

THE BENEFITS OF GENOMICS FOR MONITORING ANTIBIOTIC RESISTANCE AND DETECTING TOXI-INFECTIONS

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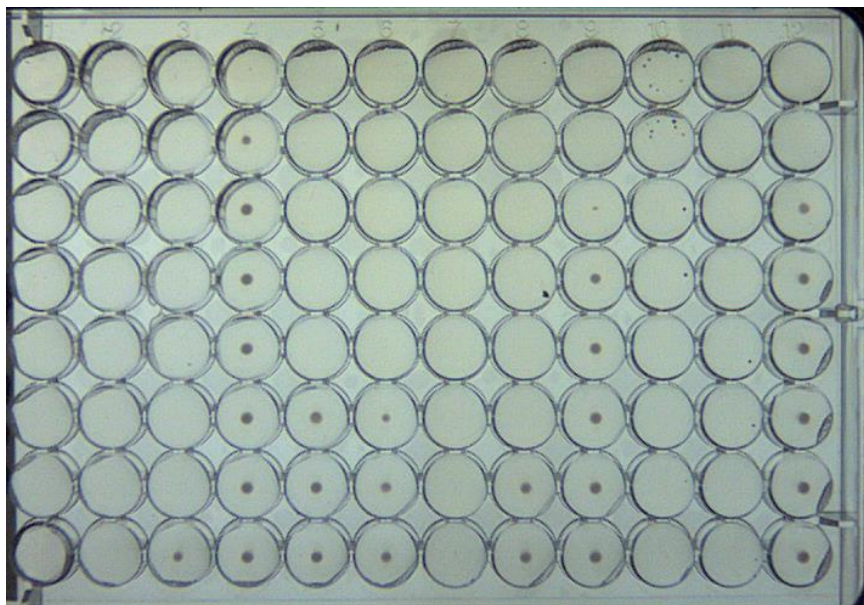
Bavo Verhaegen, Laurence Delbrassinne (Foodborne pathogens service) [.be](https://www.sciensano.be)

Antimicrobial resistance (AMR)

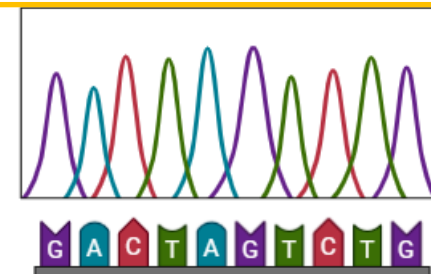


AMR: Added value phenotyping and genomics

Phenotype: expression of the resistance



Genotype:



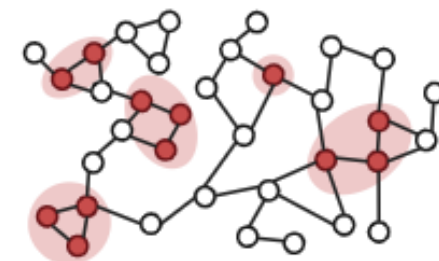
Sequencing



Resistance mechanisms

→ Transferable?

→ Co-selection?



Relatedness of the isolates

Toxi-infections

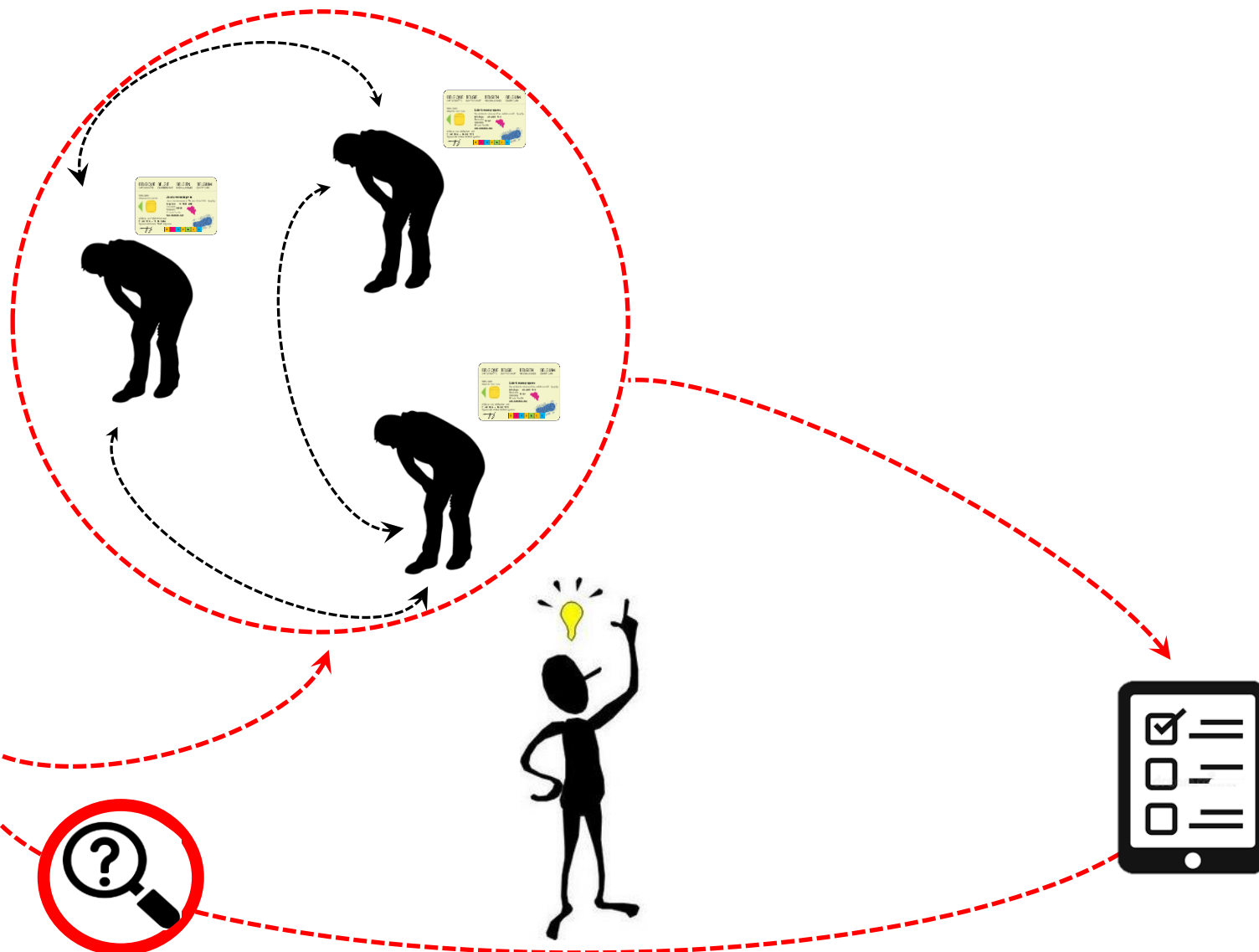


WGS



Toxi-infections: added value genomics

Molecular database

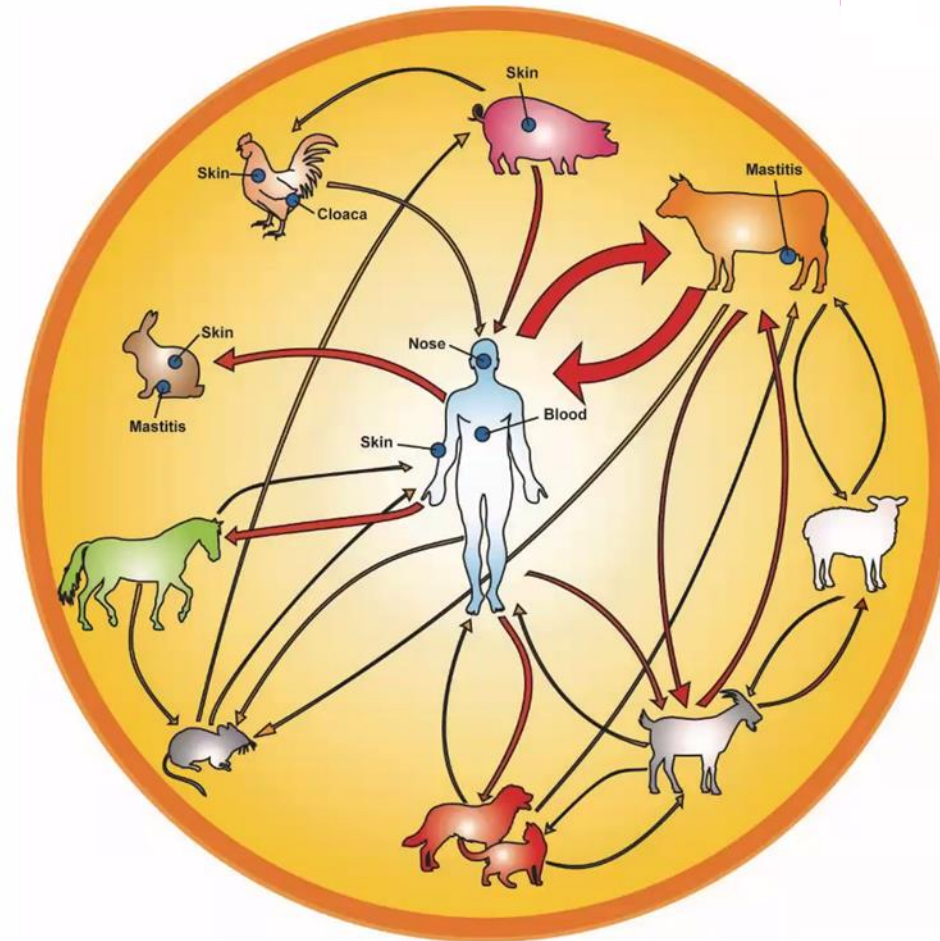


GENOMIC MONITORING OF MRSA

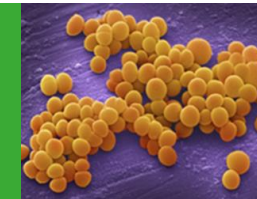
Monitoring in food-producing animals in a One-health context



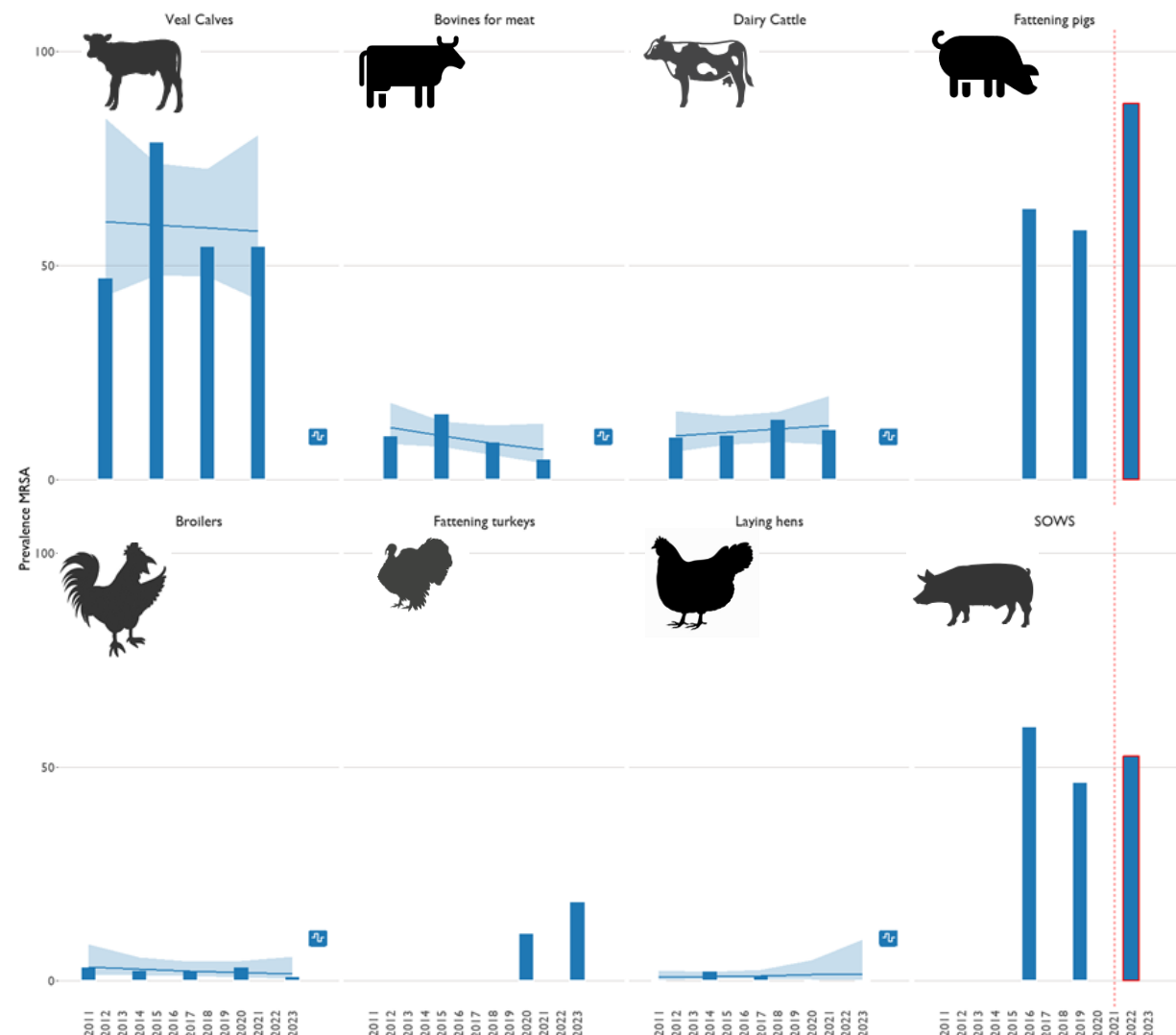
S. aureus: a multi-host pathogen



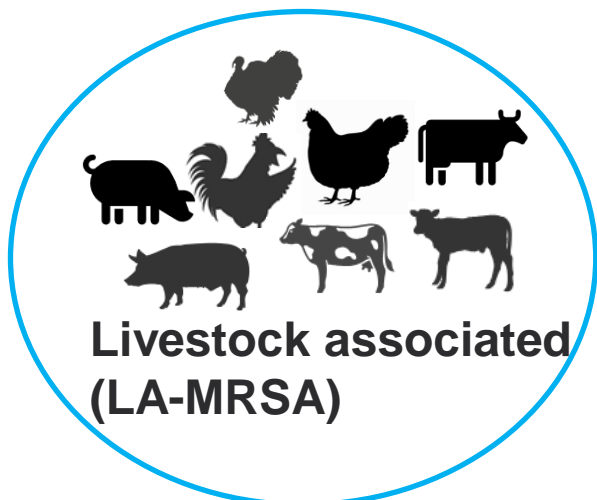
MRSA prevalence in animals in Belgium



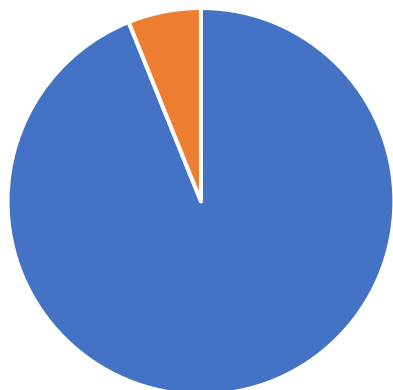
- On-farm monitoring since 2011
 - Prevalence of MRSA
 - Characterization of MRSA isolates
 - Phenotype + Basic genotype
 - In-depth genotype (WGS), since 2022
- 3-years-rotation: Poultry, Bovines, Porcines
- Highest prevalence (>50%) in veal calves and porcines



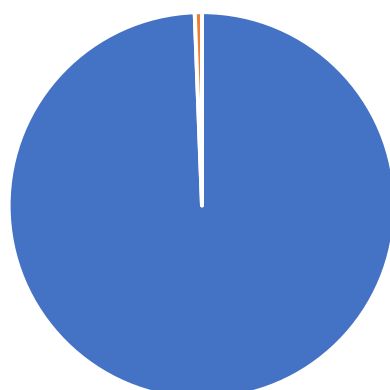
MRSA genotyping



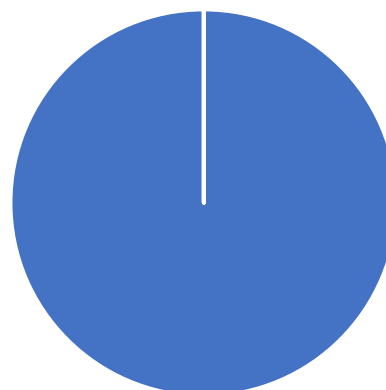
Bovins (2021)



Porcins (2022)



Volailles (2023)



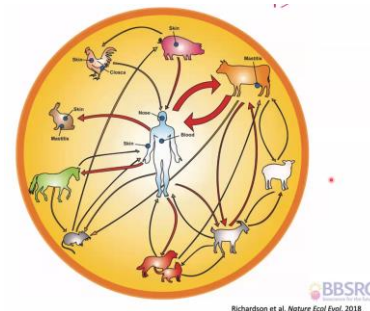
- Mostly LA-MRSA
- HA- and CA-MRSA sporadically detected in Belgium in food-producing animals:
 - porcines, bovines or poultry
 - Source not traced
 - WGS is helpful to assess genetic relatedness

Example: HA-MRSA strain detected in bovines

Isolated from meat cattle in 2018 in Belgium:

- ST22 (CC22)/ HA-MRSA
- *tst* (toxic shock syndrome)
- *sak*, *chp*, *scn* (immune evasion cluster)
- Tet S
- SCCmec typical of LA-MRSA (IV2b/ IVa2b)

- Hypothesis: a strain of human origin which is thought to have acquired resistance to methicillin in animals
- Importance of genomics for the monitoring

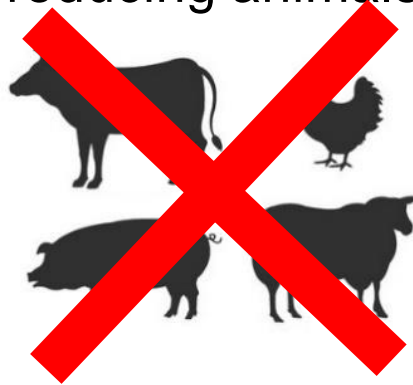


ONE-HEALTH MONITORING OF RESISTANCE TO CRITICAL ANTIBIOTICS

The linezolid case

Linezolid

- Linezolid (LZD):
 - a critically important antibiotic to treat human infections (MRSA, VRE)
 - not licensed for food-producing animals



- linezolid-resistant (LR) isolates reported in European countries in H + A



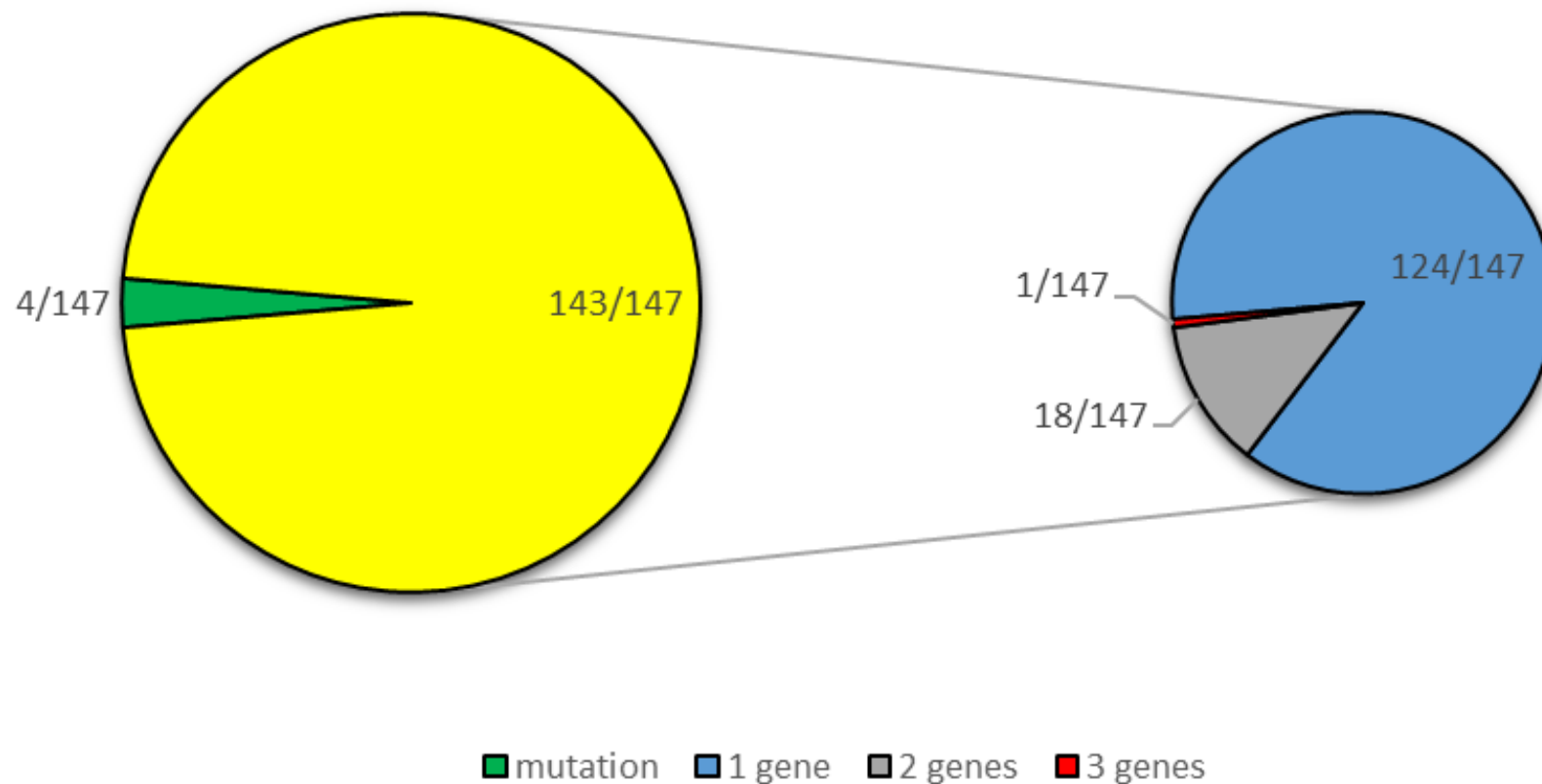
Known resistance mechanisms

Known genetic determinants conferring resistance to linezolid

transferable	Gene	Mechanism	Antibiotic classes (Resistance to)
	cfr	23SrRNA methylation	Oxazolidinones, phenicols, lincosamides, pleuromutilins, streptogramin A =« PhLOPSA »
	optrA	ribosomal protection	oxazolidinones, phenicols
	poxrA	ribosomal protection	Oxazolidinones, tetracycline, phenicols,
	Mutations in 23SrRNA	ribosomal protection	Linezolid

Common
cross-
resistance
to phenicols

Resistance mechanisms identified



→ Most of the isolates (97.3%) carried **transferable LR genes**

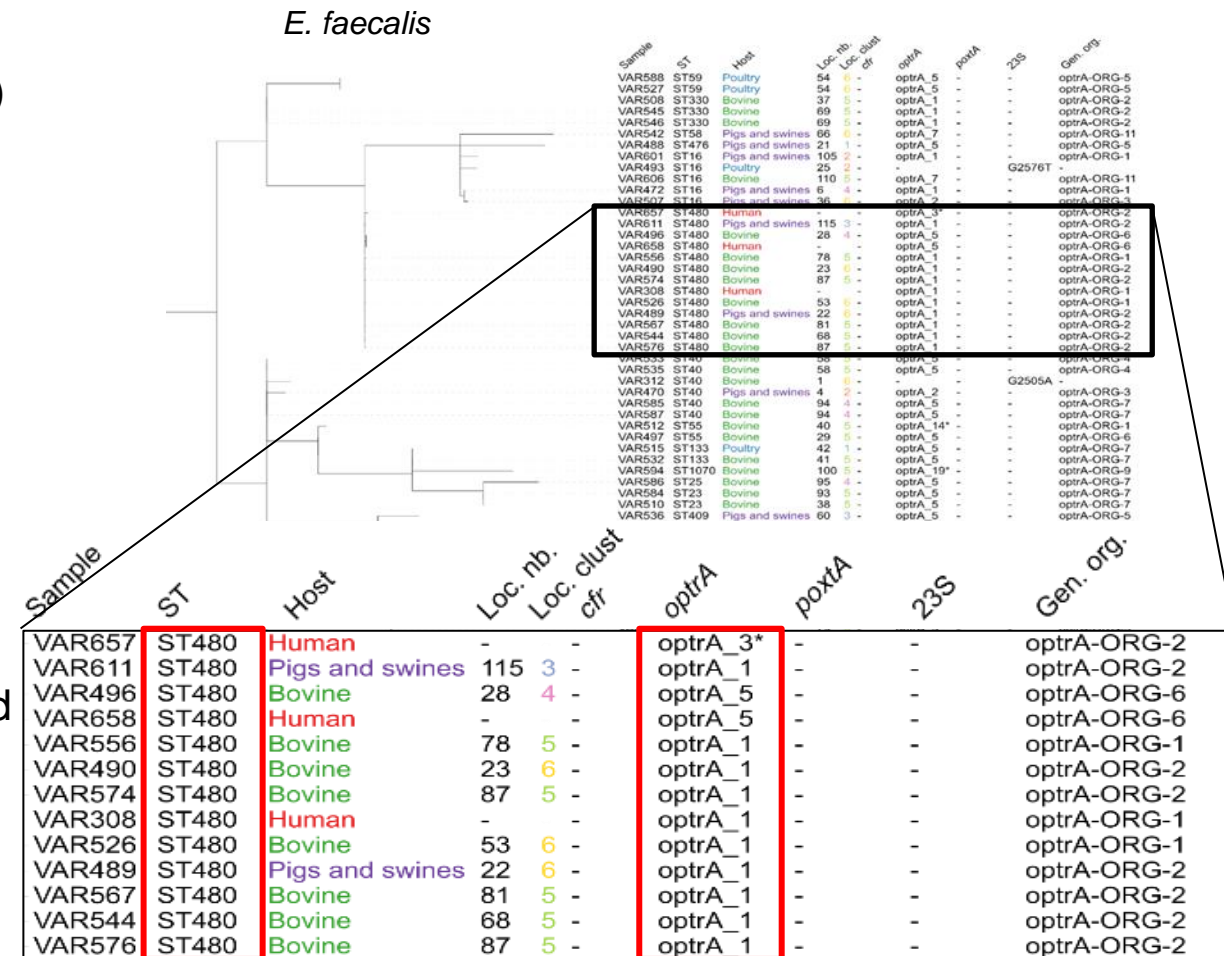
→ Mainly *optrA*: only gives **cross-resistance to phenicols** (and LZD)

Large diversity observed among LR enterococci isolates

Very large phylogenetic differences observed along with some smaller clades containing more closely related isolates

- *E. faecalis*: 28 different STs (including 3 new)
- *E. faecium*: 32 different STs (including 8 new)

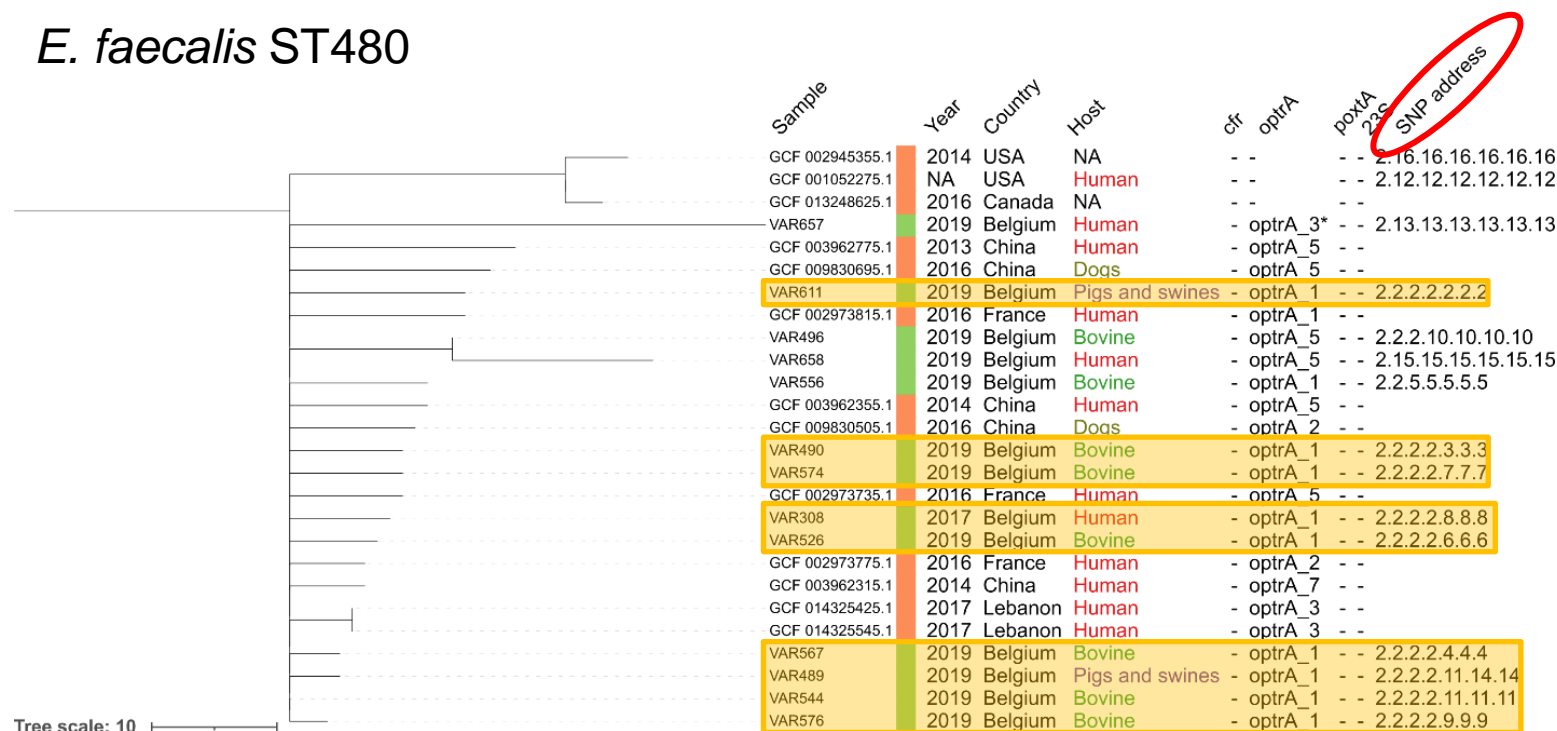
GENETIC DIVERSITY!



- No clear correlation between phylogenies and carried LR genes (alleles)
→ could indicate a facilitated transfer and **spread** of LR genes

Closely related isolates from pigs, bovines and humans

E. faecalis ST480



- 9 closely related isolates (difference of 10 to 25 SNPs based on SNP address)
- Isolates from pigs, bovines and humans
- Suggesting a potential epidemiological link

Genomic research as a basis of AMCRA advise



FOODBORNE OUTBREAK

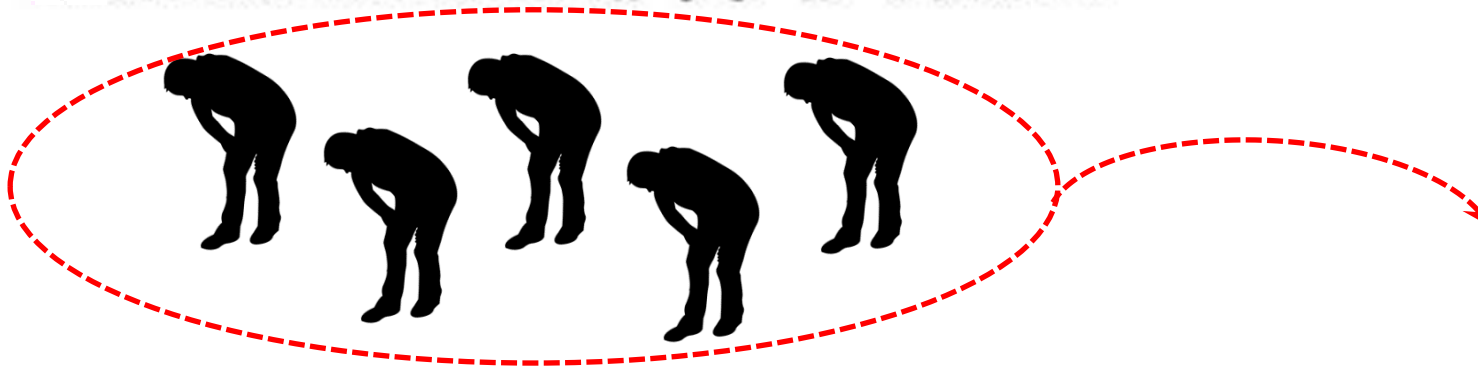
Spaghetti special

- 2024: 46 ill after spaghetti night organised by youth movement → 2 hospitalisation
- mostly within 24h: Diarrhea, fever, abdominal cramps



Epidemiological study

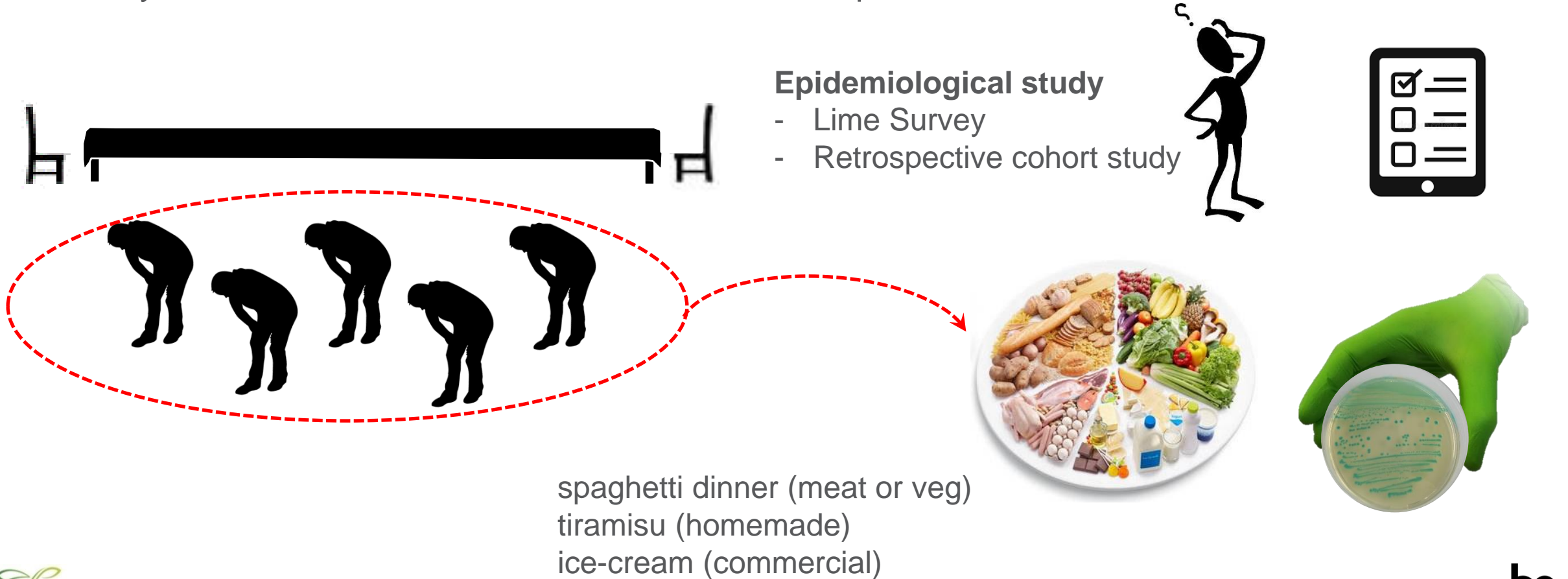
- Lime Survey
- Retrospective cohort study



spaghetti dinner (meat or veg)
tiramisu (homemade)
ice-cream (commercial)

Spaghetti special

- 2024: 46 ill after spaghetti night organised by youth movement → 2 hospitalisation
- mostly within 24h: Diarrhea, fever, abdominal cramps



Spaghetti special

- 2024: 46 ill after spaghetti night organised by youth movement → 2 hospitalisation
- mostly within 24h: Diarrhea, fever, abdominal cramps



Attack rates:

- 96% for tiramisu
- 85% for spaghetti

- Tiramisu (leftovers)
- Eggs (same batch)



- qPCR++, isolation+
 - qPCR+, isolation-
- Typing: *Salmonella* Enteritidis

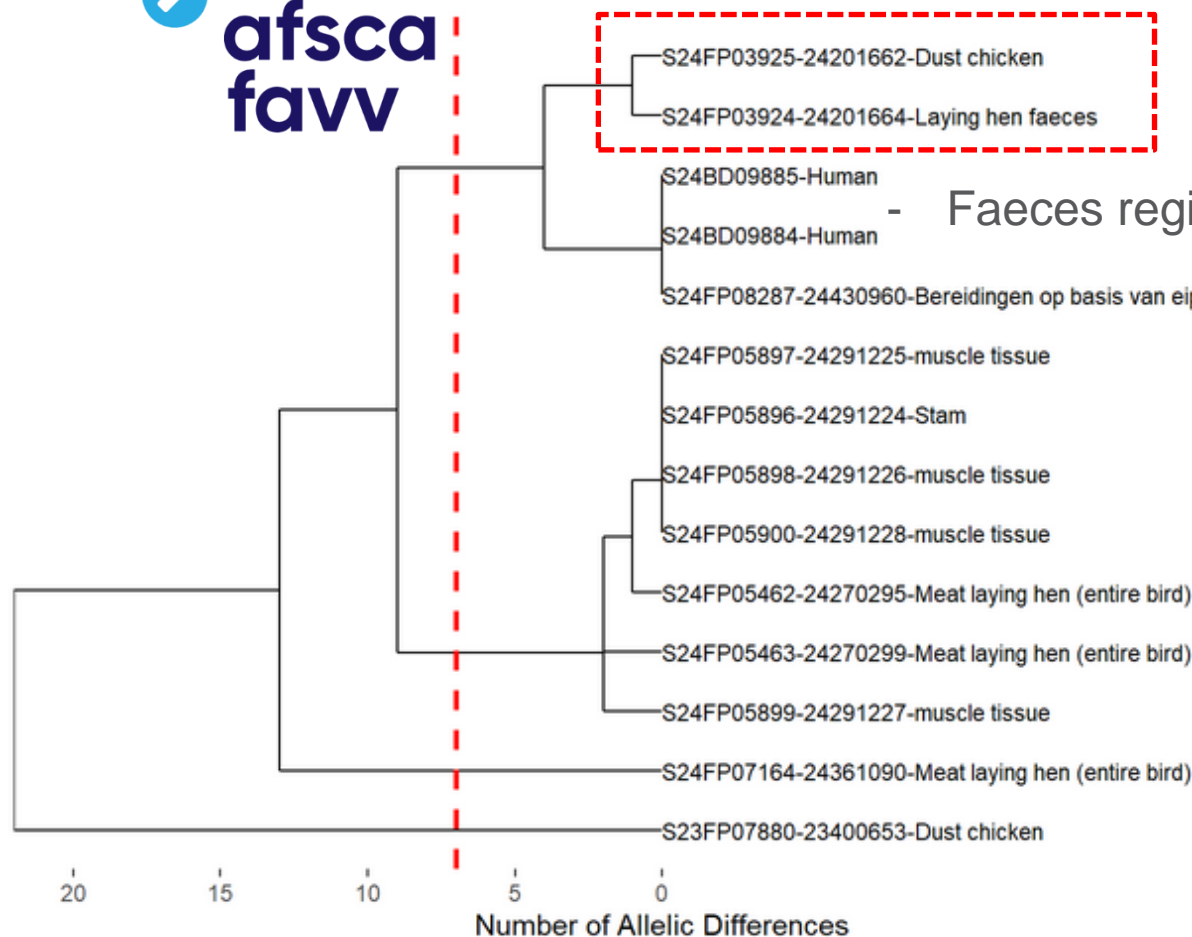
- Faeces regional hospital: *Salmonella* spp. → *Salmonella* Enteritidis
- Sent to NRC



Whole genome sequencing



afsca
favv



- Faeces regional hospital: *Salmonella* Enteritidis

- Tiramisu (leftovers)



Traceability (FAVV-AFSCA)



- same hatchery
- same transport

2 farms:

- Antwerp
- Limburg

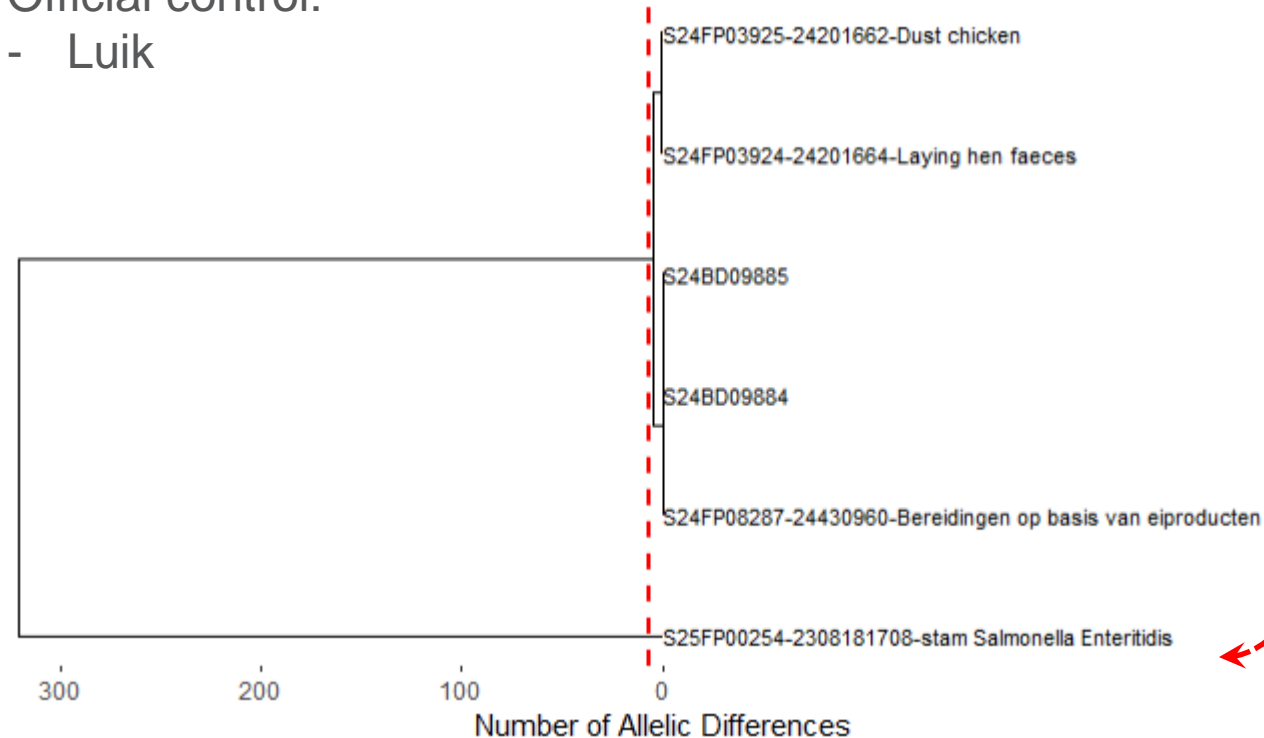
Autocontrol: no non conform results since 2022

Extra sampling: no Salmonella detected

Autocontrol: one non conform

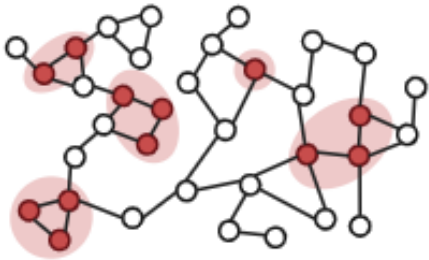
Official control:

- Luik



WGS

Conclusion: added value of genomics



- Link human and food/ animal strains
- Link outbreak strains to WGS database: source detection
- High resolution solution next to epidemiological data



Resistance mechanisms
→ Transferable?
→ Co-selection?

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**Journal of
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**Large diversity of linezolid-resistant isolates discovered in
food-producing animals through linezolid selective monitoring
in Belgium in 2019**

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Marie Hallin^{4,5,6}, Pierre Wattiau¹, David Fretin¹, Olivier Denis^{6,7} and Cécile Boland^{1*}

- The FBO investigation is a collaboration between NRL FBO, NRL Salmonella, NRC Salmonella & Shigella, the FASFC , Regional Health inspection services



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