Scientific Network for Zoonoses Monitoring Data
Minutes of the 8th specific meeting on Antimicrobial Resistance data reporting

Held on 07-08 November 2018, Parma
(Agreed on 27 November 2018)

Participants

- **Network Representatives of Member States (including EFTA Countries):**

Country	Name
Austria	Peter Much
Belgium	Cristina Garcia-Graells
Bulgaria	Hristo Daskalov
Croatia	Gordan Kompes
Cyprus	Despina Theodoridou
Czech Republic	Tomas Cerny
Denmark	Helle Bisgaard Korsgaard
Estonia	Jelena Sõgel
Finland	Suvi Nykasenoja
France	Sophie Granier
Germany	Katja Pamela Alt
Greece	Myrsini Tzani
Hungary	Zita Záborczki
Ireland	Lisa O'Connor and Rosemary Slowey
Italy	Antonio Battisti, Francesca Martinelli, Alessandro Franco
Latvia	Tatjana Ribakova
Lithuania	Asta Pereckiene
Luxembourg	Manon Bourg
Malta	Susan Chircop
Netherlands	Johan Bongers
Poland	Dariusz Wasyl
Portugal	Maria Helena Pinto
Romania	Theodora Chesiou Vasile
Slovakia	Andrea Moizisova
Slovenia	Maja Golob
Spain	Gema López Orozco and Pilar Vicente Escriche
Sweden	Oskar Nilsson
United Kingdom	Francesca Martelli
Iceland	Vigdis Tryggvadottir
Norway	Jannice Schau Slettemeås
Switzerland	Gudrun Overesch

- **Hearing Experts:**

Valeria Bortolaia: European Reference Laboratory on antimicrobial resistance (EURL-AR)

- **European Commission:**

Angela Bolufer De Gea: Directorate-General for Health and Food Safety (DG SANTE), Directorate G, Unit G4

- **EFTA:**

Diana Quiliquini

- **Others:**

Lindita Molla (Albania), Muhamed Smajlovic (Bosnia and Herzegovina), Todor Karpanchev (Former Yugoslav Republic of Macedonia), Bekim Zhubi (Kosovo), Dragana Gerbic Sekuloivc (Montenegro), Tatjana Labus (Serbia), Guzin Sahin (Turkey).

EFSA:

Biological Hazards and Contaminants (BIOCONTAM) Unit: Pierre-Alexandre Belœil (Chair), Beatriz Guerra, Krisztina Nagy.

Evidence Management (DATA) Unit: Anca-Violeta Stoicescu

1. Welcome and apologies for absence

The Chair welcomed the participants to the 8th Specific Meeting on Antimicrobial Resistance of the Scientific Network for Zoonoses Monitoring Data.

2. Adoption of agenda

The agenda was adopted without changes. No further items were added.

3. Agreement of the minutes of the 7th specific meeting on Antimicrobial Resistance data reporting of the Scientific Network for Zoonoses Monitoring Data held on 8-9 November 2017, Parma

The minutes were agreed by written procedure on 13 December 2017 and subsequently published on the EFSA website. The actions from the meeting were presented together with the status of their progress. Minutes were approved.

4. Topics for discussion

07 November 2018 (first day)

4.1 General introduction

Pierre-Alexandre Belœil gave a general introduction to the meeting, notably underlining the importance and relevance of the antimicrobial resistance (AMR) monitoring activities at the European Union (EU) level. The main objectives of the 8th specific meeting on AMR data reporting of the Scientific Network for Zoonoses Monitoring were presented and discussed with the Network members. They notably related to the 2017 data reporting and the up-coming activities related to AMR monitoring in the EU in 2019, in particular regarding the 2018 data collection and the review of the EFSA technical specifications for harmonized monitoring of AMR[1,2].

4.2 Update from the EC: state of play of implementation of the AMR action plan

Further to the 2017 publication of the European Commission EU One Health Action Plan against AMR two major reports have been published.
At the European level, the Committee on the Environment, Public Health and Food Safety (ENVI) in the European Parliament published in September 2018 a report with a series of recommendations for the European Commission, its agencies and Member States. Out of the 131 recommendations, 31 recommendations are directed to Member States asking among other topics for One Health action plans; increased awareness; harmonised monitoring and surveillance; ensuring that environmental issues are introduced into the pharmacovigilance system or incentives for the development of drugs. The European Commission is preparing a reply to this report.
At the international level, FAO, OIE and WHO presented the results of their 2nd survey on AMR which received replies from 154 countries (out of the 194 WHO members). Highlights from this survey are that 60% of the respondent countries (and 68% of respondent European countries) have an Action Plan, either developed, approved or being implemented; that the European region is more advanced compared to the global picture (especially EU/EEA region).
As regards the progress in the implementation of the action plan, two progress reports have already been published. Main achievements have been the political agreement on the veterinary medicinal products and medicated fee regulations; the EU Joint Action on Vaccination; the Better Training for Safer Food Initiative securing 15 sessions on AMR until mid-2019; a budget of around 300 million EUR for the AMR Accelerator programme under the Innovative Medicines Initiative or adding two new antibiotics to the surface water Watch List under the Water Framework Directive. Momentum on AMR continues with G7 and G20 communiqués and international cooperation with WHO and OECD.

1 EFSA (European Food Safety Authority), 2012a. Technical specifications for the analysis and reporting of data on antimicrobial resistance (AMR) in the European Union Summary Report. EFSA Journal 2012;10(2):2587, 53 pp., doi:10.2903/j.efsa.2012.2587
2 EFSA (European Food Safety Authority), 2012b. Technical specifications for the harmonised monitoring and reporting of antimicrobial resistance in methicillin-resistent Staphylococcus aureus in food-producing animals and foods. EFSA Journal 2012;10(10):2897, 56 pp., doi:10.2903/j.efsa.2012.2897

4.4 Feedback on the reporting of 2017 AMR data

The main aspects of the 2017 AMR data processing and reporting were presented by Anca Stoicescu, including the major issues encountered during the reporting process as well as specific achievements. The feedback of the MSs on the 2017 AMR data processing and reporting was collected after the official closure of the data collection through a questionnaire to assess satisfaction with EFSA's reporting tools and to identify needs for improvement. An overview of this survey results was presented and discussed with the Network. Based on survey feedback, solutions/improvements proposed for the next (2018) reporting period were presented.

The catalogues were finalized by 31/01/2018. Reporting officers were able to visualise all data, and also to reject them. The confirmation button is only available at the end of the data process. No major disruptions of DCF and DWH were encountered.

The survey was filled in by 70 experts from 35 MSs. Anca Stoicescu explained in details the comments received and the actions that have already been or will be taken in order to improve the data collection exercise.

Further to a specific question from Austria, Anca Stoicescu confirmed that there are differences in how 'total units tested' and 'total units positive' are calculated in various data models.

It is as well of note that data on genes have been not yet included in the data extraction due to a bug in the process of data migration from the DCF to the DWH. The bug is planned to be solved so that those gene data can be made available for the 2017 EUSR on AMR.

4.5 Update from the European Reference Laboratory for Antimicrobial Resistance (EURL-AR)

Valeria Bortolaia from the EURL-AR presented the main activities performed by the EURL-AR in 2018 in accordance with the EURL mandate (Regulation (EU) 2017/625). The main tasks were summarized as follows:

- Guidance on methods in relation to harmonized AMR monitoring. Validation of the protocol including extended storage time (up to 96 h) between collection of caecal samples and start of the analysis for isolation of ESBL/AmpC/carbapenemase-producing *Escherichia coli* is being finalised. Furthermore, the EURL-AR adopted a revised protocol for isolation of MRSA from food-producing animals and the farm environment based on findings by Larsen et al. 2017 (Euro Surveillance).
- Organisation and follow-up of proficiency testing. Like every year, the EURL-AR performed proficiency tests including i) antimicrobial susceptibility testing of *E. coli*, *Staphylococcus aureus*, *Enterococcus* spp., *Campylobacter* spp., *Salmonella* spp.; ii) genetic characterization of ESBL/AmpC/carbapenemase-encoding genes in *Salmonella* spp.; and iii) isolation of ESBL/AmpC/carbapenemase-producing *E. coli* from a complex matrix (caecal content and/or meat from pigs, cattle and broilers).

- Coordination and assistance of laboratories in the EURL-AR network. Like every year, the EURL-AR performed one site visit with the purpose to assist NRLs in implementing the EC action plan on AMR. The EURL-AR also continuously supported NRLs by providing reference strains (more than 280 strains were shipped in 2018) and scientific/technical support. Furthermore, the EURL-AR held the annual workshop in Denmark which ensured sharing of knowledge and future perspectives on AMR surveillance across the entire network.
- Training. This year's training course aimed at providing participants from the NRLs with theoretical knowledge and practical tools for transitioning "Towards use of next-generation sequencing for surveillance of antimicrobial resistance in zoonotic and indicator bacteria from animals and food". Furthermore, the EURL-AR participated to the development of three publicly available E-learning courses focusing on detection and characterization of antimicrobial resistance by phenotypic, WGS-based and metagenomics-based methods.
- Scientific and technical assistance to EC/Collaboration with other agencies. Among other tasks, the EURL-AR supported the EC in ensuring high quality standards of AMR data and harmonization across NRLs by performing i) the Confirmatory Testing in collaboration with the EFSA; ii) a MIC reading survey to identify drug/bug combinations for which MIC reading might be problematic; iii) a survey on NGS capacity across NRLs within the framework of the working group on NGS; and iv) the development of ResFinder 4.0 as a tool for *in silico* antimicrobial susceptibility testing to overcome the limitations of phenotypic methods.

Material referring to the above points is publicly available at www.eurl-ar.eu.

4.6 EFSA scientific validation of data supported by EURL-AR reference testing

Beatriz Guerra presented the reasons for performing the Reference Testing Exercise on 2017 AMR data: namely, to improve the quality of data, detect emerging resistance mechanisms/clones, and to assess the suitability of WGS to support AMR surveillance. She also presented the criteria which have been used to select the isolates to be provided for reference testing in 2018: primarily, confirmation of reported resistance to carbapenems, resistance to tigecycline, colistin and azitromycin, discrepancies between panel 1 and panel 2 for those antimicrobials present in both panels, confirmation of ESBL+AmpC- ESBL- and AmpC- presumptive phenotypes, *S.* Rissen and isolates showing microbiologically-R to ciprofloxacin but susceptible to nalidixidic acid (typical phenotype of plasmid mediated quinolone resistance encoding genes-PMQRs).

The results of re-testing of the 2016 data (reported in 2017) and the preliminary results of the 2017 data (reported in 2018) were presented by Valeria Bortolaia. The significant discrepancies between the 2017 AMR monitoring data reported by the MSs and the confirmatory testing results will be accounted for in the corresponding 2017 EU Summary Report.

4.7 The 2017 EUSR on AMR: Preliminary Main Findings

Pierre Alexandre Beloeil briefly presented the preliminary main findings on AMR in *Salmonella,* indicator *Escherichia coli*, *Campylobacter jejuni* and Methicillin

Resistant *Staphylococcus aureus* (MRSA) in food and food-producing animals from the draft 2017 EUSR on AMR. The 2017 EUSR on AMR is the fourth EUSR based on AMR data collected and reported in accordance with the requirements of Commission Decision 2013/652/EU. The 2017 EUSR on AMR focuses on AMR in pigs and veal calves. Analyses of AMR occurrence are performed per combinations of bacteria-animal populations/food categories. The occurrence of multi-drug resistance (MDR), combined resistance to critically important antimicrobials and rates of complete susceptibility are also analysed.

For *Salmonella*, preliminary results on the occurrence of resistance, geographical distribution of ciprofloxacin-R and cefotaxime-R, data on combined resistance to these antimicrobials, and information on the main resistant serotypes were presented. Preliminary results on the prevalence of AMR and MDR in *E. coli* and *C. jejuni* were presented and discussed. The occurrence, genetic diversity and MDR-profile of MRSA from different categories of food and animal species reported voluntarily were presented.

Beatriz Guerra presented some key findings on the occurrence of ESBL-/AmpC-/carbapenemase-producing *E. coli*/*Salmonella* deriving from the routine monitoring and the occurrence/prevalence of ESBL-/AmpC-/carbapenemase-producing *E. coli* from pigs and calves and from pig meat and bovine meat collected within the specific monitoring. Results regarding the presumptive carbapenemase-producing microorganisms specific monitoring were also described.

It was highlighted that the results presented, although they give a good overview of the epidemiological situation regarding AMR, are preliminary as some MSs are still correcting data. A more complete view of the results will be presented in the draft version of the 2017 EUSR on AMR sent for consultation.

4.8 Production of the 2017 EUSR on AMR: next steps

The Chair re-iterated the steps for the consultation and publication of the 2017 EU Summary Report (EUSR) on AMR. The draft 2017 EUSR on AMR will be sent for consultation at the beginning of December and owing to the strict deadlines with the publisher MSs were requested to send their comments by beginning of January 2018 at the latest. DCF has been opened in November to allow the results from the reference testing to be updated in the EFSA database; for certain MSs, some alterations may still be accepted in December and accounted for in the final version of the report. The 2017 EURS on AMR will be published by mid-February 2019.

4.9 Update of the activities of the EFSA WG on the review of the Technical Specification for AMR monitoring

The current harmonised monitoring of antimicrobial resistance (AMR) in bacteria from food-producing animals and meat derived thereof, as defined by Commission Implementing Decision 2013/652/EU, has benefited from the harmonisation of the antimicrobial susceptibility testing method used (microdilution), in particular regarding the sets of antimicrobials and dilution ranges to be tested, as well as the interpretative criteria of resistance (EUCAST ECOFFs) and the representative sampling design. The EURL-AR also provides external quality assurance for susceptibility testing. This high level of harmonisation of susceptibility testing between MSs has enabled comparison between the levels of resistance or the resistance profiles reported for bacterial

targets by the MSs. The European Commission issued a request of scientific and technical assistance to EFSA on harmonised monitoring of antimicrobial resistance in bacteria transmitted through food in the view of reviewing the current EU implementing legislation (Commission Implementing Decision 2013/652/EU). To address the mandate, the EFSA has set up an ad hoc Working Group, working in close liaison with the EURL-AR and the EURL-*Campylobacter*.

An update on the current activities of the EFSA Scientific WG on the review of the technical specifications for the harmonised AMR monitoring in food-producing animals and food (art. 31 EC mandate) was provided jointly by EFSA and the EURL-AR (member of the WG). The approach followed by the EFSA WG and the guiding principles for the preliminary draft proposals were first presented. The intention is notably to continue the phenotypic monitoring of AMR and to update it, where needed, accounting for the recent scientific and technological trends in AMR.

The intention is to slightly alter the harmonised panel of substances for *Salmonella* and indicator *E. coli* (panel 1) and for MRSA. It is proposed to take full advantage of the caecal content sampling to construct the AMR monitoring. It is also put forward to expand the scope of the routine AMR monitoring, by performing complementary baseline surveys and to complement the phenotypic monitoring with molecular monitoring.

The possible structure of a workflow implementing WGS for AMR currently under discussion was presented, as well as the vision and the added value of using WGS in AMR surveillance, while emphasizing that the discussions are still at a preliminary stage. WGS has a notable added value compared with phenotypic antimicrobial susceptibility testing as it can truly provide surveillance data for action. For example, phenotypic antimicrobial susceptibility testing can only provide occurrence of specific resistance phenotypes and thereby conveys limited information on pathways of AMR transfer. On the contrary, by using the detailed genetic information obtained by WGS, it is possible to accurately assess if there is transfer of antimicrobial resistance genes and/or antimicrobial resistant bacteria along the food chain and from animals to humans, and this information is necessary to evaluate the need and plan any public health intervention aimed at protecting consumers' health.

This key agenda topic gave the opportunity to have a preliminary exchange of views with the MSs. It was underlined that the proposals presented were preliminary and may be subject to change. The corresponding EFSA Scientific Report is planned to be published in April 2019.

The Network notably discussed the issues of the implementation of the current specifications in the countries with small production sectors and the use of the 'slaughter batch' of fattening pigs as epidemiological unit. Those 2 points will be addressed by the EFSA WG. Regarding the monitoring in pigs in 2019, the EC and the EFSA will liaise to propose a temporary solution regarding the definition of the epidemiological unit.

The difference between the EFSA WG and the EURLs WG on WGS has also been clarified.

08 November 2018 (second day)

5. Welcome and apologies for absence

The Chair welcomed the participants to the second day of the 8th specific meeting on AMR data reporting of the Scientific Network for Zoonoses Monitoring Data.

6. Topics for discussion

6.1 Milestones for the production of the 2018 EU Summary Report on AMR

Krisztina Nagy presented the planned milestones for the 2018 EUSR on AMR data reporting and validation exercise. The Network discussed all timelines and agreed on the following milestones:

- Opening of the DCF for 2018 data reporting on 1 April 2019;
- Closure of the reporting period on 31 May 2019. Data sent in after 31 May (new data) will not be scientifically validated for the 2018 EUSR and will neither be included in the 2018 EUSR;
- First validation period for EFSA: 1–13 June 2019;
- 14 June 2019: letters requesting scientific clarifications and/or amendments (if needed) sent to the MSs by EFSA;
- First period for data correction for MSs: 17 June – 28 June 2019;
- Final validation period for EFSA: 6 – 10 July 2019;
- Final period for data correction for MSs: 11 – 17 July 2019;
- 24 July 2019: EFSA validates the final submitted and corrected data (against a number of criteria, the same used in the first and second validation period). After 24 July 2019, data cannot be changed, as the data extracted on this date will be used to draft the 2017 EUSR. Wrong data (combination of matrix/pathogen) will not be included in the analysis for the 2018 EUSR;
- Amendment of 2018 data and historical data can be carried out between 1 and 30 November 2019. These data will be used in the National reports and in the EFSA DWH but will not be included in the analysis of EUSR 2018.

6.2 The 2019 reporting period: the technical and scientific reporting requirements regarding 2018 AMR data

Anca Stoicescu presented the changes in the reporting process of 2018 AMR data to be implemented for the 2019 reporting period. Most of the improvements regarding the 2018 data collection were previously described while presenting the feedback of 2017 data reporting when solutions to solve the identified issues were proposed. Improvements will be implemented in the Microstrategy reports, business rules, catalogues and reporting manuals. New business rules will be added for improved validation at the data entering the DCF.

The catalogue updates will be sent to MSs for consultation on 11 January 2019 and the final version will be ready by 31 January 2019. MSs were requested to send to EFSA any additional *Salmonella* serovars newly isolated and not currently listed in the catalogue by 23 November 2018.

6.3 Production of a 'mini' EUSR on AMR

The intention is to produce a short EUSR mainly based on the 'main findings' sections of the 2015 and 2016 EUSR on AMR covering all the food producing animals populations monitored. The document is under finalisation and should be sent soon for consultation. The intention is to publish it before the 2017 EUSR on AMR.

6.4 The monitoring of MRSA in pigs in Switzerland: an update

The Swiss delegate, Gudrun Overesch, presented an update on the monitoring of MRSA in pigs in Switzerland. In Switzerland, the occurrence of MRSA in fattening pigs at slaughter has increased constantly since the detection of MRSA became part of the monitoring. Starting at 2% in 2009 and increasing to 20.8% in 2013, the MRSA prevalence reached 44.0% in 2017. Moreover, a similar increasing trend, though at a lower level, has been observed for MRSA carriage in veal calves. The actual prevalence equaled 8.1% in 2017. The MRSA monitoring results have confirmed that *spa*-types t034 and t011 are becoming widespread in Switzerland's population of slaughtered pigs. These genotypes belong to the clonal complex CC 398, which is typically livestock-associated (LA-MRSA). The zoonotic potential of such strains via meat or direct animal contact is of public health concern. So far, the risk for public health due to ingestion of MRSA-positive meat and products is assumed to be low. This was underlined by Swiss data, as the prevalence of MRSA in Swiss pork, beef and chicken meat is very low. MRSA were only detected in chicken meat from abroad, but with a decreasing trend from 2014 to 2016. In contrast, the risk of humans being colonized by MRSA via close contact to animals carrying MRSA is evident. Persons at risk, such as farmers, veterinarians and slaughterhouse workers, are more likely to be colonized with MRSA than the community at large. Our study with Swiss veterinarians and farmers in 2017 revealed that 6.1% of the sampled veterinarians and 5.1% of the tested Swiss farmers carried MRSA in their nasal mucosa. The increasing MRSA colonization of Swiss livestock may lead to an increasing MRSA colonization of Swiss persons at risk and, in consequence, to a higher proportion of patients entering Swiss medical care facilities. The detection of a LA-MRSA in two patients in 2017 indicates that the above-mentioned transmission can occur in Switzerland.

6.5 Surveillance and control of LA-MRSA in the Norwegian pig population: an update

Jannice Schau Slettemeås, the Norwegian delegate, presented an update on LA-MRSA in Norway[3]. Norway produces ~1.6 million slaughter pigs and 60 000 sows each year and has approximately 2000 herds divided on 1200 sow and 800 fattening herds. The breeding pyramid shows a unidirectional flow of animals with about 40 herds of pure breeds on top (genetic nucleus) followed by 50 sow herds (multipliers), 1100 piglet producers and 800 finisher herds.

Surveys conducted in 2008, 2011 and 2012 indicated a very low prevalence of MRSA positive swineherds in Norway. The MRSA belonging to the animal associated CC398 t034 was detected in swine samples for the first time in 2011. In 2013/14, three clusters of MRSA CC398 positive swine herds were detected, and measures to eradicate LA-MRSA from positive swineherds were imposed.

[3] Personal communication, Laura Lindholm, National Institute for Health and Welfare.

The rationale behind this strategy was to avoid the swine population becoming a reservoir of MRSA with the potential of zoonotic transmission. The LA-MRSA eradication strategy includes restrictions on trade of live animals upon suspicion, depopulation of pigs in LA-MRSA positive swineherds, thorough cleaning and disinfection of premises, negative samples from the environment and mandatory downtime before restocking with pigs from MRSA negative herds. After restocking, samples are collected from animals and the environment several times to assess the effectiveness of MRSA eradication. From 2014, a yearly surveillance programme on MRSA in the swine population was implemented where > 800 herds are tested yearly. In all positive herds, measures to eradicate MRSA are imposed.

A socio-economic analysis was performed in collaboration with the government, producers, the Norwegian Food Safety Authority and the Norwegian Institute of Public Health. The NVI produced prospective transmission models for introduction and further dissemination of LA-MRSA. In total six different control options were identified and several transmission models were produced regarding prevalence of MRSA in a 10-year period in the pig herd population and in occupationally exposed persons considering the control options. The total costs for a 10-year period, including insurance premiums for the farmers, were estimated. Considering the different control options and performing monitoring at a low scale showed that the prevalence of MRSA in both groups would increase after 3-4 years. After 10 years, the MRSA prevalence in pig herds and occupationally exposed persons would be approximately 60 and 10 %, respectively.

6.6 Shall we monitor AMR in sea food?

Sophie Granier, the French delegate, gave a presentation on whether monitoring of AMR in sea food should be considered. She thanked ASK network members for their work contributing to the guidelines.

6.7 Moraxella, is it the origin of *mcr*-1?

Francesca Martelli, the UK delegate presented an update on Moraxella. The Presentation "Moraxella, is it the origin of *mcr*-1?" described work carried out at the Animal and Plant Health Agency in the United Kingdom to determine the occurrence of *mcr*-1 and *mcr*-2 genes in Gram-negative bacteria isolated from healthy pigs in Great Britain. Six hundred and fifty seven Gram-negative bacteria isolated from pigs between 2014 and 2015 were examined by WGS. Variants of *mcr*-1 and *mcr*-2 were identified in Moraxella spp. isolated from pooled caecal contents of healthy pigs at slaughter collected from six farms in Great Britain. Other bacteria, including Escherichia coli from the same farms, were not detected harbouring *mcr*-1 or *mcr*-2. A Moraxella porci-like isolate, MSG13-C03, harboured -1.10 with 98.7% identity to MCR-1, and a Moraxella pluranimalium-like isolate, MSG47-C17, harboured an MCR-2.2 variant with 87.9% identity to MCR-2, from E. coli; the isolates had colistin MICs of 1–2 mg/L. No intact insertion elements were identified in either MSG13-C03 or MSG47-C17, although MSG13-C03 harboured the conserved nucleotides abutting the ISApl1 composite transposon found in E. coli plasmids and the intervening 2.6 kb fragment showed 97%identity. Six *Moraxella osloensis* isolates were positive for phosphoethanolamine transferase (EptA). They shared 62%–64.5% identity to MCR-1 and MCR-2, with colistin MICs from 2 to 4mg/L. Phylogenetic

analysis indicated that MCR and EptA have evolved from a common ancestor. In addition to *mcr*, the b-lactamase gene, blaBRO-1, was found in both isolates, whilst the tetracycline resistance gene, tetL, was found in MSG47-C17. The results of this study add further evidence for the mobilization of the *mcr*-pap2 unit from Moraxella via composite transposons leading to its global dissemination. The presence of *mcr*-pap2 from recent Moraxella isolates indicates they may comprise a reservoir for *mcr*. This research is published in the Journal of Antimicrobial Chemotherapy (2018)1;73(10):2904.

6.8 Ongoing/concluded WGS-related activities from BIOHAZ and BIOMO respectively

Beatriz Guerra provided a presentation on the EFSA activities in the area of Whole Genome Sequencing: including the results of a questionnaire on WGS activities in the EU, the activities of the EFSA WGS umbrella project, including capacity building, Mandates from EC, EFSA funding activities, and others (work packages 1 to 6) and the EC joint mandate to EFSA an ECDC for "Technical support to collect and analyse whole genome sequencing (WGS) data in the joint ECDC-EFSA molecular typing database". A joint Working ECDC-EFSA WG is defining the needs and requirements of such a molecular typing system, and existing "solutions" (covering data collection, analysis, visualization) are being explored. Also the results of the capacity building benchmarking exercise on AMR tools were presented. This exercise highlighted the need for harmonisation and the influence of each change in parameters on the results.

6.9 New Mandates on AMR:

- **The JIACRA III project (EFSA-Q-2018-00058)**

Pierre-Alexandre Beloeil shortly presented the JIACRA III project to be performed in close collaboration with the ECDC and the EMA in order to analyse the relationships between AMR and AMU in food-producing animals, food and humans. The third JIACRA exercise should be finalised by the end of 2020.

- **Self-tasking mandate for scientific opinion on the application and use of next generation sequencing (including whole genome sequencing) for risk assessment of food-borne microorganisms (EFSA-Q-2018-00058)**

Maria Teresa Da Silva Felicio presented the background and ToRs of the ongoing self-task mandate from the BIOHAZ Panel on 'the application and use of next generation sequencing (including whole genome sequencing) for risk assessment of foodborne microorganisms'. The work plan for this mandate, WG composition and expertise were presented. A scientific opinion will be adopted by October 2019 providing answers to two ToRs: (1) evaluate the possible use of NGS (e.g. WGS and metagenomic strategies) in foodborne outbreak detection/investigation and hazard identification (e.g. generation of data on virulence and AMR genes, plasmid typing) based on the outcomes of the ongoing WGS outsourcing activities, experience from different countries and underlining the added value for risk assessment; and (2) critically analyse advantages, disadvantages and limitations of existing NGS-based methodologies (including WGS) as compared to microbiological methods cited in the current EU food legislation (e.g. *Salmonella* serotyping, STEC monitoring, AMR testing), taking into account benchmarking exercises.

No AOB was raised.

7.1 Date for next meetings

The 9th Specific Meeting on AMR (November 2019) is planned to be arranged in week 45 or 46 of 2019 shared with the participants.

8. Conclusions

An overview of the main discussions and agreements reached during the meeting was presented. It can be retained that the update from the European Commission on the 'One Health' Action Plan against the threat of AMR recalled the importance of the fight against AMR and the reduction of the use of antimicrobials in food-producing animals. The harmonised monitoring of AMR is a key element of the Action Plan.

The analyses of the 2017 AMR data, the production of the 2017 EUSR on AMR and the phenotypic reference testing exercise have been conducted in parallel for mutual advantage. The meeting was an opportunity to exchange about the preliminary outcomes of AMR monitoring in 2017. The preliminary draft report is planned to be sent for a 2-week consultation in December. Further to the confirmatory testing still under finalisation, the data not yet altered in the EFSA database in November can be modified in December, only for those MSs concerned.

In 2018, in accordance with a mandate of the EC, the EFSA has started to review the technical specifications underpinning the EU legislation on harmonised monitoring of AMR in the light of the constantly evolving epidemiological situation and feedback from practical implementation experience. The intention is to propose to continue a slightly altered phenotypic monitoring for the routine AMR monitoring and to extend the scope of monitoring with complementary molecular typing (WGS), notably further to a formalisation of the Confirmatory Testing, and with specific baseline surveys in the period of 2021-2016. The EURL-AR has already started to provide training to the NRLs on the sequencing activities. **EFSA Network delegates were also kindly requested to come back to the EFSA by e-mail with specific comments in the coming weeks so that the EFSA WG can address them.**

Regarding the 2019 reporting process, the intention is to speed up a bit the procedure of data validation over June-July 2019. As business rules facilitate the data validation and the subsequent steps of data analysis, it is also planned to complement the set of business rules while receiving 2018 data. Business rules and selection criteria for reference testing will be circulated to the MSs at the beginning of 2019, so that they can be used by the MSs to validate AMR data before reporting to EFSA. The suggestions for improvement of the reporting tools and procedures will be addressed by EFSA when preparing the 2019 reporting season (of 2018 data). The importance of reporting representative and already fully validated AMR data by the MSs to EFSA in May 2019 was also emphasised.

Four reporting countries have provided specific updates on their own situation regarding AMR; two of them on MRSA in pig sector notably. There is an intention to propose to re-run the baseline survey on MRSA in pigs in 2021-2026.

9. Closure of the meeting

The Chair thanked the Network members for their invaluable contribution to the AMR monitoring in food-producing animals and food as well as for their engagement and their constructive contributions to the discussions. The meeting was duly closed at 13.25.

Appendix: List of Action Points

Scientific Network for Zoonoses Monitoring Data
Minutes of the 8th specific meeting on Antimicrobial Resistance data reporting

Held on 07-08 November 2018, Parma

List of the action points agreed at the meeting

Agenda Point	What	Agreement/Comment	Deadline
	To account for the issues encountered during the 2017 reporting exercise.	EFSA will implement the solutions presented during the meeting.	31 January 2018
	To solve the bug in gene data migration process from the DCF to the DWH	EFSA will implement a solution.	30 November 2018
	To keep the *Salmonella* serovars catalogue of the EFSA database updated.	MSs are kindly requested to send to EFSA any additional *Salmonella* serovars newly isolated and not currently listed in the catalogue.	23 November 2018
	To provide the documentation for the 2018 data collection exercise on time.	Reporting Manuals and Catalogues will be sent for consultation on 11th of January and published on 31st of January 2018.	31 January 2018
	To refine the definition of total unit tested and total units positive, in particular for ESBL-/AmpC-producing and carbapenemase-producing E. coli	Reporting Manuals will be sent for consultation on 11th of January and published on 31st of January 2018.	31 January 2018
	To insert again an indicator of occurrence of resistance at the EU level based on the weighting mean and animal population size in the 2017 EUSR on AMR	EFSA will implement a solution in the final 2017 EUSR on AMR	31 January 2018
	MSs to send by email to EFSA specific comments on the AMR monitoring	Comments to be addressed by the EFSA WG while reviewing the technical specifications.	30 November 2018
	To arrange a TC with the countries with small production sectors to support the activity of the EFSA WG.	-	30 November 2018
	To liaise with the EC on the 2019 AMR monitoring to about the epidemiological unit in pigs.	-	30 November 2018
	To communicate the exact dates of the Network meeting in 2019	EFSA	31 January 2018