

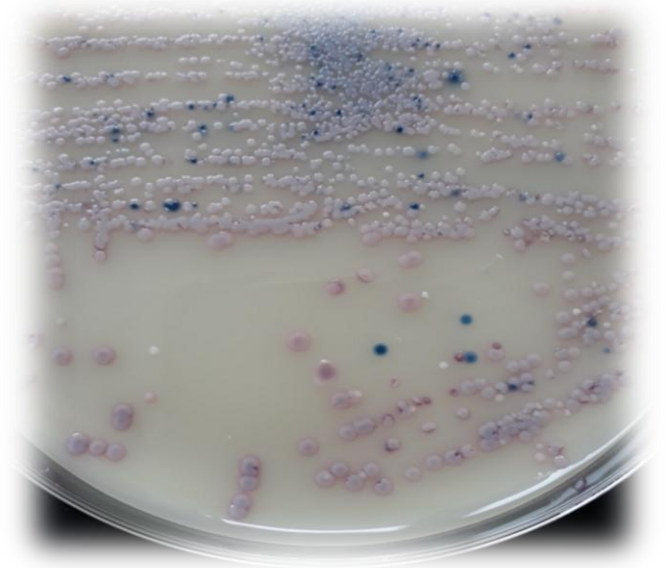


## **TECHNICAL SPECIFICATIONS FOR A BASELINE SURVEY ON MRSA IN FATTENING PIGS**

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on behalf of the EFSA WG

# Objectives

1. To assess **MRSA prevalence** in fattening pigs in the EU and in the EU MSs
  2. To inform on **genetic diversity**, **AMR** and **virulence factors** of MRSA in pigs
- EU-wide cross-sectional survey at the slaughterhouse
  - Should target slaughtered fattening pigs
  - Should provide comprehensive, comparable and reliable information
  - Should provide detailed characterisation of MRSA strains and lineages, virulence and host-adaptation factors



# Sampling framework

- Sampling design: **at the slaughterhouse**
- Sampling approach **already in place** for routine AMR monitoring at the slaughterhouse
- Assessing MRSA prevalence **in batches of slaughter pigs**
- Sampling point: post-stunning
- Sample type: **nostril swabs**

Sampling concept	Sampling of nostril samples at slaughter
Target populations	Domestically produced fattening pigs (slaughtered in the SH representing 60% of fattening pigs slaughtered in the MS)
Strata (1 <sup>st</sup> stage)	Slaughterhouses (60% of domestic production of FP)
Proportional allocation	Sample size proportionate to the slaughterhouse throughput
2 <sup>nd</sup> stage	Batches of fattening pig carcasses originating from the same herd of pigs
Epidemiological Unit	Slaughter batches of fattening pigs
Sample	4 pooled samples of 20 nostril swabs per epidemiological unit

# Sample collection: Nostril swabbing of slaughter pigs

- The slaughter batch should be of a sufficient size to allow the sampling of at least 20 carcasses, given the speed of the slaughter line (to be pragmatic!: for small batches: 4 pooled samples of less than 5 swabs)
- To avoid any misidentification and mixing of batches, samples should be taken from the carcasses situated around the middle of the given slaughter batch sampled
- For the operator/sampler's comfort and for proper sample handling, there is no need to sample successive carcasses of the same slaughter batch
- To account for the speed of the slaughter line, to **sample only one nostril per carcass**
- To rotate 5 times the swab within the nostril sampled
- Sampling of nostril swabs shall be performed **after stunning** of the pigs but **before scalding** of the carcasses (to be pragmatic!):
  - Optimally **before** the **bleeding** post/ If not possible, after the bleeding post
  - To be recorded: a data element added.
- Unique numbering system of the 4 composite samples (identification of the batch, SH, sample)



# Sample size

- **Number of batches**

- **50%** (between) **batch prevalence** or if unknown prevalence:

⇒  $N_b = 194$  batches to be sampled (vs. 300 batches for ESBL)

- Example: 77% (between) batch prevalence

⇒ #batches =  $97/pr \rightarrow$  e.g.  $97/0.77 = 126$  batches

- Maximum number of batches:  $N_b = 194$  batches

- Accounting for lost adjustment (+7%): **208 batches**

- + 5% to consider missing data
- + 2% to consider possible loss of strains during storage

- **Finite population correction**

- $N_b > 5\%$  of the total population size of the batches of the MS
- Downward adjustment
- Required number of slaughter batches tabulated in MRSA Tech. Spec. (Table 2)

. In the case of unknown prevalence of MRSA *a priori*, **a sequential quarterly procedure has been proposed.**

. **A higher prevalence requests a lower sample size to be tested.**

. The approach requires a thorough follow up all along the survey so that the adaptation is implemented every quarter of the survey!

. The adjustment needs to be performed after each quarter and can go in both directions

To be documented by quarterly exchange with EFSA

Cf. Table 3 of Tech. Spec.

- **Proportional allocation of sample size per strata and per quarter**

> Proportional allocation of  $N_b$  per strata (slaughterhouse:  $f_t$ : fraction of throughput):  $N_b * f_t$

> Number of batches to be collected per quarter:  $N_b * f_t / 4$



# Sample size

- **At the batch level**

- > **20 nostril swabs** (individual samples) per batch
- > **4 pooled samples** (of 5 nostril swabs) per batch
- > Batches with less than 20 pigs: 4 pooled samples

The sample size allows a sensitivity of 80% for detecting as positive a batch characterised with a within batch prevalence of 10%.

- **Robust randomised sampling procedure currently in place for routine monitoring of AMR**

- > **Even distribution over the quarter (-> over the year)**



# EXPECTED OUTPUTS

- **Data analyses**
  - MRSA Prevalence assessment at MS-level and EU-level
  - Assessment of the diversity of MRSA
  - Accounting for the hierarchical structure of the data



# DATA REPORTING (1)

- Existing EFSA Data Models to be used with limited adaptations
- **Isolate-based Data Model**
  - Isolate-level quantitative AMR data
  - WGS data: **pre-defined list of genes in catalogues to facilitate the reporting**
  - Reported according to the AMR data model of EFSA used in routine
- **Sample-based Data Model**
  - detailed analytical results of all samples taken (positive and negative) reported using the EFSA standard for reporting laboratory results (Standard Sample Description version 2 (SSD2))
  - Limited number of epidemiological data to be reported
    - durations of transport
    - duration of lairage
    - stunning method
    - Sampling performed before or after bleeding

**Reporting  
is  
Recommended !**





## DATA REPORTING (2)

- **Data Model**

- To collect epidemiological information on Slaughterhouses and Farms
- Number of animals in the farms involved
- Annual throughput of the slaughterhouses involved

- **... through XML files**

- Like the reporting of AMR data from routine monitoring
- Reporting tools will be made available: from Excel file to XML file



# INFO-SESSIONS

- **Info Session 1**

- April 2024
- To address points for harmonisation
- Documentation available on Teams

- **Info Session 2**

- Dedicated to data reporting
- ... Last Questions

**A EFSA info-session  
dedicated to data reporting  
is planned  
on 23 October 2024**



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Thank you  
for your attention!

## Acknowledgements

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