Thank you for your attention!**

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