

# EFSA-EURL Confirmatory testing 2020 data

Jette Sejer Kjeldgaard &  
Anne M. Seyfarth

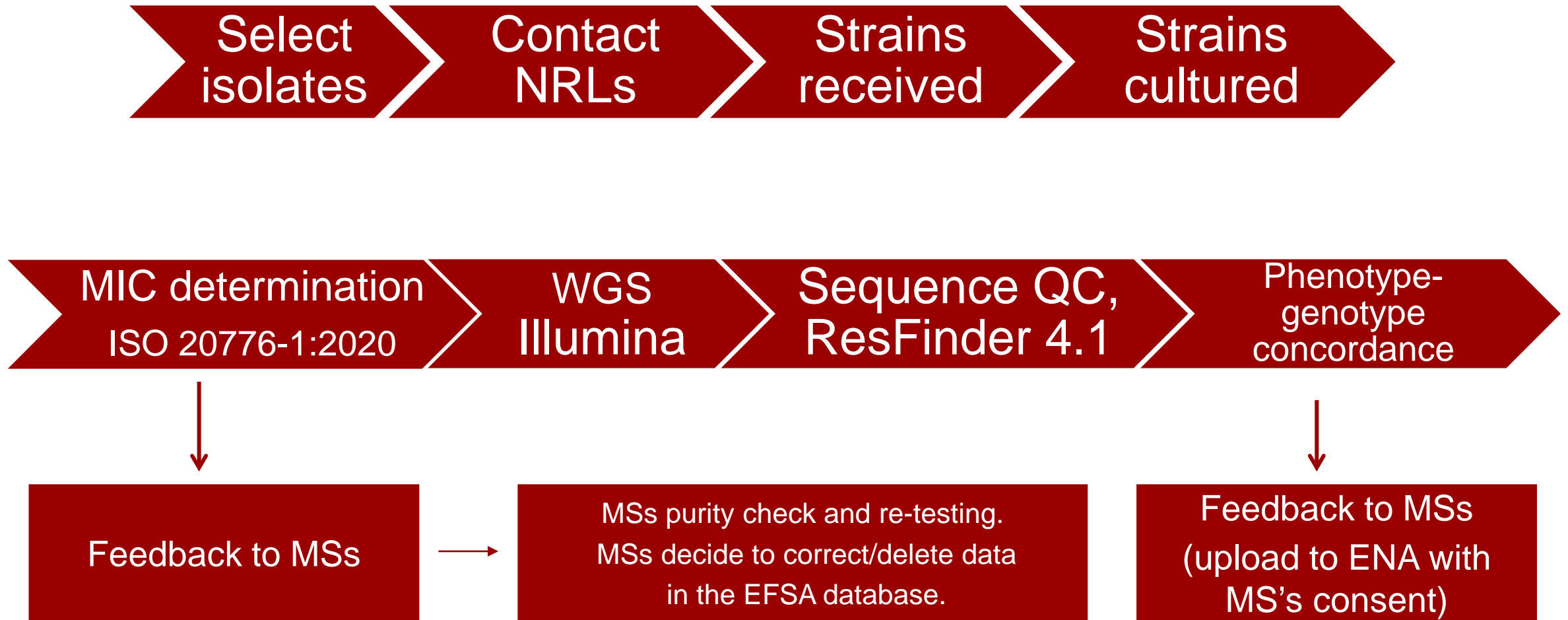
# Term of Reference, EURL-AR

The EURL-AR will provide confirmatory testing on bacterial isolates of particular relevance upon request by the NRLs, the European Commission and EFSA:

- To support the activities related to the implementation of the Decision 2013/652/EU
- To confirm the AMR phenotypes observed by MSs
- To determine the AMR genotypes and to evaluate phenotype-genotype concordance

*Relevant Material Transfer Agreements (MTAs) between the EURL and MSs ensure the legal aspects of strain ownership.*

# Workflow for the confirmatory testing activities



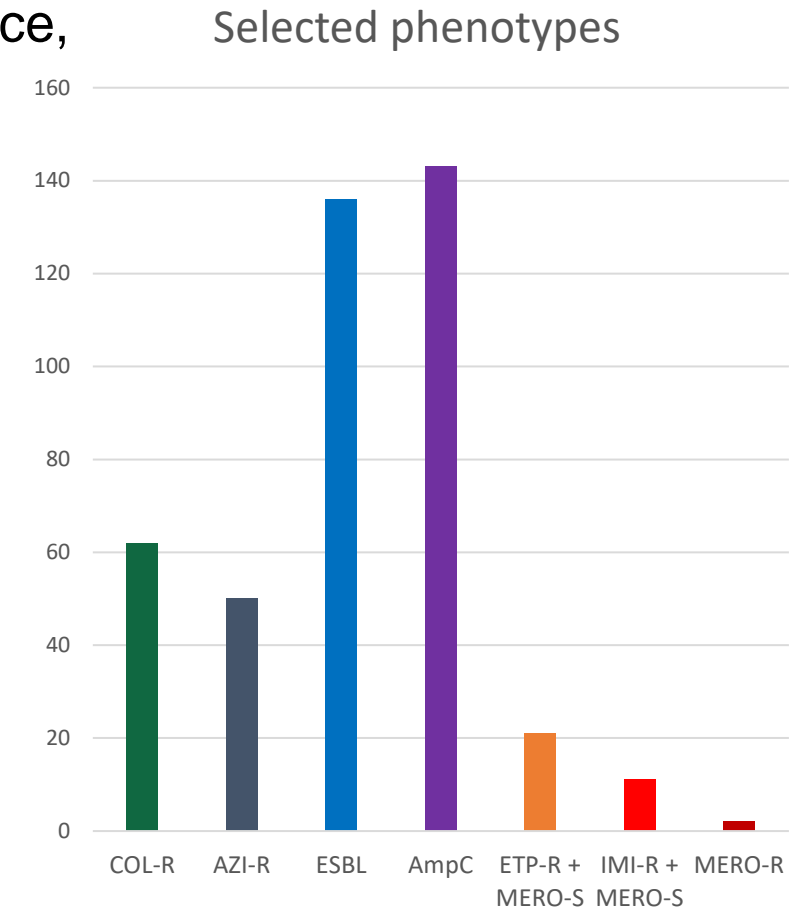
# Changes compared to last year's presentation

- Due to lab issues we are not ready to present the **genotypic data** yet. This presentation only covers the comparison of MIC-results between MS and the EURL-AR
- The selection criteria by EFSA for the 2020-isolates were the same as for last year, except for including **AZI-R profiles** again
- Last year with the panels and ECOFFs for the "old" legislation. Next year amikacin will be included and some ECOFFs are changed

# Selection criteria by EFSA

- The selection criteria for the 2020-isolates relates to colistin resistance, azithromycin resistance, the presumptive ESBL/AmpC profiles and carbapenem resistance:

- COL-R profile: 62 isolates
- AZI-R profile: 50 isolates (with ESBL profile)
- ESBL profile: 136 isolates (incl. the AZI-R profiles)
- AmpC profile: 143 isolates (FOX MIC=16; FOX MIC>16)
- ETP-R + MERO-S: 21 isolates (cephalosporin-resistant)
- IMI-R + MERO-S: 11 isolates (cephalosporin-resistant)
- MERO-R: 2 isolates (cephalosporin-resistant)



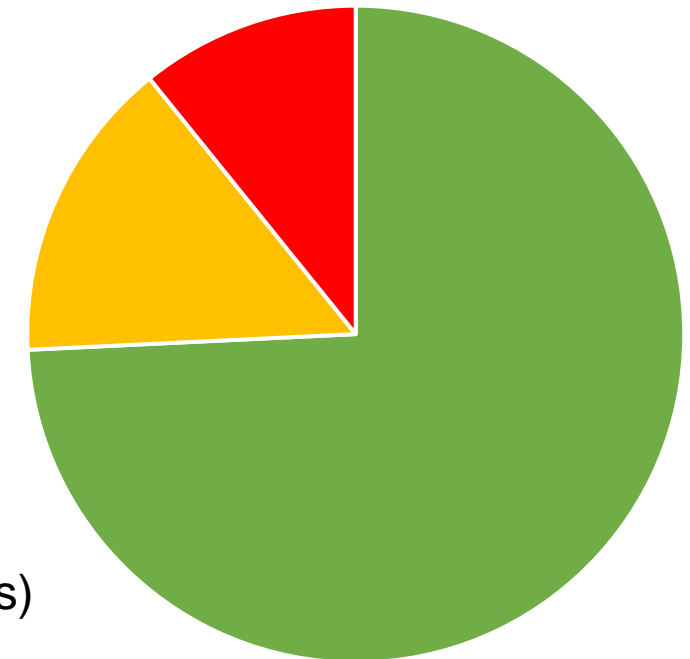
# Isolates

- **2020 was a poultry year**
- **372 isolates were selected (29 countries)**
  - 348 *E. coli* and 24 *Salmonella* (range 1-39 per country)
  - 15 of the 24 *Salmonella* were selected because of colistin.
- **364 isolates were received at the EURL (29 countries)**
  - 3 isolates were not tested (1 *Klebsiella*, 1 heavily contaminated, 1 lost)
  - **361 isolates MIC-tested → 9,025 bug/drug tests (i.e. 9,025 MIC-values)**
- **8 isolates were not received at the EURL**
  - Data changed by MS for 4 isolates (3 isolates from CARBA-R to S)
  - 3 isolates were not viable anylonger at MS.

# Comparison of phenotypes at MS and EURL

Comparison of phenotypes

- 268 of the isolates (74.2 %) were in fully agreement:
  - Identical R/S phenotypes according to the applied ECOFFs
  - MIC-values were within the acceptable deviation of the method (i.e. within  $\pm 1$  dilution step difference).
- For the remaining 93 isolates (25.8 %) R/S discrepancies were observed:
  - 54 isolates - within the acceptable deviation of the method.
  - 39 isolates (10.8 %) - above the acceptable deviation (14 MSs)



**The levels of discrepancies are the same as for last year.  
Very fine, pure cultures received at the EURL this year.**

- Full agreement
- Acceptable deviation
- Above acceptable deviation

# Isolates with MICs within the acceptable deviation

- No critical issues were identified for the 54 isolates with R/S discrepancies caused by differences in MIC-values within the acceptable deviation of the method

The R/S discrepancies were primarily observed for:

- Cefepime (FEP): MIC 0.12 vs. 0.25 mg/L (24 isolates)
- Cefoxitin (FOX): MIC 8 vs. 16 mg/L (12 isolates)
- Ertapenem (ETP): MIC 0.06 vs. 0.12 mg/L (7 isolates)

ECOFF considerations based on the results in the 2020-dataset :

- The EUCAST ECOFF for *E. coli* and FEP is 0.25 mg/L
- The EUCAST ECOFF for *E. coli* and ETP is 0.03 mg/L (tentative)



# Isolates with MICs above the acceptable deviation

For the 39 isolates with R/S discrepancies caused by differences in MIC-values above the acceptable deviation of the method, the 14 MSs were asked to check the purity of their culture, to do a re-testing and report the results.

## **Outcome of the re-testing performed by the MSs:**

- Data for 30 isolates were corrected. Corrections were mainly for carbapenems (13 cases of R→S), SMX (11 cases of R→S) and COL (7 cases of R→S).
- Data for 4 isolates were not corrected after re-testing. The discrepancies were concluded to be caused by testing of non-identical material at MS and EURL.
- By a mistake, the data for 1 isolate was not corrected after re-testing (IMI R→S) and 4 isolates were not re-tested by two MSs.

# Phenotypic profiles and the selection criteria (1)

- COL-R profiles: **95.2 %** of 62 profiles were confirmed as COL-R
- AZI-R profiles: **98.0 %** of 50 profiles were confirmed as AZI-R
- ESBL profiles: **100 %** of 136 profiles were confirmed as ESBL-profile  
(data was of course deleted for the *Klebsiella* isolate)
- AmpC profiles: **92.9 %** of 141 profiles were confirmed as AmpC profiles and the rest (10 isolates) was categorised as ESBL profiles by the EURL-AR. In all 10 cases, the difference in profile evaluation was caused by FOX

Awaiting WGS results, but remember to check for synergy!

## Phenotypic profiles and the selection criteria (2)

Carbapenems:

- IMI-R + MERO-S: 0 % of the 11 profiles were confirmed as IMI-R
- MERO-R: 50 % (1 isolate) of the profiles were confirmed as MERO-R
- ETP-R MERO-S: 14 of the selected 21 isolates were not really resistant, as they were reported by the MSs with MICs at 0.064 mg/L\*.

Four of the remaining 7 isolates were confirmed as ETP-R (and are expected to harbour the CMY-2 gene).

*\* The applied ECOFF for ETP is 0.06 mg/L. Many countries report this MIC-value as 0.064 mg/L (which is the correct concentration) and therefore, MIC-values at 0.06 mg/L were regarded as resistant by EFSA when selecting isolates for the confirmatory testing.*

## Final words...

- Thanks to all NRLs and EFSA for a fine collaboration!
- Thanks to our lab technicians at DTU, especially Birthe, for all the work done in the lab!
- The genotypic results for the 2020-data are expected to be ready and mailed to you by the end of June.

**THANK YOU FOR YOUR ATTENTION 😊 !!**