D6.6: Report on Short Term Missions (STMs)

Year 2 (2019)

Responsible Partner: UoS, UK (P23)

GENERAL INFORMATION

European Joint Programme full title	Promoting One Health in Europe through joint actions on foodborne zoonoses, antimicrobial resistance and emerging microbiological hazards
European Joint Programme acronym	One Health EJP
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DOCUMENT MANAGEMENT

Work Package 6 Task #	Task 6.2: Workshop Programme satellite to the Annual Scientific Meeting
Co-ordinating Institutes	The WP6 Team: University of Surrey (United Kingdom) Wageningen Bioveterinary Research (the Netherlands)
Co-ordinating Team	Professor Roberto La Ragione, Professor Wim van der Poel, Dr Piyali Basu and Dr Dan Horton
Institutes awarded grants and institutes visited respectively	IZLER (Italy) > RIVM (the Netherlands) VISAVET UCM (Spain) > Hasselt University (Belgium) VISAVET UCM (Spain) > DTU (Denmark) FHI (Norway) > SSI (Denmark)
Due month of the report	**26**
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Type *R: Document, report* *DEC: Websites, patent filings, videos, etc.* *OTHER*	R
Dissemination level *PU: Public* *CO: confidential, only for members of the consortium (including the Commission Services)*	PU

Contents

This document is part of the European Joint Programme One Health EJP. This programme has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 773830.

Aims and Objectives

Short Term Missions (STMs) provide small travel grants with the aim of sharing scientific expertise, methodologies, equipment and facilities to harmonise the existing approaches and methodologies within the large OHEJP network, and to drive the research forward in a collaborative and non-duplicative fashion to strengthen both the scientific capacity within the OHEJP and also future prevention, preparedness, detection and response of the EU to foodborne and other emerging threats across human-animal-environmental sectors.

The OHEJP aimed to fund ten STMs in every year of the Programme, with the first set commencing in Y2 of the Programme.

Selection of STMs

The Work Package 6 Team co-ordinate the call and selection of the STMs following the validated procedure which involves the following steps: the call is launched and after the deadline closes, the WP6 Team perform an eligibility check with pre-determined criteria (see protocol in annex 1 for more information), and then applications and supporting documents are sent to three independent reviewers. The reviewers were nominated by the Scientific Steering Board (SSB). The WP6 Team compiled the scores and validated the selection with the Project Management Team (PMT), and the final decision is then communicated to the SSB and applicants.

Call Promotional Campaign

The first call for the Short Term Missions was launched on 8th January 2019 and closed on 18th March 2019 to align with the Training and Education activities timeline provided by the Coordination Team. The original deadline of 11th March was extended by one week as we only received five applications.

When the call was launched, a promotional email marketing strategy was used to disseminate the information to the SSB, PMT, Project Leaders and Communication Contact Persons who were instructed to disseminate the email which contained key information presented in a visually attractive format with OHEJP branding, and a branded graphic (see annex 2) announcing the launch. The email also contained instructions on how to join the 'Call for Short Term Missions 2019' group on the private space of the website, where they could download the guidelines, application form and templates required to apply. These were also disseminated regularly on our social media channels Twitter and LinkedIn to increase traffic to the website. The launch of the call was also disseminated on the public space of the website and the OHEJP consortium newsletter. After the call was launched, reminders of the deadline and announcement of the deadline extension was sent via the same methods one month, two weeks, one week, one day before, and finally on the day (annex 2).

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Short Term Mission 1 Report

Skills development mission with focus on development of a framework for reporting outbreak investigations using consumer purchase data in cooperation with researchers in SSI

1. Name of applicant	Solveig Jore
2. Institute of Affiliation/ Contact information	Norwegian Institute of Public Health (NIPH) Address: Postboks 222 Skøyen, 0213 Oslo Telephone: +47 21076516 Email: solveig.jore@fhi.no
3. Host institute and names of scientists involved	Statens Serum Institute Uffe Christian Braae, Steen Ethelberg & Frederik Trier Møller
4. Dates of STM or workshop	23.06.2019 – 29.06. 2019
5. Key aims of STM or Workshop	The purpose of this scientific mission was to develop a framework for reporting outbreak investigations using consumer purchase data. This is a task under WP2 in the NOVA project (Joint Research Project). We looked at the use of purchase data and other possible sources of "surveillance data" as well as description of best practice on the area. In addition, the outcome of this research cooperation should be publication of several scientific articles related to foodborne zoonoses.
6. Impact and relevance of scientific mission	This mission focuses on best practice exchange with other scientists working in foodborne zoonoses. Both the applicant and the hosting organisation is going to gain on this activity by daily contact of the applicant with SSI's scientists. The applicant wishes further to build up her competence in foodborne zoonoses surveillance and contribute to harmonisation of research tools among scientists within the EJP network.
7. Benefits to OHEJP	Scientific mission to carry out tasks under WP2 in the NOVA project.

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Summary

During this week of short term-mission, we worked on developing a framework for reporting outbreak investigations using consumer purchase data. We also looked at the current and previous use of purchase data and the potential future use. We worked on a description of “best practice” for using purchase data with the aim of harmonising the use of this kind of surveillance data amongst the European countries. In addition, we started drafting an opinion paper describing the method and existing barriers for the benefit of new users and with the hope that these barriers eventually can be overcome.

Technical Report

Brief Background:

The purpose of this scientific mission was to look more in detail around the use of consumer purchase data and to develop a framework for reporting outbreak investigations using consumer purchase data. This is a task under WP2 in the NOVA project.

The tasks performed during this short-term mission:

During this one-week stay at SSI we worked on developing a framework for reporting outbreak investigations using consumer purchase data. We also looked at the current and previous use of purchase data and the potential future use. We worked on a description of “best practice” for using purchase data with the aim of harmonising the use of this kind of surveillance data amongst the European countries. In addition, we started drafting an opinion paper describing the method and existing barriers for the benefit of new users and with the hope that these barriers eventually can be overcome.

Conclusion:

We managed to look at previous, present and possible future use of consumer purchase data and we developed a framework of the best practice for using this kind of data. In addition, we started drafting an opinion paper describing the method and existing barriers for using consumer purchase data.

Dissemination and Communication activities

N/A

Scientific outputs

We are working on an opinion paper describing the method and existing barriers for the use of consumer purchase data. This is expected to be published in 2020.

Testimonial and Photos

The testimonial and photo of the awardee has been uploaded along with the summary to the ‘Short Term Missions 2019’ page of the website.

These testimonials are also included in the consortium and external newsletters as they have been completed and were also shared on our social media channels mentioned above.

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Short Term Mission 2 Report

Training on source attribution modelling

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3. Host institute and names of scientists involved	RIVM (the Netherlands) Dr. Lapo Mughini Gras
4. Dates of STM or workshop	10/06/2019 - 14/06/2019
5. Key aims of STM or Workshop	Training on source attribution modelling approaches
6. Impact and relevance of scientific mission	Harmonization of data analysis approaches, added value to data collected for surveillance, direct impact on the territory
7. Benefits to OHEJP	Ease of communication between professionals, strengthening of relationships between institution to favour future collaborations

Summary

The aim of the visit to the RIVM was to enhance source attribution skills through an ad hoc structured and supervised training, which included exercises with real data and validation of learnt competences. The need for this mission fell within the context of an ongoing process of updating the current routine surveillance of foodborne pathogens with sequence based techniques at IZSLER. IZSLER carries out surveillance plans for the most populous region of Italy, Lombardy, producing large amounts of data. Therefore, the integration of surveillance data with source attribution analyses, could be of great usefulness to improve the positive outcomes on the regional territory. During the mission the participant has been informed on the activities and research ongoing in the hosting institute, with the possibility to interact with other professionals and receive input for future collaborations. During the training the participant received a general introduction on source attribution approaches, with a special focus on source attribution based on microbial subtyping. The Dutch, Hald, Asymmetric Island and STRUCTURE models were included in the training, with particular reference to MLST and MLVA

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data. The use of WGS in source attribution studies was discussed as well. After each training session, the participant was engaged in consolidating the learnt topics through simulation of attribution with data on *Listeria monocytogenes* retrieved from public databases. During the staying, it was organized a seminar in which the participant had the possibility to introduce herself and her institute to professionals from the hosting institute to share some highlights about her research activity.

Technical Report

The aim of the visit to RIVM was to enhance source attribution skills through an ad hoc structured training supervised by Dr. Mughini Gras, which included exercises and validation of learnt competences. The need for this mission fell within the context of an ongoing process of updating the current routine surveillance of foodborne pathogens with sequence based techniques at IZSLER. IZSLER carries out surveillance plans for the most populous region of Italy, Lombardy, producing large amounts of data. Therefore, the integration of surveillance data with source attribution assessments, could be of great usefulness to improve the positive outcomes and impact on the regional territory.

On the first day of training the participant received an overview introduction on source attribution modelling, the different approaches, and the criteria for choosing the most appropriate model or assessment strategy. The approaches regarded were:

- Microbial subtyping
- Comparative exposure assessment
- Case-control studies
- Data from outbreaks
- Expert elicitation

The training then focused on source attribution based on microbiological subtyping. Four models were considered, Dutch, Hald, STRUCTURE and Asymmetric Island Model (AIM). For each model the participant was instructed on:

- principles of the modelling approach and development of the model
- data suitable to be fit in the model
- overview of the software needed for calculation and where to retrieve it
- input data formatting
- how to run the model
- assessment of uncertainty
- results interpretation
- presentation of findings

Simulation on datasets previously analysed by the supervisor were then run and discussed. Following, the participant was encouraged to consolidate the concepts learnt by applying the models to data retrieved from an on-line database of *Listeria monocytogenes* typing data, namely the Italian *L. monocytogenes* online database (www.listeria.it). This database was used in all attribution exercises and consisted of 1007 isolates of food and food environment isolates, and clinical isolates, collected

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in Italy between 1992 and 2014. The clinical isolates were 285, while the source isolates were classified by the participant in six categories, namely dairy (n=136), fish (n=103), poultry (n=45), pork (n=252), bovine meat (126), and other RTE or vegetables (n=60). All isolates were typed with both MLST and MLVA.

For the Dutch, Hald, and STRUCTURE models, MLST data were used. The AIM instead, was applied both to MLST and MLVA data, using the typing data separately (i.e. 7 and 6 alleles), and coupled (i.e. 13 alleles).

Overall, the results were comparable among all models, and identified dairy products as the main source of listeriosis.

As an example:

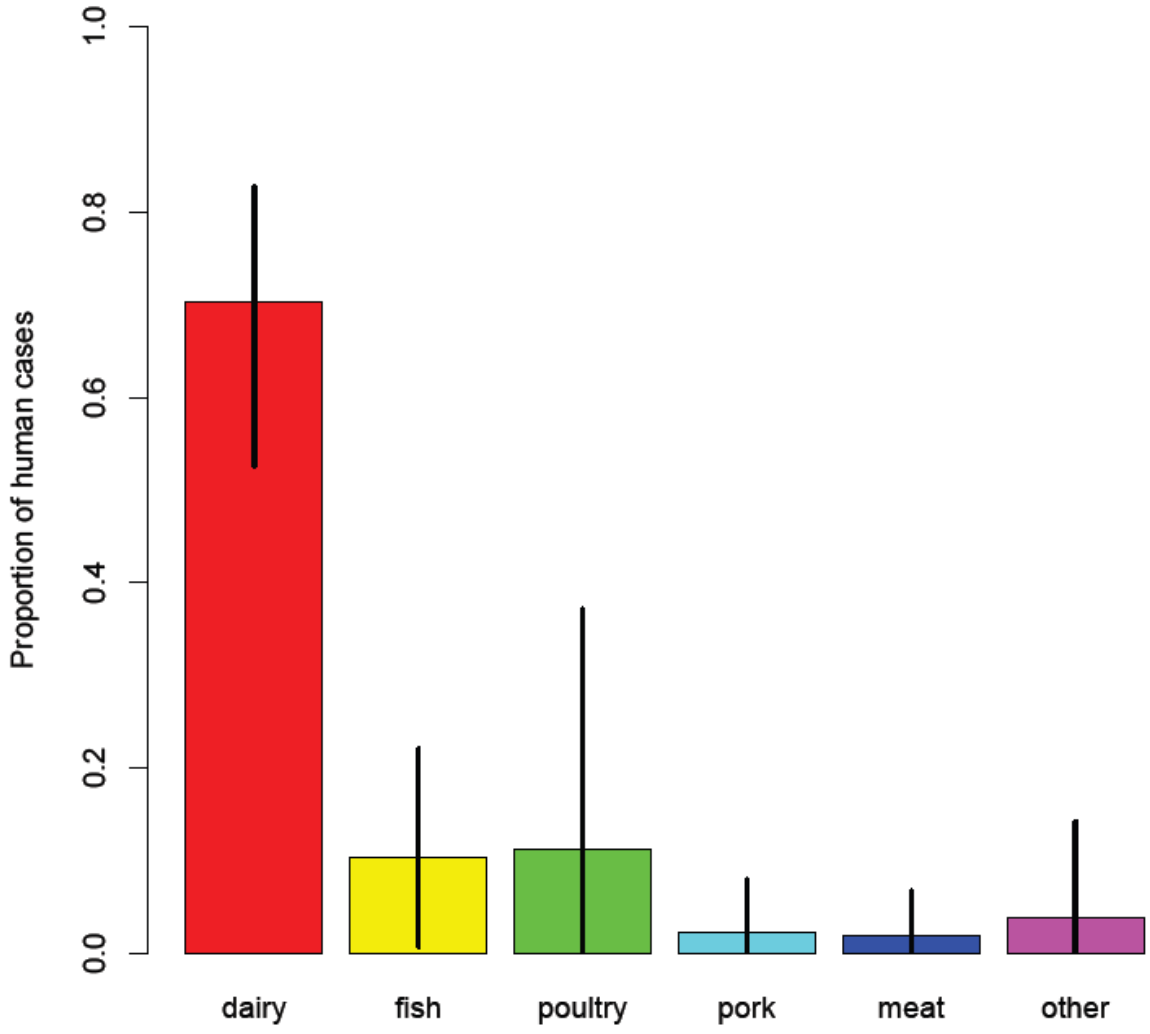

Figure 1: Histograms of the distribution of the proportion of isolates attributable to the each source using the AIM approach with coupled MLST and MVLST data.

Similar graphs were prepared for all the models run.

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On the fourth day of the staying the participant was invited to give a speech to discuss with other RIVM professionals her previous and current work on *L. monocytogenes* surveillance.

By the end of the mission the participant was able to independently run the different models studied and plan a source attribution assessment.

Dissemination and Communication activities

N/A

Scientific outputs

A report with the main findings will be forwarded to the Lombardy Region authority for veterinary public health (July 2019).

In the case where all contributors agree the results of the different modelling approaches could be published in a scientific paper (by the end of 2019).

Testimonial and Photos

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Short Term Mission 3 Report

Dynamics of *E. coli* in laying hens: Training in Bioinformatic Analysis of Whole Genomic Sequences

1. Name of applicant	Irene Aldea Ramos
2. Institute of Affiliation/ **Contact information**	Institute: Veterinary Health Surveillance Center (VISAVET). Complutense University of Madrid (UCM). Address: Avenida Puerta de Hierro, s/n. 28040 Madrid, España Telephone: 913 943 999 Fax: 913 943 795 Email: ireneald@ucm.es
3. Host institute and names of scientists involved (N/A workshop)	National Food Institute, Technical University of Denmark (DTU), Denmark. Dr. Valeria Bortolaia and Dr. Pimlapas Leekitcheroenphon.
4. Dates of STM or workshop	September, 2nd- 29th 2019
5. Key aims of STM or Workshop	Training in bioinformatic analysis of whole genomic sequences (WGS). Learning in the use of tools for the identification of resistance genes and mobile genetic elements.
6. Impact and relevance of scientific mission	Use the different tools available more efficiently and learn about new tools to optimize analysis of WGS data.
7. Benefits to OHEJP	Antimicrobial resistance (AMR) is a top health priority under the One Health perspective since spread of antimicrobial resistant bacteria do not recognize borders across humans, animals and the environment. The analysis of the WGS data could improve understanding of the flow of AMR resistance.

Summary

I visited the Technical University of Denmark with the aim to improve my knowledge on bioinformatics. The National Food Institute of DTU is part of the Centre of Genomic Epidemiology which has several web services for the analysis of whole genome sequences. Along this month, I have been learning to perform phylogenetic analysis based on the whole DNA sequences. We have worked in the construction of phylogenetic trees with both programs of the Centre of Genomic Epidemiology

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and with other web-available programs. We also analysed the resistance genes and how they move between bacteria. To do this, we tried to describe the genetic context of the genes and also to rebuild the mobile genetic elements. I have learned not only how to use some tools for the search of this mobile genetic elements but also how to read the results properly. They have also helped me to further analyse the data I already had, and they have given me some guidelines and ideas for the work that I can do next, as well as to relate the results that I obtain with the objectives of my project. During the staying I also had the opportunity to attend some sessions of a course in which we were taught to use some tools for the analysis of WGS data.

Technical Report

The objective of this WP1 is to enable the student to perform analyses of whole genome sequence data independently. The training will encompass all steps of WGS data analysis from assessment of the quality of raw data to output of results useful for epidemiological

investigations.

Task 1: Training in bioinformatics analyses of whole genome sequence (WGS) data. This WP is divided into tasks covering all different steps of WGS data analysis, as detailed below. Of note, the training focuses on analyses of WGS data obtained by Illumina technology which, at present, is the most widely used technology by sequencing laboratories worldwide.

- Work done in this task: Task 1 has been carried out throughout the month of stay. With the results obtained in some of the bioinformatics programs, we could relate some of the problems we were seeing with the low quality of some sequences.

Task 2: Detection of genes and mutations mediating antimicrobial resistance in Escherichia coli. Furthermore, the student will familiarize with the principles behind different alignment/mapping algorithms available for detection of AMR genes/mutation in WGS data.

- Work done in this task: We have carried out the analysis of resistance genes with Resfinder, CARD, ARG-ANNOT ... and other tools for the detection of AMR genes and mutations. Not only have we analyzed the results of each one, but we also have compared these results from the different programs, being able to see the impact of the different algorithms that the tools have, finding ones more genes and mutations than others.

Task 3: Examine the genetic context of the AMR genes, which is essential to infer possible pathways of transmission of AMR across bacteria and animal populations. Resolve both the immediate genetic context of the AMR genes (integron/transposons) and the location (chromosome/plasmid) of these AMR gene cassettes. This work will focus on a selection of AMR genes identified in task 2.

- Work done in this task: We used the Plasmidfinder tool and, based on the type of replicon and on the resistance genes found, we searched the databases for the reference plasmid that most closely resembled the one we have in each sample. The sequences of the reference plasmids were compared with the samples by BLAST, and the contigs that theoretically formed

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part of the plasmid were pooled together. The reference sequence was compared again with the bound plasmids and we were able to analyze the percentages of identity and query cover to study what part of the plasmid was missing. Thus we have managed to form some of the plasmids present in my samples and we have also noticed errors in sequencing (task 1).
We have also studied the genetic context of resistance genes, to know if the same resistance genes have the same evolutionary origin even if they are not in the same mobile gene element. For this, we have used the ISfinder program to see the insertion sequences attached to the gene, and the Prokka program to annotate the genes of the sequences.

Task 4: Learning the theory and practice of the two most used methods for clustering of WGS data, i.e. cgMLST and SNP.

- Work done in this task: To perform the cluster of WGS data, we have done the SNPs analysis. With the CSI phylogeny tool we can see the SNPs between samples and others to establish clonal relations. I have also made and modified a phylogenetic tree based on SNPs with the iTol web-based tool. Thanks to this we have been able to make hypotheses about possible epidemiological scenarios of transmission of AMR isolates. We couldn't perform the cgMLST analysis because we weren't able to get the sequences in fastq format.

Task 5: the progress of the student will be checked by host institute, and also support will be provided for additional information needed for improving the training of the student at DTU.

Dissemination and Communication activities

N/A

Scientific outputs

N/A

Testimonial and Photos

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Short Term Mission 4 Report

Application of advanced epidemiological analytical methods for antimicrobial resistance data in Salmonella in pigs

1. Name of applicant	Kendy Tzu-Yun Teng
2. Institute of Affiliation/ **Contact information**	Institute: VISAVET Health Surveillance Centre UCM Address: Avenida de Puerta de Hierro, s/n 28040 Madrid España Telephone: +34688343740 Email: tteng@ucm.es
3. Host institute and names of scientists involved (N/A workshop)	Centre for Statistics, Hasselt University Prof. dr. Marc Aerts Dr. Stijn Jaspers
4. Dates of STM or workshop	5th August to 20th September 2018 (7 weeks)
5. Key aims of STM or Workshop	The aim of the visit is to develop skills in analysing data on phenotypic antimicrobial resistance (AMR) to identify associations between the occurrence of resistance and different antimicrobials in an attempt to better understand its dynamics in *Salmonella* of swine-origin
6. Impact and relevance of scientific mission	This STM explored methodology that can be used to identify the dynamics and relationships of the emergence of AMR in *Salmonella* from swine source. The results of the investigation allow us to better understand the complexity of AMR in *Salmonella* and draw inferences.
7. Benefits to OHEJP	This STM focused on the dynamics of the emergence of AMR, areas prioritised by the OHEJP in *Salmonella* spp. and dominant serotype strains in swine. As the persistence of *Salmonella* or specific serotypes in the animal reservoir may likely contribute to the reversal of the decreasing trend in *Salmonella* incidence in humans. The usefulness of the analysis of AMR surveillance data is demonstrated by this STM, enriching the current NOVA project. Cutting-edge skill sets to draw inferences from AMR isolate-based data have been under development and introduced into the OHEJP network, facilitating the utilisation of the regularly collected AMR isolate-based data by institutes in the OHEJP consortium.

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Summary

The short term mission (STM) was taken place at the Centre of Statistics, the University of Hasselt. The aim of the visit was to develop skills in analysing data on phenotypic antimicrobial resistance (AMR) to identify patterns among the occurrences of resistance of different antimicrobials in an attempt to better understand the interactions and dynamics in *Salmonella* of swine origin. Data containing AMR information on the minimum inhibitory concentration results of seven antimicrobials from a total of 1,150 *Salmonella* isolates in 2001-2013 were collected through the Spanish Veterinary Antimicrobial Resistance Surveillance Network programme and analysed during the STM. The antimicrobials included Cefotaxime, Chloramphenicol, Ciprofloxacin, Florfenicol, Gentamicin, Nalidixic acid and Tetracycline. Multiple techniques, including principal component analysis, multiple correspondence analysis, hierarchical clustering, and latent class analysis, were performed to detect potential patterns and clusters among the (categorised) minimum inhibitory concentration results for antimicrobials. Generalised estimating equations were conducted to examine the evolution of the proportion of the resistant strains of each of the seven antimicrobials. Additionally, the structures of relationships among the antimicrobials were examined by Bayesian network analysis. We also made an effort to develop new approaches to Bayesian network analysis in Stan. The work performed during this STM demonstrated useful analytical techniques to explore the interactions among AMR and associations between AMR and *Salmonella* serotypes. On the base of this action, development to explore AMR phenotypes continues to be carried on.

Technical Report

Background of the mission

The short term mission (STM) took place at the Centre of Statistics at the University of Hasselt with collaboration with Prof Marc Aerts, the director of the Centre of Statistics, and Dr Stijn Jaspers. Both of them are the authors of the European Food Safety Authority report, *Development and application of statistical methodology for analysis of the phenomenon of multi-drug resistance in the EU: demonstration of analytical approaches using antimicrobial resistance (AMR) isolate-based data*. During the STM, these newly arrived skills for the analysis of AMR isolate-based data were applied to a dataset from the Spanish Veterinary Antimicrobial Resistance Surveillance Network programme in Spain, including information of AMR in *Salmonella* isolates in pigs from 2001 to 2013. The program has been coordinated by the VISAVET Health Surveillance Centre UCM (VISAVET) since its inception. Its objective is to monitor multiple foodborne zoonoses, including *Salmonella*, *Escherichia* coli and *Campylobacter* in swine, poultry and cattle. This dataset has been incorporated into an OHEJP research project, NOVA (Novel approaches for design and evaluation of cost-effective surveillance across the food chain). Based on the initial results which show the varying prevalence of *Salmonella* in pigs in Spain depending on regions and serotypes, the STM generated knowledge to help to determine the magnitude of the contribution of AMR to the persistence of *Salmonella* and specific strains/resistotypes in pigs and humans. These findings can be translated into other hosts such as poultry and bacterial species.

During the STM, a database containing seven AMR information on the minimum inhibitory concentration results to antimicrobials from a total of 1,050 *Salmonella* isolates between 2001 and

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2013 were analysed. Data included the resistance phenotypes, serotypes, year and geographical origin of the samples, and information of the sampled farms.

Tasks

Two Tasks were performed. The first one was to determine the temporal trends in and patterns of the resistance to antimicrobials in *Salmonella* in pigs, and the second focused on the dynamic among them.

Task 1

Task 1 explored the temporal trends in and the relationships among the resistance to various antimicrobials in *Salmonella* in swine in Spain. Multiple multivariate statistical analyses were employed, allowing the simultaneous consideration of more than one antimicrobial. Generalised estimating equations were conducted to examine the evolution of the proportion of the resistant strains of each of the seven antimicrobials. Identification of clustering in the distribution of resistance using data segmentation (e.g., principal component analysis, multiple correspondence analysis and hierarchical clustering) and modelling (e.g. latent class analysis) was performed. How serotypes could play a role in these clusters identified was also explored.

Task 1 Results

Results of generalised estimating equations showed that the proportion of isolates resistant to Ciprofloxacin and Nalidixic acid increased and to Chloramphenicol, Gentamicin, and Tetracycline decreased, respectively, over the years (Fig 1). Quadric year terms of Cefotaxime, Ciprofloxacin, Florfenicol, Gentamicin and Tetracycline were retained in the model, indicating nonlinear relationships between the antimicrobials and year. Six clusters were recommended for hierarchical clustering, and the categories that had a high frequency in each cluster are shown in Table 1. In contrary, four clusters were suggested by comparing the information criteria of the models for latent class analysis.

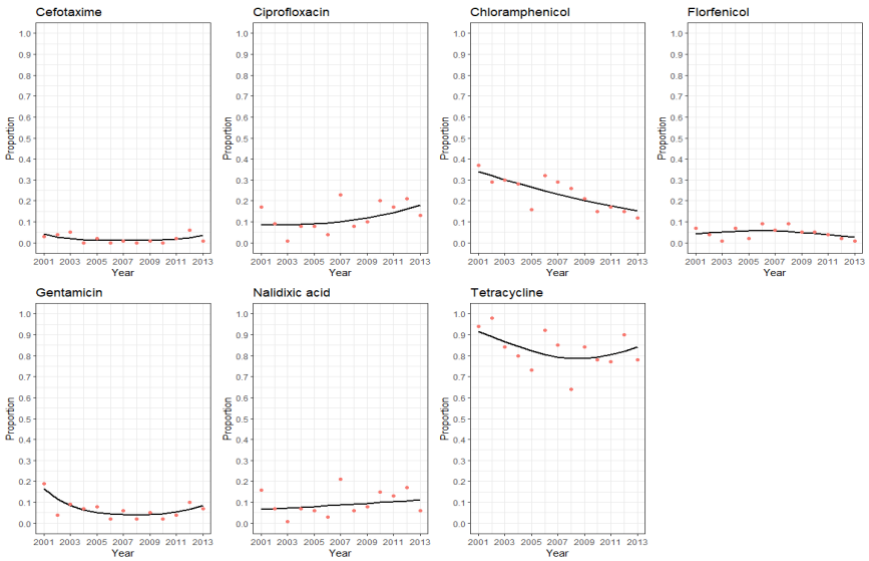

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Figure 1. Prediction of the proportion of isolates resistant to each of the antimicrobial using the generalised estimating equation (black line) and the observed proportion (red dot)

Table 1. Categories of high frequency in each cluster in hierarchical clustering result.

Cluster 1	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**
TET_s	TET_r	GENT_r	FFC_r	CEFOT_r	CIPR_r
S. Bredeney	CIPR_s	S. Brandenburg	CLOR_r	*S.* Typhimurium	NAL_r
CLOR_s	NAL_s	CLOR_r	*S.* Typhimurium	CLOR_r	*S.* Kapemba
NAL_s	GENT_s	TET_r	TET_r	TET_r	*S.* Wien
S. Montevideo	FFC_s	*S.* Monophasic	GENT_r	NAL_r	*S.* Essen
GENT_s	*S.* Rissen	*S.* 4,12:i:-			FFC_s
FFC_s	CLOR_s	NAL_s			*S.* Choleraesuis
CIPR_s	CEFOT_s	*S.* Braenderup			*S.* 4,12:d:-
S. 4,5,12:d	*S.* Derby	FFC_s			*S.* Brikama
S. Enteritidis	*S.* Berta	*S.* Virginia			S. London

TET: Tetracycline, CLOR: Chloramphenicol, NAL: Nalidixic acid, GENT: Gentamicin, FFC: Florfenicol, CIPR: Ciprofloxacin, CEFOT: Cefotaxime, _s: susceptible, _r: resistant.

Task 2

Bayesian network analysis (BNA), a form of graphical modelling, was performed to detect and quantify the associations between the resistances. BNA is ideal for this task due to its competency in the disclosure of structures and patterns in complex data. We conducted BNA using an R package “abn” (Fig 2), but we also explored new approaches of BNA with Stan (mc-stan.org). Stan is a probabilistic programming language that allows extensively flexible statistical modelling with high-performance computation. With Stan, BNA was performed by following steps. Firstly, seven multivariable logistic regression models were built with the rest antimicrobials that were not the outcome variable as the predictors in the models. Secondly, covariate selection for each of the model was performed with “projpred” package and the Bayesian network was constructed in Stan. This development is still underway.

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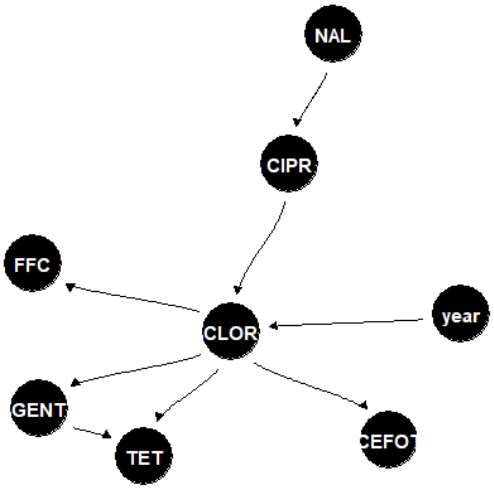

Figure 2. A Bayesian network among the seven antimicrobials.

Conclusion

The work performed during this STM demonstrated useful analytical techniques to explore the interactions among AMR and associations between AMR and *Salmonella* serotypes. On the base of this action, development to explore AMR phenotypes continues to be carried on.

Dissemination and Communication activities

The work will be submitted to be presented at the One Health EJP Annual Scientific Meeting 2020.

Scientific outputs

We are keeping working on more analyses and will produce one scientific paper on the application of the analyses and, hopefully, another one on the development of one of the analytical technique. We will present the study on at least one scientific conference.

Testimonial and Photos

The testimonial and photo of the awardee has been uploaded along with the summary to the 'Short Term Missions 2019' page of the website.

These testimonials are also included in the consortium and external newsletters as they have been completed and were also shared on our social media channels mentioned above.

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Annex 1: Protocol for selection of Short-Term Missions 2019

Protocol for the One Health EJP 'Short Term Missions'

WP6 Education and Training

INTRODUCTION

Short Term Missions (STMs) are small travel grants with the aim of sharing scientific expertise, methodologies, equipment and facilities to harmonise the existing approaches and methodologies within the large OHEJP network, and to drive the research forward in a collaborative and non-duplicative fashion to strengthen both the scientific capacity within the OHEJP and also future prevention, preparedness, detection and response of the EU to foodborne and other emerging threats across human-animal-environmental sectors. The OHEJP aims to fund 10 STMs every year of the Programme, with the first set commencing in Y2 of the Programme.

OHEJP SHORT TERM MISSION PROCESS

1. Develop scoring system for reviewers and additional information for applicants

- A pre-approved scoring system was created based on the following criteria:
  - Scientific Quality
  - Benefit to OHEJP: includes considerations to match aims, potential for collaboration (between partners or brings new innovation into OHEJP from outside), overarching EU benefits, acquisition of new expertise not yet available within the institute
  - Value for money
  - Overall recommendation
- All criteria will be equally weighted (up to 10 points available), with the exception of overall recommendation (5 points available). The max score is 35.

2. Contact partners for reviewer nominations

- SSB members will be contacted by WP6 team to nominate potential reviewers of STM applications from within their institutes (not an Institute Representative or Scientific Representative), to cover the three areas: Food borne zoonoses, AMR and emerging threats.
- They will be asked to sign the No conflict of interest document.
- WP6 will ensure selection of potential evaluators that have no conflict of interest with the proposed partners.

3. Launch call

- **The call for the first round of STMs will be launched on 08 January 2019.**

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- This must be communicated to all mailing lists (which includes the Communication Contact Points within every organisation) in the consortium via email as a primary means of communication, but should also be uploaded onto the OHEJP website, and promoted on social media. Reminders of deadlines should be promoted via all of these communication channels when appropriate.

4. Eligibility check by WP6 team and Review by experts

After submission, applications will be first checked for eligibility by the WP6 team using the following eligibility rules.

a. Applicant eligibility

All staff working in any of the member institutes of the OHEJP are eligible to apply for the STM grants. PhD students should either be registered through their institute or be based at a member institute. **Only scientific staff from, and PhD students based at, the partner institutes of the OHEJP are eligible to apply**.

Applicants must fill in the STM application form, and are strongly encouraged to compile the following documents with the main application:

1. Detailed Work Plan of the professional activities during the visit/workshop programme (max. two pages and should help justify length and associated costs) ❑
2. Detailed budget (max. one page) ❑
3. Letter of recommendation from home institute ❑
4. Letter of recommendation from host institute ❑
5. Curriculum Vitae of STM applicant or workshop speakers ❑
6. List of Publications (if any) ❑

b. Call Topics

STM applications must relate to the following key OHEJP priority areas:

- One Health Missions- Veterinary, Food, Medical and or Environmental research
- Skills development missions (e.g. genomics, bioinformatics, big data epidemiology)
- Exchange with researchers, policy makers, and risk managers to complement WP5- Science to Policy translation
- Risk research
- Integration of microbiological, risk assessment and surveillance activities
- Harmonisation of diagnostics tests, platforms and research

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c. STM locations

- STMS can take place at any external institute to that of the applicant.
- STMs implemented in one of the OHEJP member institutes will have priority over other application for STMs outside the OHEJP.
- However, applications that propose to bring in scientific tools or expertise in key areas beyond those available at OHEJP institutes will also be welcomed.

d. Budget

Costs

- STMs will be 44% EU funded and 56% co-funded by the institute of affiliation of awardees.
- The total costs for each mission should not exceed €5000.
- **Applicants must fill all yellow fields in each tab of the budget template,** detailing all expected direct to deliver the mission. This template must be submitted with the application form. The template is sent out as a separate document in the call, however can also be requested from the WP6 Project Manager. Applicants can liaise with the Support Team (ohejpcoord@anses.fr) for guidance on how to complete this budget template.

Receipts / External Funding

Receipts consist of sponsorship money. These additional amounts will top-up the maximum allocated costs funded by the OHEJP (€5000)

Note: 100% of these external funds must be allocated to fund the cost of the mission.

All financial contributions by any third parties must be detailed in the budget template.

External Funding may be discussed within WP6 and Coordination. If permitted, sponsorship can help to either reduce the costs of the mission, increase the options during the mission, or raise the profile of the OHEJP. Additional funding and must be declared as a receipt.

Using the budget template, applicants must provide a detailed and realistic budget indicating clearly sources of any top-up funding (e.g. sponsorship money) and aspects of the trips that will be covered using such additional funds. Applicants can liaise with the Support Team (ohejpcoord@anses.fr) for guidance on how to complete this budget template.

5. Review by experts

- Following an initial check for eligibility by the WP6 leaders, applications and relevant templates will be anonymised by WP6 and sent out for review by experts selected by SSB from within the OHEJP partner network according to their expertise and independence from the proposed activity.

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- Reviewers will be asked to score the applications using the pre-approved scoring system (see above), and to make comments on specific criteria, concerns or conflicts of interest.

6. WP6 Ranking and suggested decision

- The WP6 team will review and audit the reviewers' scores, detecting and resolving any typographical or administrative errors before submitting to the PMT.
- The WP6 team has the right to propose a modification of the score-based ranking. However, this must be justified and then agreed by the SSB.
- The top 10 (or however many will be funded, which is dependent on budget and amounts requested) will be suggested to PMT to be awarded the funds. In the case of a tied score at the bottom, WP6 will suggest a decision to PMT based on the actual comments of reviewers out a list of missions recommended for funding. This decision will require final validation from PMT.

7. PMT teleconference

- The PMT will meet by teleconference to discuss and validate the ranking based on the reviewers' scores and written feedback.

8. Final decision to SSB, award letters and feedback to other applicants

- Final decisions will be distributed to applicants and the SSB, along with a list of approved missions which will also be made available on the OHEJP website.
- Award letters will be sent to successful applicants.
- Feedback using the reviewers' scores and comments will be made available for applicants upon request who are not successful. The availability of this feedback will be communicated to the unsuccessful applicants.

9. WP6 STM final report validation

- After the mission has been completed, the awardee is responsible for the completion of a scientific and financial report within 30 days of completion of the mission, which should be sent to **Piyali Basu,** p.basu@surrey.ac.uk.
- WP6 will ask reviewers to confirm that the STM or workshop has been conducted as originally approved.
- Recipients are expected to help the OHEJP promote its scientific activities. The final report template includes a request to write a testimonial for publishing on the OHEJP website and provide a photograph if possible.

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TIMELINE

Deadline for completion

- Applicants must aim to complete their missions by the **end of October 2019**
- A scientific report (using validated template) for the mission must be completed within 30 days of completion of the mission. Final reports must be submitted by end of September 2019. Reimbursement details and evidence should be submitted as part of the financial report.
- This timeline is necessary to process the reports of each mission through the required levels of approval, and to ultimately meet the deadline of Deliverable D6.6. This deliverable requires a report of the 10 STMs that are completed in Y2, and for these to be uploaded on the OHEJP website.
- Reports of the 10 short term missions per year completed also uploaded onto the OHEJP webpage.

Short Term Missions Protocol	Start Date	End Date	Duration
Develop scoring system for reviewers	08/10/2018	22/10/2018	14
Develop documentation for applicants	08/10/2018	07/11/2018	30
PMT approval of documentation	08/11/2018	08/12/2018	30
Contact partners for reviewer nominations	15/01/2019	24/02/2019	40
Launch call	07/01/2019	09/01/2019	2
Application preparation	09/01/2019	10/03/2019	60
Application deadline	10/03/2019	12/03/2019	2
Eligibility check by WP6 team	10/03/2019	13/03/2019	3
Review by experts	13/03/2019	03/04/2019	21
WP6 ranking and suggested decision	04/04/2019	11/04/2019	7
PMT teleconference	11/04/2019	18/04/2019	7
Final decision to SSB	19/04/2019	24/04/2019	5
Award letters to successful applicants	19/04/2019	21/04/2019	2
Feedback to other applicants	19/04/2019	21/04/2019	2
STMs organisation, activities, report writing	19/04/2019	30/08/2019	133
WP6 STM final report validation	30/09/2019	30/10/2019	30

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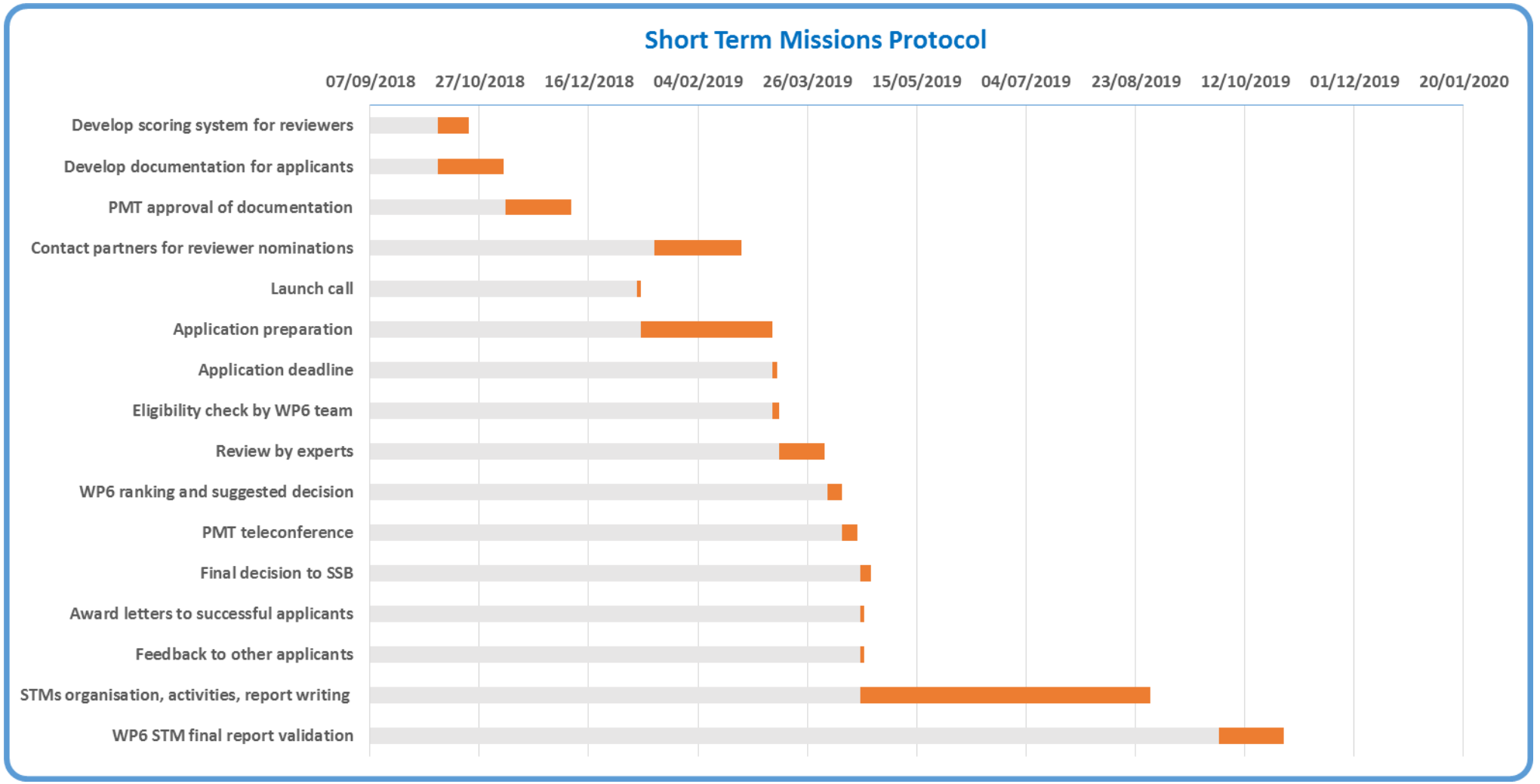

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Annex 2: Promotional graphics

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