FIRST DETECTION OF HIGHLY PATHOGENIC AVIAN INFLUENZA VIRUS IN NORWAY

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Keywords: Anseriformes, Charadriiformes, HPAI, H5N8, hunting, surveillance

Introduction

Several outbreaks of highly pathogenic avian influenza (HPAI) caused by influenza A virus of subtype H5N8 were reported in wild birds and poultry in Europe during autumn 2020.

However, Norway was one of the few countries in Europe that had not previously detected HPAI virus, despite widespread active monitoring of both domestic and wild birds since 2005 (Sjurseth *et al*., 2020).

Objectives

The aim of the national surveillance program for avian influenza in wild birds is to study and understand the threats posed by wild birds in relation to influenza viruses of avian origin, with special emphasis on H5 and H7 viruses (Sjurseth *et al*., 2020).

Methods

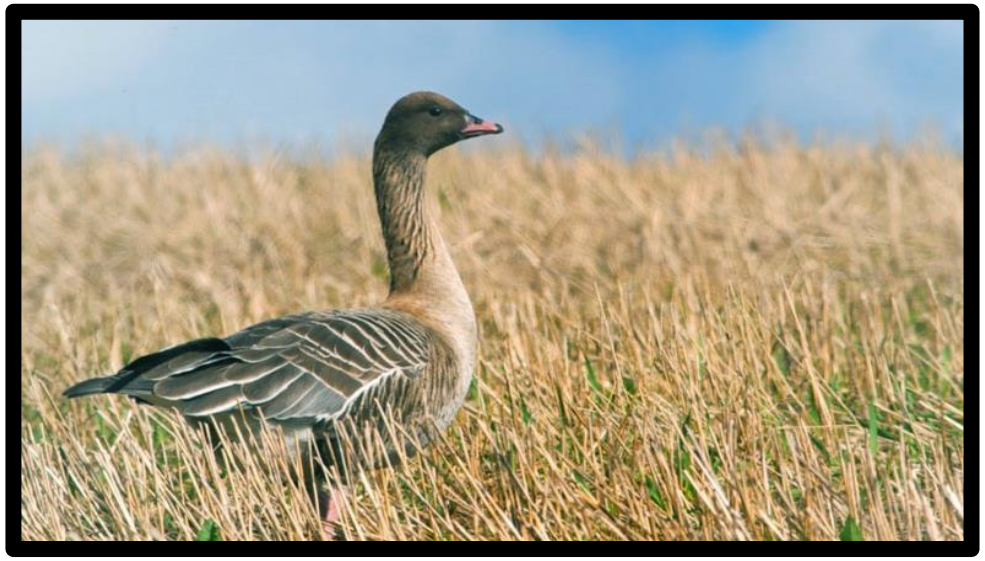
The Norwegian Food Safety Authority (NFSA) is responsible for implementing the active surveillance program for avian influenza (AI) in wild birds in Norway. The program started in 2005 and is based on screening of cloacal and oropharyngeal swabs from healthy birds shot during the hunting season in the autumn (Sjurseth *et al*., 2020). Directly after sampling, swabs are placed in virus transport medium and mailed to the Norwegian Veterinary Institute (NVI) in Ås. Samples are either processed immediately or frozen at − 70 °C upon arrival. In addition, dead birds considered to be high risk species for HPAI (geese, ducks and gulls) are sampled in the field by inspectors from the NFSA and submitted directly to NVI for PCR analysis.

Analyses

Virus detection is performed with realtime RT-PCR targeting the matrix gene of the Influenza A virus, followed by subtype-specific PCRs and sequencing of the cleavage site of the haemagglutinin molecule for determination of the pathogenicity, following the protocols from the Animal and Plant Health Agency (APHA).

Results

We report detection of HPAI virus subtype H5N8 in a wild pink-footed goose (*Anser brachyrhynchus*), and several other geese (2), ducks (5) and gulls (2), from south-western Norway in November and December 2020 (Madslien *et al*., 2021). This is the first detection of HPAI virus in Norway.



Pink-footed goose (*Anser brachyrhynchus*) in Norway. Picture: Wikipedia

Conclusions

HPAI virus has been detected for the first time in Norway, but the mode of introduction remains unclear. However, a northward migration of infected geese or gulls from Denmark or the Netherlands during the autumn of 2020, is currently our main hypothesis for the introduction of HPAI to Norway.

Although HPAI of subtype H5N8 has been reported to have very low zoonotic potential, this is a reminder that HPAI with greater zoonotic potential in wild birds may pose a threat in the future. This underpins the importance of implementing a One Health strategy in handling avian influenza in Norway.

References

Sjurseth SK, Madslien K, Gjerset B, Er C. *The surveillance programme for avian influenza (AI) in wild birds in Norway 2019*. Annual Report 2019. Norwegian Veterinary Institute. 2020.

Madslien K, Moldal T, Gjerset B, Gudmundsson S, Follestad A, Whittard E, *et al*. *First detection of highly pathogenic avian influenza virus in Norway.* BMC Vet Res. 2021 Jun 12;17(1):218. doi: 10.1186/s12917-021-02928-4.

Acknowledgments

The authors are grateful to all waterfowl hunters for providing samples for avian influenza virus analysis on a voluntarily basis. We appreciate the excellent work by inspectors from the NFSA for sampling dead and sick birds in the framework of the increased passive surveillance that was implemented after the first detection of HPAI virus in Norway.

One Health in the 21st Century Conference

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Veterinærinstituttet
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Mattilsynet

ViltHOP
Helseovervåkings-programmet for vilt

CORNELIA – Antimicrobial Resistance (AMR) in One Health Interfaces

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Project information

- The CORNELIA project (Project #320249) is funded by the Research Council of Norway for 2021-2024, as a "Collaborative project to meet societal and industry-related challenges".
- The project is a collaboration between several universities (NMBU and UiT), institutes (FHI, NIBIO and NIVA), and commercial companies within wastewater technology (BlueShift AS and Sustaintech AS), as well as VEAS wastewater treatment plant and Oslo University Hospital (OUS).
- A reference group with national and international stakeholders is associated with the project.

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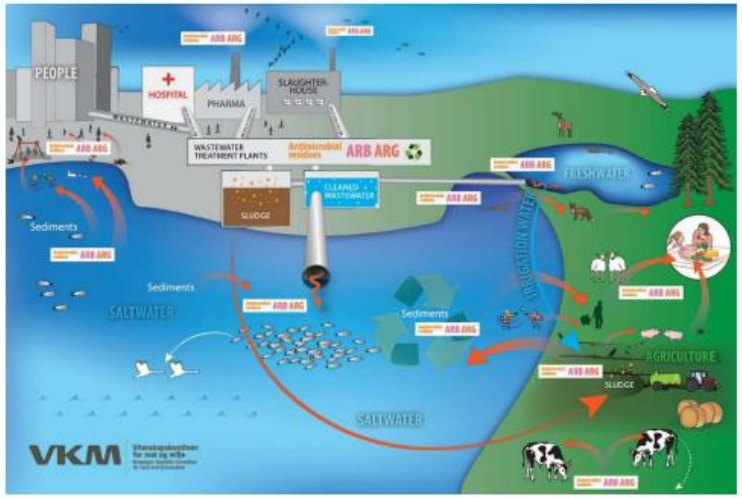
Project background

- AMR is regarded as the essence of One Health, as it affects all sectors. The environment, however, is often neglected in One Health-AMR initiatives, although the environment is the most dynamic and complex sector of the three (1).
- The VKM-report Assessment of the impact of wastewater and sewage sludge treatment methods on antimicrobial resistance from 2020 (2) emphasizes the complex interplay between resistance carriers, traits, various sources of variation, and the wastewater systems, as well as lack of harmonized methods and protocols to compare studies from different systems.

Objectives

Wastewater, sludge and manure are breeding grounds for bacteria, and melting pots of genes from humans and animals. These interfaces may provide good conditions for the development, exchange, and dissemination of AMR. In CORNELIA, our targets are to:

- Unravel AMR patterns and dynamics among critical and highly pathogenic, enteric and environmental bacteria in aquatic and soil interfaces.
- Study the development, transmission and resilience of AMR in aquatic and soil interfaces and the role of these interfaces as important AMR reservoirs.
- Define a basis for the establishment of surveillance programs as NORM-ECO and One Health Resistome Surveillance System.
- Develop and demonstrate technical ARB/ARG-mitigating systems for targeted wastewater treatment at the source and wastewater treatment plant effluents.
- Demonstrate the value of the One Health approach in combating AMR.



The figure demonstrates the potential recycling of AMR. Used with permission from VKM.

Studies of the AMR challenge

CORNELIA will:

- Compare methods for detection and identification of ARBs/ARG in wastewater
  - Cultivation of single isolates
  - Chip-based high-throughput system
  - Metagenomics and whole-genome analyses
- Conduct experimental studies of persistence, transmission and expression of AMR in environmental interfaces

Do we need a surveillance system?

CORNELIA will:

- Compile information and determine matureness of other initiatives
- Develop a framework for "NORM-ECO"

Providing interventive solutions

CORNELIA will test innovative mitigation systems for targeted removal of ARG from wastewater.

- A combined ozonation/ advanced oxidation unit
- Next-generation UV-C irradiation
- Interventions will be operated separately and in series for the most optimal treatment result
- VEAS and OUS as testing locations

References

1. Essack, SY., 2018. Environment – the neglected component of the One Health Triad. Lancet Planet Health, 2(6) 238-239.
2. VKM, Yngvild Wasteson, Hege Salvesen Blix, Erik Joner, Elisabeth-Henie Madslien, Jakob Ottoson, Henning Sørum, Wolfgang Uhl, Siamak Yazdankhah, Øivind Bergh, Ole Martin Eklo, Kaare Magne Nielsen and Pål Trosvik (2020). Assessment of the impact of wastewater and sewage sludge treatment methods on antimicrobial resistance. Scientific opinion of the Panel on Microbial Ecology of the Norwegian Scientific Committee for Food and Environment.

Forecasting human gastrointestinal outbreaks in Norway with Campylobacter broiler farm surveillance data and results dissemination to health authorities

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Keywords: infectious disease, surveillance, forecasting, data visualization

FHI

Mattilsynet

Veterinærinstituttet
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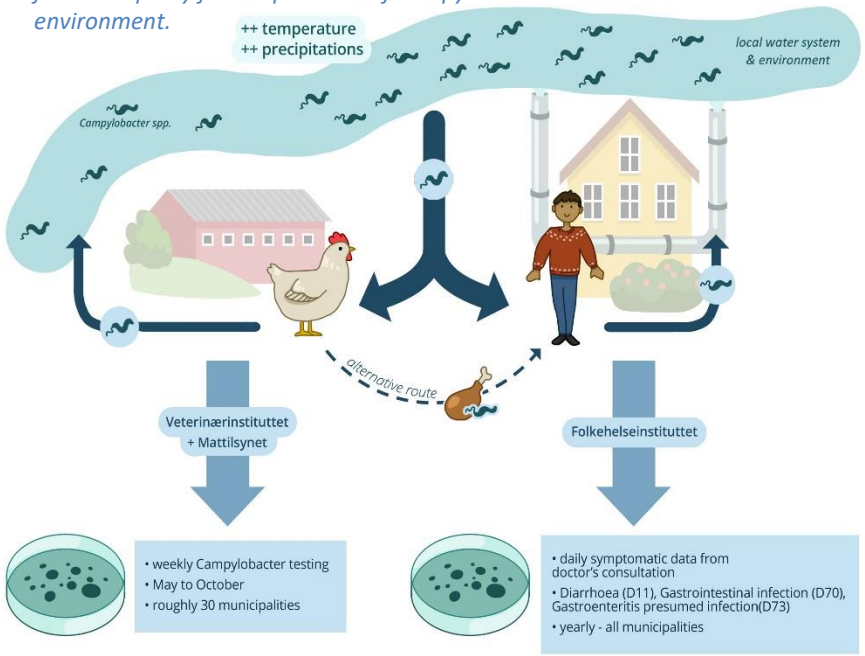
INTRODUCTION

Campylobacter is a **leading cause of food and waterborne illness** in Norway and countries worldwide. People can get Campylobacter infection by eating undercooked poultry, unpasteurized milk, by contact with animals and by drinking untreated water, among other causes. Broiler farms in Norway are monitored for Campylobacter to limit entry into the food chain. **Effective monitoring and modelling has the potential to limit its impact on human health**.

Diagram of a simplified Campylobacter spp. transmission cycle and our sources of data. Our model uses the presence of Campylobacter in broiler farm as a proxy for the presence of Campylobacter in the local environment.



OBJECTIVES

- **Forecast human gastrointestinal outbreaks** using Campylobacter farm surveillance and meteorology data.
- Share data and model predictions in real-time via an interactive R Shiny website to **communicate risk to health authorities** in order to **increase responsiveness** when facing possible Campylobacter outbreaks.

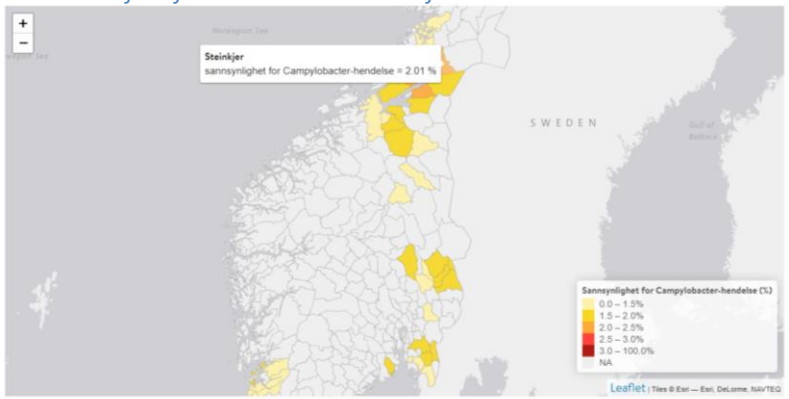
METHODS & RESULTS

We developed a random effects model of weekly gastrointestinal consultations in Norwegian municipalities to estimate a baseline level of gastrointestinal burden. We modelled extreme deviations from this baseline with logistic regression using Campylobacter monitoring and weather data to give 1- and 2-week forecasts of gastrointestinal outbreaks.

Covariate (lag)	Coefficient	p-value
Intercept	-3.5	<1e-14
precip (1wk)	0.0052	0.015
temp (1wk)	-0.012	0.0028
precip (2wk)	-0.0053	0.023
temp (2wk)	-0.021	0.000058
freeze (2wk)	0.15	0.000034
temp range (2wk)	0.0082	0.032
precip (3wk)	-0.009	0.000063
temp (3wk)	0.022	8.4e-08
temp SD (3wk)	0.06	0.0017
temp range (3wk)	-0.022	0.0001
campy prop (2wk)	0.0082	0.00023
herds (2wk)	0.028	0.00025

Two-week lagged Campylobacter positive status, as well as higher temperatures and precipitation, was associated with higher levels of gastrointestinal consultations. Significant inter-municipality variability was observed in outbreak forecasts.

Web interface for the communication of model results.



CONCLUSIONS

Campylobacter surveillance can be a useful element in gastrointestinal outbreak forecasting. **Surveillance of its pathway to illness such as via water system monitoring** is likely a critical part of accurate forecasting. Effectively **communicating forecast results to health professionals** is important to reduce the impact of Campylobacter contamination.

REFERENCES

Paul, M., et al. (2008). "Multivariate modelling of infectious disease surveillance data" *Statistics in Medicine* **27**(29): 6250-6267

Jonsson, Malin E., et al. "Effect of climate and farm environment on Campylobacter spp. colonisation in Norwegian broiler flocks." *Preventive veterinary medicine* 107.1-2 (2012): 95-104.

FUNDING

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Veterinærinstituttet
Norwegian Veterinary Institute

Human and canine exposure to anthrax in a One-Health perspective

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INTRODUCTION

Bacillus anthracis is the causative agent of anthrax which is a zoonotic disease with a broad spectrum of susceptible species and up to 100% high mortality in herbivores. Anthrax causes a high burden of disease in rural areas at the human-livestock-wildlife interface, and is endemic to low-income countries in Asia and Sub-Saharan Africa (WHO, 2008). In these areas, sample conservation and -integrity are often challenging due to conditions in the field and limited laboratory infrastructure. We conducted a serological study in humans and dogs as part of a more extensive study of the epidemiology of anthrax in Northern Tanzania (Mwakapeje et al., 2018). Samples were collected conventionally and on filter paper to assess the applicability of filter paper for transportation under challenging field conditions.

OBJECTIVES

- Confirm exposure to anthrax in dogs and humans in hotspot areas in Tanzania.
- Compare the antibody responses to immunodominant anthrax antigens in humans and dogs.
- Assess the impact on efficacy of antibody detection by ELISA in serum diluted from filter paper and in serum on ready-to-use Western blot membrane strips.
- Explore the possibility for using sampling of dogs to reflect human exposure to anthrax in an epidemiological setting.

METHODS

The fieldwork was conducted between September and November 2016 in districts of the Arusha and Kilimanjaro regions. Serological sampling of humans and dogs was performed in villages with confirmed cases of human anthrax reported by the local hospitals and extension clinics and in neighbouring villages. Samples were transported both in cooled cryovials as well as on filter paper (Whatman™) in ambient temperature. Serum from vials and serum eluated from filter papers was analysed by in-house ELISA and ready-to-use Western blot membrane strips (Dupke et al., 2019) at the Robert Koch Institute (RKI) and the Norwegian Veterinary Institute (NVI). Serological results were combined with GPS data for studies of spatial distribution and analysed visually in QGIS.

RESULTS

Seroprevalence of anthrax in humans and dogs and its spatial distribution are shown in Table 1 and Figure 1. Seroprevalence varies between districts, and spatial distribution suggests correlation between anthrax exposure in humans and dogs. Serum from dogs was analysed at NVI (Figure 2) and serum from humans at RKI. Analyses of serum eluted from filter paper was performed at RKI (Figure 3). All positive ELISA results were confirmed by Western blot. Comparison between the human and canine antibody responses in eluated serum show that canine responses was significantly higher than the human responses (mean: 2,0 and 0,7 respectively, P=<0,0001) (Fig 3).

		Human samples			Canine samples		
Regions	**Districts**	No	Positive	Seroprevalens (CI 95%)	No	Positive	Seroprevalens (CI 95%)
Arusha	Ngorongoro	12	2	0,17 (-0,08-0,41)	23	7	0,30 (0,10-0,51)
Kilimanjaro	Siha	11	5	0,45 (0,10-1,81)	7	6	0,86 (0,51-1,20)
	Hai	9	4	0,44 (0,04-0,85)	2	2	1
	Meru	2	0	0	1	1	1
	Rombo	4	2	0,50 (-0,42-1,42)			
	Moshi	3	2	0,66 (-0,77-2,42)			
Total		41	15	0,36 (0,21-0,52)	33	16	0,48 (0,30-0,66)

Table 1 Seroprevalence in humans and dogs in regions and districts of Northern Tanzania as shown by ELISA results

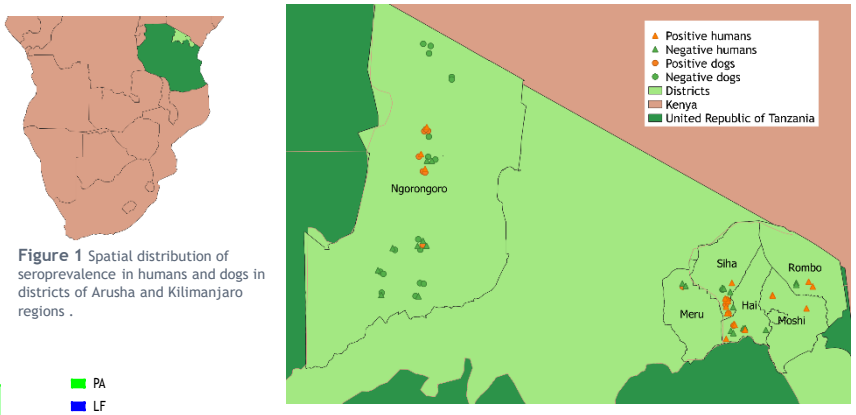

Figure 1 Spatial distribution of seroprevalence in humans and dogs in districts of Arusha and Kilimanjaro regions .

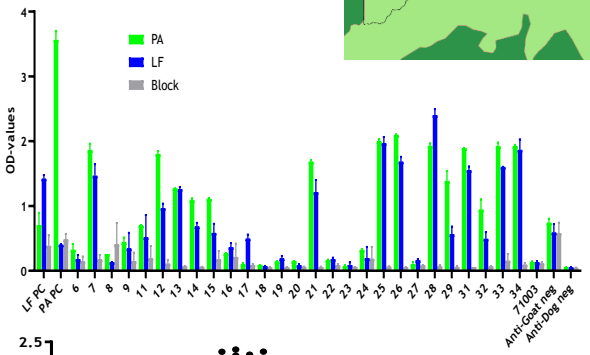

Figure 2 ELISA results of canine serum from cryovials. Green bars represent reactivity towards recombinant protective antigen, blue bars towards recombinant lethal factor and grey bars represent background signals for each sample.

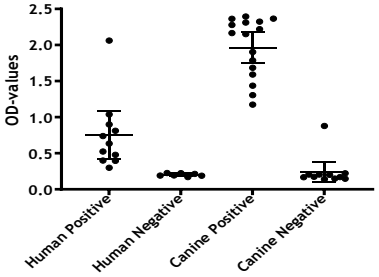

Figure 3 ELISA results of human and canine serum eluated from filter paper.

CONCLUSIONS

- Results suggest a correlation between the anthrax disease burden of in humans, and seropositivity in dogs in hotspot areas.
- Seropositive dogs have significant higher levels of protective antibodies to known immunodominant antigens than seropositive humans.
- Antibody detection by ELISA in serum eluated from filter paper and on Western Blot strips can be performed without loss of efficacy.
- The use of serological tests in dogs can be a cost-effective way to survey the interface areas in endemic anthrax regions.

References

WHO (2008). Anthrax in humans and animals: World Health Organization

Dupke, S., Bardohn, A., Forna, T., Leendertz, F. H., Couacy-Hymann, E., Grunow, R., & Klee, S. R. (2019). Analysis of a newly discovered antigen of Bacillus cereus/thuringiensis/anthracis for its suitability in specific serological antibody testing. Journal of Applied Microbiology, 126(1), 311-323. doi:10.1111/jam.14114

Mwakapeje, E. R., Hogset, S., Fyumagwa, R., Nonga, H. E., Mdegela, R. H., & Skjerve, E. (2018). Anthrax outbreaks in the humans -livestock and wildlife- interface areas of Northern Tanzania: a retrospective record review 2006-2016. Bmc Public Health, 18, doi:ARTN 106 10.1186/s12889-017-5007-z

Acknowledgements and ethical considerations: The permission to carry out this study was sought from and granted by the Tanzanian National Institute for Medical Research (NIMR) with reference number: NIMR/HQ/R.8aVol.IX/2286. Permissions were also sought from Arusha and Kilimanjaro region authorities and local district authorities.

This project was funded by the Norwegian Veterinary Institute

Quinolone resistant *Escherichia coli* from Norwegian livestock, wild animals and humans

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Keywords: Quinolone resistance, *Escherichia coli*

Introduction

Characterization of the quinolone resistance mechanism in animal isolates, comparison to human isolates and the population structure of quinolone resistant *Escherichia coli* (QREC) have been studied through several projects at the Norwegian Veterinary Institute.

The aim of the current study was to combine results from previous studies to investigate if the QREC population found in animals could in any way contribute to the occurrence of QREC in humans.

Methods

A selection of QREC isolates (n=418) from poultry, pig, red fox and wild birds collected in NORM-VET and human isolates collected through NORM and Public Health Institute were Illumina sequenced (1). Strains harbouring plasmid resistant quinolone resistance (PMQR) genes were long read sequenced using MinION (ONT).

Genomes were assembled with SPAdes (2) or using the Bifrost pipeline (3). AMR detection was done using the ARIBA tool with the ResFinder and MegaRes databases for acquired genes and chromosomal point mutations, respectively.

For hybrid assembly, plasmid- and AMR gene detection, and annotation, the ELLIPSIS pipeline was used (4).

Results

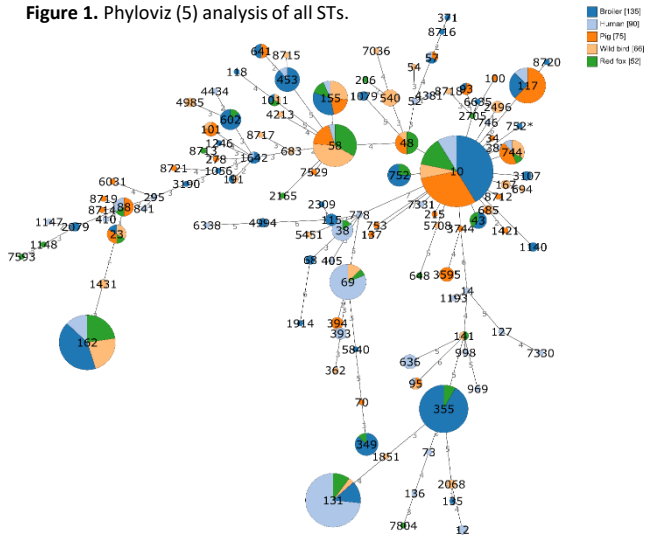
Several unique sequence types (ST) were detected (Figure 1). Some were shared between human and animal QREC isolates. Point mutations were the main resistance mechanism identified (Figure 2). PMQR genes (n=59) were detected on plasmids of different incompatibility (Inc) groups from both human and animal isolates (Figure 3), predominantly in wild animals.

Conclusions

There was **some overlap of QREC isolates** with same STs isolated from animals and humans. Overall **few PMQR genes** were detected in all isolates.

Results

Figure 1. Phyloviz (5) analysis of all STs.



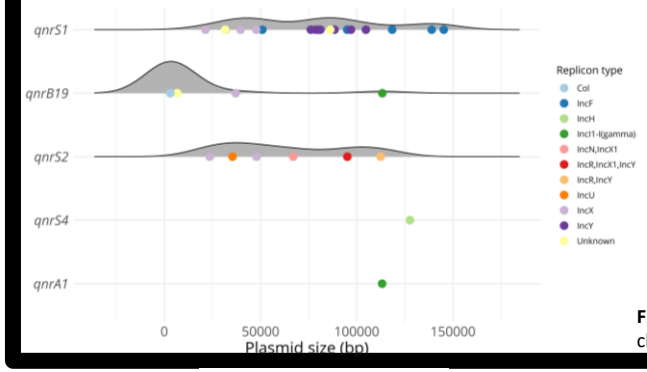


Figure 3. Density plot of plasmid sizes with respective Inc-groups characterized from the 59 isolates harbouring PMQR genes.

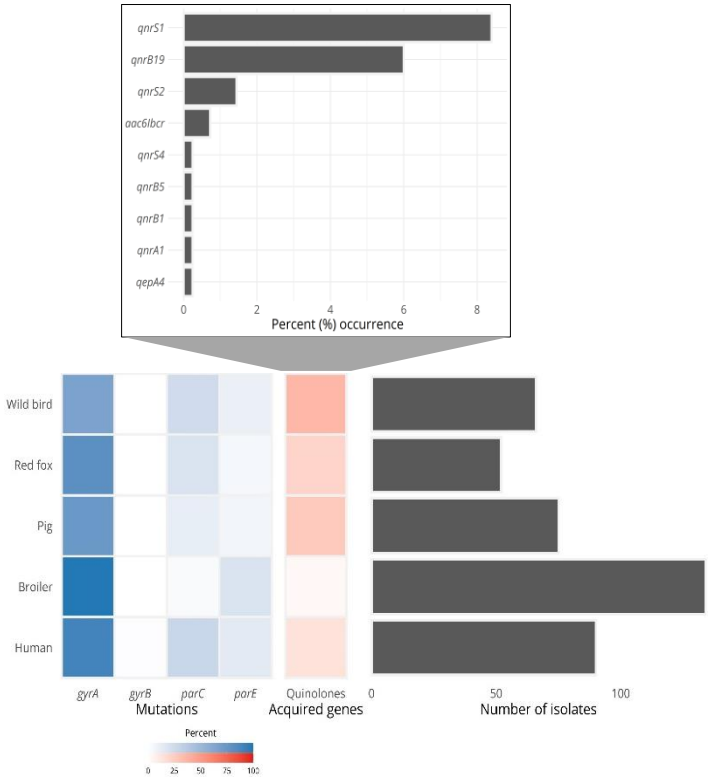


Figure 2. The mechanisms of quinolone resistance in all QREC.

References

1) Kaspersen *et al.* 2020 (DOI: 10.1128/aem.02769-19)
2) Bankevich *et al.* 2012 (DOI: 10.1089/cmb.2012.0021)
3) Bifrost (DOI: 10.5281/zenodo.3984659)
4) ELLIPSIS (https://zenodo.org/badge/latestdoi/279863701)
5) Francisco *et al.* 2009 (DOI: 10.1186/1471-2105-10-152)

Acknowledgments/Funding

The Norwegian Research Funding for Agriculture and Food Industry funded this work; grant number 244140 and 255383, and One Health EJP project, which has received funding from the European Union's Horizon 2020 research and innovation program (grant number 773830).

Detection of *Campylobacter* in air samples from poultry houses using shot-gun metagenomics

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Norwegian Veterinary Institute, Oslo, Norway
presenter

One of the major causes of food-borne infections in Europe are *Campylobacter* spp. Thus, broiler production facilities need to be closely monitored for the presence of *Campylobacter* using effective methods. Here we use metagenomic sequencing of ambient air samples in combination with real-time PCR to detect *Campylobacter* in broiler houses.

METHODS

- Air samples from two Norwegian broiler houses were collected using a Sartorious AirPort MD8 device with 80 mm diameter disposable gelatine filters [1]. Two filters were divided into four equal parts, respectively, and spiked with different amounts of *C. jejuni* 927 (Table 1).
- Two sterile gelatine membrane filters were divided into eight equal parts and spiked with ZymoBIOMICS Microbial Community Standard II. Four samples were spiked with *C. jejuni* CCUG 11284T and four samples with MOCK communities served as blanks (Table 1).
- Air filter pieces were vortexed in ddH2O with alkaline protease until they were dissolved. The solution was centrifuged, and the pellet was used for DNA extraction using the gram-negative protocol for DNeasy Blood and Tissue kit (Qiagen).
- Real-time PCR was performed as described by [2].
- Shotgun sequencing of samples and the two isolates was performed using a Illumina HiSeq 3000 at the Norwegian Sequencing Centre.
- Metagenomic data was analyzed using the Sunbeam pipeline [3].
- The *Campylobacter* genomes were assembled using Bifrost [4].

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

RESULTS

Figure 1. Genus level Taxonomic classifications of metagenomic shotgun sequences. Sequences were classified with Kraken using the Refseq database of genomes. Only genera with a maximum abundance of 0.1 % in at least one sample are vizualized here. The relative abundance is scaled using different bubble sizes. This indicated the presence of several possible pathogenic genera in the house samples.

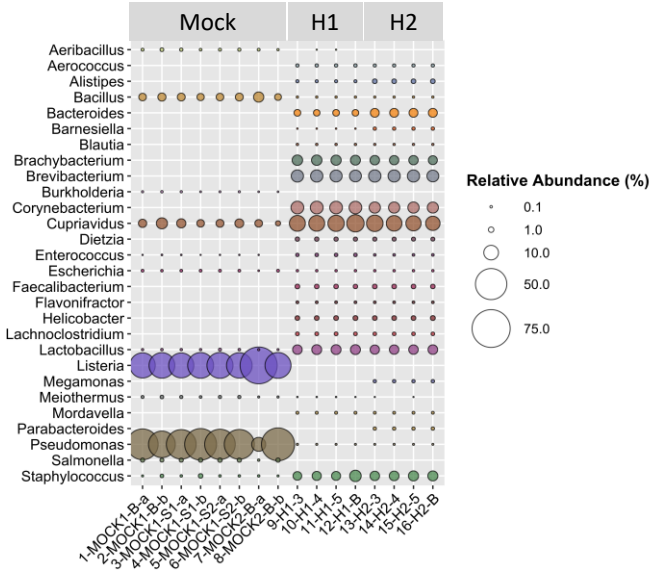

Figure 2. Campylobacter species sequence abundances as detected using Kraken classification. The samples with 200 CFU had 4 in 1 million reads assigned to *C. jejuni*, while the blank samples had on average 2.6 reads assigned to the same species. The house samples showed a similar trend as the real-time PCR results for *Campylobacter* abundance. Since the house samples were naturally contaminated with *Campylobacter*, multiple species could be detected besides *C. jejuni*.

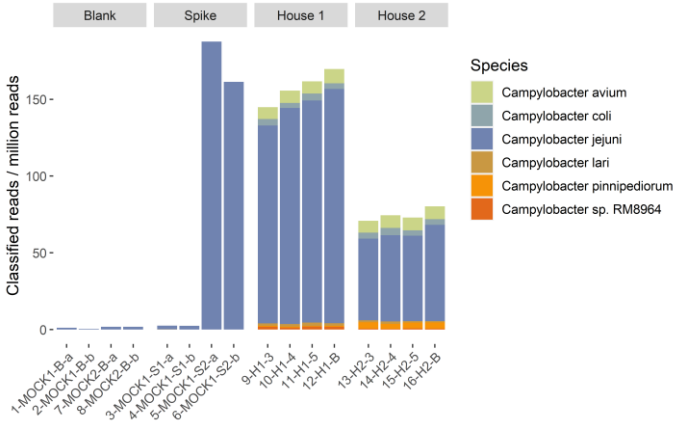

Table 1: Description of samples and real-time quantification of *Campylobacter* 16S rRNA copies for all samples. Low Cq values indicate a high abundance of 16S rRNA copies.

Sample ID	Sample - *C. jejuni* spike	Spike (CFU)	Mock amount (µl)	Cq 16S rRNA
MOCK1-Ba	Mock – no spike	0	75	43,1
MOCK1-Bb	Mock – no spike	0	75	N/A
MOCK1-S1a	Mock - CCUG 11284T	200	75	37,21
MOCK1-S1b	Mock - CCUG 11284T	200	75	35,19
MOCK1-S2a	Mock - CCUG 11284T	20000	75	29,11
MOCK1-S2b	Mock - CCUG 11284T	20000	75	29,16
MOCK2-Ba	Mock – no spike	0	125	41,11
MOCK2-Bb	Mock – no spike	0	125	N/A
H1-3	House 1 - 927	5650	-	29,39
H1-4	House 1 - 927	565	-	30,42
H1-5	House 1 - 927	56,5	-	30,28
H1-B	House 1 – no spike	0	-	31,07
H2-3	House 2 - 927	5650	-	30,62
H2-4	House 2 - 927	565	-	31,26
H2-5	House 2 - 927	56,5	-	31,32
H2-B	House 2 – no spike	0	-	32,56

CONCLUSIONS

***Campylobacter* species can be detected using airfilters in broiler house samples with a lower limit of 200 CFU. However, false positive identification is possible in samples where *Campylobacter* 16S rRNA was detected at the detection limit with real-time PCR. In the house samples multiple *Camplyobacter* species could be detected besides *C. jejuni*.**

REFERENCES

1) Johannessen et al., Food Microbiol **2020**, 90, 103455
2) Josefsen et al., Appl Environ Microbiol **2010**, 76, 5097-5104
3) Clark et al., Microbiome **2019**, 22, 46
4) Bifrost https://github.com/NorwegianVeterinaryInstitute/Bifrost

ACKNOWLEDGEMENTS

The farmer who provided access to the chicken houses is thanked for his kind collaboration. The NSC and Sigma2 are thanked for help with the library preparation, sequencing and access to the Saga HPC cluster.

Inspiring a Nutrition Revolution

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Keywords: Planetary Health,

Introduction

With food systems accounting for around 20% of greenhouse gas (GHG) emissions in the UK , and obesity levels rising in Scotland and globally, a food transformation is needed. Though there is enthusiasm amongst students for healthy, "planet responsible" eating, dietary support and information is limited.

Objectives

1. To develop and implement a Planetary Health Meal Plan for students in Dundee and Edinburgh
2. To develop knowledge and behaviour change resources to facilitate scale-out

Methods

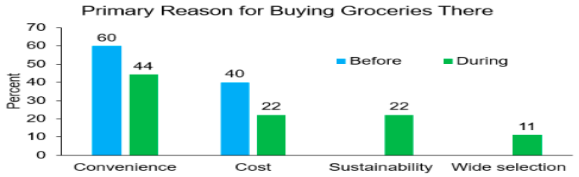
Stakeholders including local businesses; third sector representatives; students; teachers; nutritionists; and academics were brought together in a focus group. An initial 2-week meal plan, aligning with EAT-Lancet guidelines was developed, including shopping lists; dietary alternatives, and carbon footprint data. A website was launched showcasing the meal plan, and university participants recruited for a pilot through social media.

A follow up survey was rolled out to participants. Using feedback, the meal plan was refined and adapted into a 1-month recurrent plan for launch across participating Scottish universities in September 2021.

37 participants recruited for 2 week pilot → 16 survey responses (7 fully completed) → 241 participants recruited to 1 month meal plan (ongoing)

Pilot Results

The results demonstrated a change in the purchasing habits of our participants, with an increase from 10% to 33% of participants buying ingredients from local/smaller retailers.



Food expenditure per week was also noted to increase, with those spending >£40 a week rising from 25% to 43%.

Fidelity - 71% of participants followed 2-3 meals each weekday, reducing to 21% and 43% for weekends 1 and 2, respectively.

Perceptions of the meal plan - Whilst most agreed the meal plan was **tasty, healthy and sustainable,** some participants disagreed on aspects of **affordability, and convenience**. The most challenging aspects of the meal plan included the time and cost expenses (33% and 17%), and the lack of vegan substitutes.

Impact - Following the pilot, participants said they were more likely to try new recipes (83%), shop locally (67%), eat more vegetables (67%), and waste less food (33%). 76% said they would recommend the meal plan to family and friends.

Learning outcomes

The results from the survey influenced the development of the month long September Meal Plan. To increase reach, accessibility, ease and affordability, the following changes were integrated:

- Increased alternatives for vegan, vegetarian and gluten-free diets
- Meal planning and ingredients lists developed to limit food waste
- Recruitment of chef, nutritionist, carbon accountant
- Recruitment of social media manager to promote the plan, and to develop engagement events

Conclusions

The pilot survey demonstrated participant interest and willingness to change their food consumption behaviours going forward from the pilot. We also revealed a set of concerns relating to the affordability, convenience and lack of vegan alternatives which hindered engagement in the pilot meal plan.

Building on these, we increased options for alternative dietary requirements, produced shopping lists and recipes which limited food waste and sourcing of expensive ingredients, and coordinated recipes across weeks.

241 people signed up to participate in the September Planetary Health Meal Plan, an increase from 37 for the pilot in June.

The Planetary Health Meal Plan was aligned with the Planetary Health Diet guidelines. All recipes also included details on the emissions linked to the ingredients.

References

https://www.planetaryhealthrevolution.com/

Acknowledgments/Funding

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BUILDING POLITICAL WILL FOR ONE HEALTH RISK ANALYSIS SYSTEM

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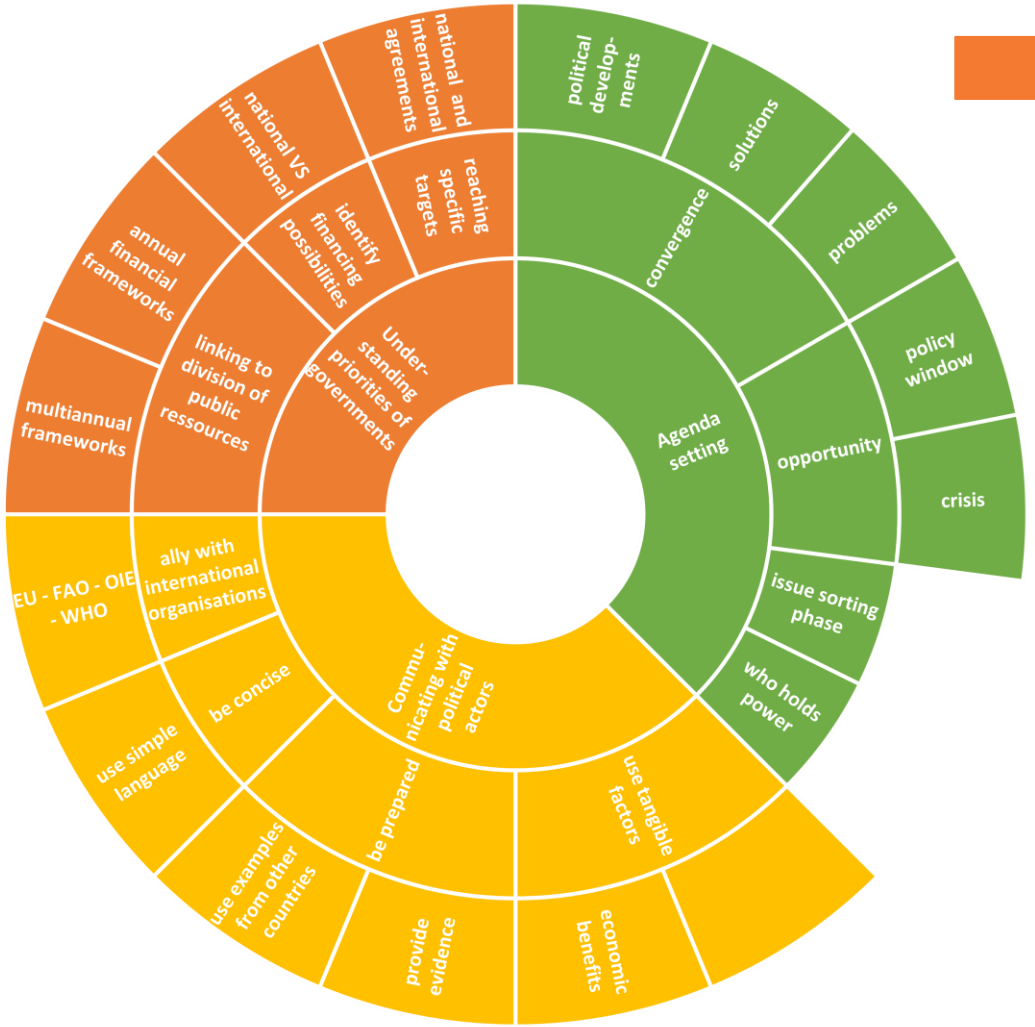
Aim: understand how One Health professionals can build political will and with results of this research build a political will tool as an element of the COHESIVE implementation guidelines for risk analysis of zoonoses (a poster presented at ASM 2020).



Methods

A transdisciplinary research method was applied. Professionals working in the field of One Health and zoonoses in the European region participated in the different workshops and focus groups between 2018 - 2021. During the sessions, methods such as brainwriting and group discussions were used. In addition, 12 semi-structured interviews (SSIs) were performed in the period of 2019 and 2020 with One Health professionals from national food safety, public and veterinarian health institutions from Czech Republic, Denmark, Italy, Netherlands, Norway and United Kingdom. In addition, OH professionals from the WHO, FAO and OIE. The sessions and interviews were recorded and transcribed for thematic analyses.

Results

The preliminary outcomes of the research resulted in practical advices aimed at building political will illustrated in the diagram

Conclusions

Understanding political will in the context of OHRAS is an essential element for the implementation of OHRAS. Following the proposed guidelines, professionals working in the area of One Health and zoonoses will be able to build political will to support the implementation of OHRAS.

COHESIVE project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 773830.

Assessment of communication strategies for future One health policy: lessons learned from COVID-19

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research authors: Eduardo Ramirez, Helena Domingues and Saeka Zafar

Keywords: communication strategy, Risk communication, health policy, guidelines, COVID-19

Introduction

In order to control outbreaks as quickly as possible, effective communication strategies can be one of the best tools to achieve this goal. Countries around the world can follow international guidelines but also develop their own plans to tackle pandemics. The challenges presented by the disease will require constant adaption and most importantly collaboration between different agents and stakeholders.
As one of the most important international organizations, the World Health Organization (WHO), has published outbreak Communication guidelines that outline improved risk communication based on lessons learned from past health crises. The main purpose is to control the outbreak quickly, avoiding massive social disruptions. These guidelines are based on a set of principles that aim to ensure the flow of information between the WHO, international community, policymakers, individuals, and health care providers (WHO, 2017).

WHO's risk communication guidelines address health issues by acknowledging that uncertainty is transversal to every communication strategy; it influences the interactions between relevant stakeholders and their response to health emergencies (WHO, 2017). Acknowledging this, the International Health Regulations (IHR) address the importance of developing risk communication capacities in member States and their continuous assessment. In practice, these capacities are tested whenever a health emergency arises; In this article strategies such as information, dissemination of information, contact tracing and quarantine protocols will be the most accessed ones.

Objectives

Communication strategies are important to strengthen the public response during pandemics. The responsibility of acting and providing these strategies are under the supervision of international organizations such as the World Health Organization (WHO). However, understanding and adherence to the guidelines can be limited by existing gaps in communication. The purpose of this article is to identify these gaps, map the implementation of communication guidelines in selected countries, highlight successful policies, understand the ongoing challenges of vaccine acceptance, and provide recommendations for future strategies.

Methods

Literature review of the communication guidelines and strategies published by WHO and an assessment of their implementation in Norway and selected countries during the COVID-19 crisis.
We reviewed 'WHO outbreak communication guidelines" and the more recent "COVID 19 Global Risk Communication and Community Engagement Strategy" to understand the guidance on pandemic communication. It helped us identify the engagement methods suggested by WHO with different stakeholders (citizens, government, companies, environment).

We did a literature review with search term {"Communication strategies" OR "Risk communication") AND ("best practices" OR lessons) AND Policy AND (stakeholder*) AND (COVID*)} on Google scholar, to find 4240 results. The results are filtered since 2020 as we wanted to know the most recent & relevant work on the topic since the start of the pandemic.
To identify the stakeholders for risk communication at different stages of the pandemic we further searched for terms {"different stakeholders" AND engagement AND "risk communication" AND covid-19"} since 2020. This showed 281 results. We review the top 20 articles to find out the different stakeholders for COVID-19 risk communication.
We analyzed risk communication strategies at different stages of the pandemic starting from information dissemination, contract tracing & quarantine protocols, prevention measures and vaccine policy.
We added each of the different stages of pandemic in the main search terms and found narrower results. e.g ("Communication strategies" OR "Risk communication") AND ("best practices" OR lessons) AND "XX" AND Policy AND (stakeholder*) AND (COVID*) e.g. when we replace XX with contact tracing we got 649 results "Information dissemination" gave 300 results; "quarantine protocols" gave 13 results ; "prevention measures" gave 263 results and "vaccine policy" OR "vaccine hesitancy" gave 203 results.

Analyses

The analyses involve identifying the stakeholders involved for successful engagement of communication strategies at global, National & sub-national levels (i.e., Governments, private organizations, NGOs, community leaders, citizens, and the Environment). The guidelines by WHO, CDC, European CDC emphasize the role of stakeholders to roll out communication strategies for COVID -19 prevention, policy, Vaccination.

Further, we analysed how each stakeholder performed in best and worst-case scenarios through the literature of communication strategies at each of the different stages of the COVID-19 pandemic: Information dissemination, Contact tracing, Quarantine protocol policy, Prevention measures, and Vaccine policy.
The role of all stakeholders in each stage of the pandemic was crucial. However, we wanted to formulate a method to quantify the importance of each stakeholder. We ranked the stakeholders in the order of importance at each stage of pandemic communication from the literature review. Through the literature review, we realize that the role of the environment as a stakeholder was not mentioned either in the WHO guideline or other guidelines for communication.
For each of the stages, the kind of communication recommendation was identified, and the best practices were summarised at the national & subnational level to develop a knowledge of best practices for future epidemic management.

Identify stakeholder viz. Governments, Private organisation, Community, NGOs, Citizen & Environment

Analyse & understand their role at different stages of info-demic - Information dissemination, Quarantine policy, Prevention, Vaccination

Identify the gaps in implementation of risk communication and highlight the best practices across national & subnational levels

Results

During the COVID-19 pandemic, risk communication and community engagement have been one of the pillars of WHO's strategy to support preparedness and response. All these strategies are based on six main features: **trust, understanding, planning, action, and accessibility**. Although WHO's guidelines have the goal of informing key audiences in order to promote health, in practice, we observe differences in their adoption, with different implications. Based on the reviewed literature, we found **that initial conditions in terms of infrastructure, stakeholder involvement, and preparedness** mattered when it comes to deploying a successful communication strategy. **Countries like Senegal and South Korea, both with different levels of income and infrastructure development, performed well in diseminating information during the initial stages of the pandemic.** Their strategy relied on the existing channels that had been developed as a response to past health emergencies.

Similarly, in the implementation of communication strategies for **prevention measures** – countries with **strong leadership and clear messaging** from the initial days of the COVID-19 pandemic have worked better. **An example of the same has been New Zealand and the leadership communication of Jacinda Ardern**. In a bid to implement a **vaccination program and tackle vaccine hesitancy** communication played a crucial role. Here again, clear messaging since the start of the pandemic helped countries to increase uptake of vaccines. However, **trust in government & healthcare authorities are the main drivers for the implementation of communication strategies for vaccination. In examples across the world, low trust in government has been the common factor that increases vaccine hesitancy**. However, the Government in the UK successfully implemented focused strategies for communities to mitigate such risk. **The communication involved empathy, respect, and engagement** with community leaders to develop credibility for the communication strategies.

The importance of **governments & healthcare authorities** as stakeholders in implementation of communication strategies is highest in all stages of pandemic management. Additionally, the role of community engagement in prevention, vaccination acceptance is crucial. **Partnership with NGOs and civil society helps in successful implementation of communication program to disseminate information about a healthcare emergence**.
In a broader dimension of health, future communicational guidelines must address the challenges that increased urbanization, migration, trade, and climate change represent to humans, wildlife, and the environment. Communicating risks and promoting behavioural change while adapting institutions and response mechanisms to this context is key to the management of future health crises. **In the guidelines reviewed for this article, although these challenges are mentioned as concerns, there is no outline of a strategy that addresses or provides comments on the need to change current practices**.

For example, involving stakeholders seemed to be relevant mostly for early information sharing, rather than for decision-making itself. Therefore, the prevention and management of future pandemics depend on assessing these issues at an international, national and local level while addressing the changes in population, urbanization, and environment, and the challenges these imply.

Conclusions

One health policy requires addressing the dynamics of different stakeholders, focus on their behaviour, interrelations, and contextual differences to simplify the implementation of communication strategies. Thus, the constant revision and inclusion of new strategies are essential for One health governance to effectively address future health emergencies.

This article highlighted some of the challenges and limitations of the existing communication guidelines and brought some practical examples of countries that were able to implement successful programs such as New Zealand, Senegal, and South Korea. While the UK, for example, failed in some aspects such as trust in government but succeeded in focused strategies within local communities to mitigate this lack of trust.

One of the lessons of the ongoing pandemic is that detecting, supporting, and isolating early cases is crucial for the management of the crisis. However, how should communities, researchers, and policymakers interact when there is no apparent threat of an outbreak remains a relevant question and an open ground for improvement. To instill and maintain public trust in the response systems are one of the objectives of risk and outbreak communication, this should include local, national representatives of the health system and allow for the coordination between public health and veterinary experts, communities, international organizations, and authorities.

References

George W. Warren & Ragnar Lofstedt (2021) Risk communication and COVID-19 in Europe: lessons for future public health crises, Journal of Risk Research, DOI: 10.1080/13669877.2021.1947874

Kraaij-Dirkzwager, M. M., Schol, L. G., Schuitmaker-Warnaar, T. J., Timen, A., & Van Steenbergen, J. E. (n.d.). Stakeholder Involvement in Outbreak Management: To Fear or Not to Fear? International Journal of Information Systems for Crisis Response and Management.

Reed, M. S., Graves, A., Dandy, N., Posthumus, H., Hubacek, K., Morris, J., Prell, C., Quinn, C. H., & Stringer, L. C. (2009). Who's in and why? A typology of stakeholder analysis methods for natural resource management. Journal of Environmental Management, 90(5), 1933–1949. https://doi.org/10.1016/j.jenvman.2009.01.001

Reid, J. A., & Mabhala, M. A. (2021). Ethnic and minority group differences in engagement with COVID-19 vaccination programmes – at Pandemic Pace; when vaccine confidence in mass rollout meets local vaccine hesitancy. Israel Journal of Health Policy Research, 10(1). https://doi.org/10.1186/s13584-021-00467-9

Sauer, M. A., Truelove, S., Gerste, A. K., & Limaye, R. J. (2021). A Failure to Communicate? How Public Messaging Has Strained the COVID-19 Response in the United States. Health Security, 19(1). https://doi.org/10.1089/hs.2020.0190

WHO. (2005). Outbreak Communication Guidelines. Available at https://www.who.int/publications/i/item/who-outbreak-communication-guidelines.

WHO. (2012). Communication for behavioural impact (COMBI): A toolkit for behavioural and social communication in outbreak response. World Health Organization.

WHO. (2017). Communicating risk in public health emergencies: a WHO guideline for emergency risk communication (ERC) policy and practice. World Health Organization.

Sustainable Electrochemical Reduction of contaminants of emerging concern and Pathogens in WWTP effluent for Irrigation of Crops (SERPIC)

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Keywords: AMR, environment, interventions, water reuse, contaminants of emerging concerns (CECs)

Project background

- Our food, sanitation and potable water systems form an interdependent system that provides a foundation for public health. This is the essence of the One Water - One Health paradigm that guides the SERPIC project (Figure 1).
- The reuse of reclaimed water is promoted by the EU regulations on minimum requirements for water reuse for agricultural irrigation and the WHO sanitation safety plans and by the circular economy principles. SERPIC connects the urban water cycle with the water cycle in agriculture and industry.
- However, wastewater treatment plants (WWTPs) face an increasing amount of contaminants of emerging concern (CECs) such as chemicals, antibiotics, antibiotic resistant bacteria (ARB), and antibiotic resistant genes (ARGs).

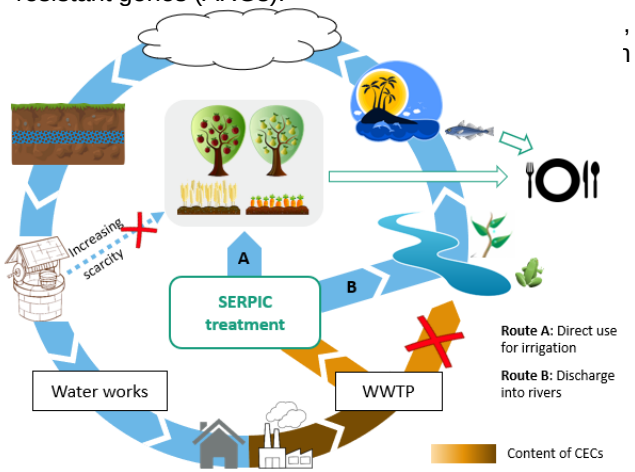

Figure 1. Application of SERPIC project.

Objectives

The SERPIC projects aims to:

- Investigate and minimize the spread of CECs, including ARB and ARGs with a focus on additional water sources for food production.
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- Reduce CECs from WWTPs effluent by developing innovative multi-barrier treatment, based on membrane filtration and light driven electrochemical processes.

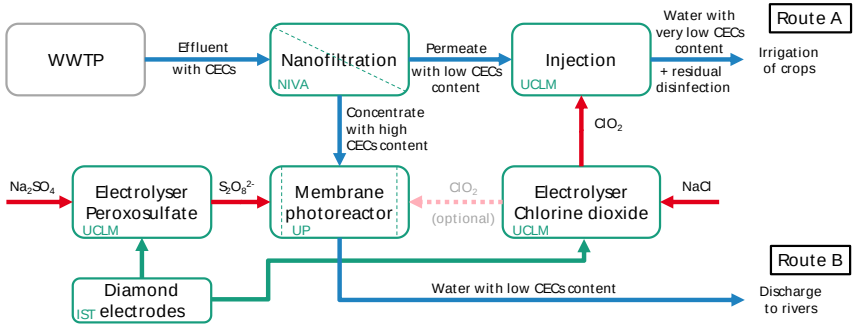


Figure 2: Process chain of the SERPIC proposed intervention.

Providing solutions

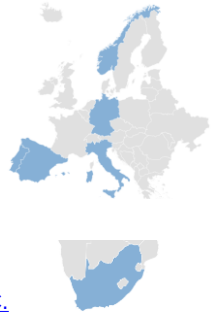
- Membrane nanofiltration (NF) to reduce CECs, including ARB/ARGs, by at least 90% while retaining the nutrients. Upon chlorine dioxide disinfection, the water will be used for crops irrigation (Figure 2).
- The CECs in the polluted concentrate stream will be reduced by at least 80% by light driven electrochemical oxidation before its discharge to the aquatic environment.
- A prototype treatment plant will be set-up on-site of a Spanish WWTP and evaluated for irrigation in long-term field tests using agricultural test pots.

AMR related activities

- Investigation of CECs and ARB/ARGs spread at four regional showcase in Europe and Africa.
- The occurrence and reduction of ca. 30 compounds, including ARB and ARGs, will be monitored in water.
- Real effluent a WWTP in Oslo will be used for experimental assessment of NF for the removal of ARB and ARGs.
- Methodologies and tools for monitoring, health and environmental risk assessment and implementation of new reuse concepts including new treatment technologies to support policy- and decision-making.

Project information

- The SERPIC project is funded by national and EU funding under the AquaticPollutants call co-organized by the JPI AMR, Water JPI and JPI Oceans.
- The project is a collaboration between the R&D institute sector (Fraunhofer Institute and NIVA), the university sector (UCLM, UNIFE, UP and SU), and the business sector within water treatment and reuse (AdP, SolarSpring).



- Project website: www.aquatic-pollutants.eu/Projects/Taking+Actions/SERPIC.html

Acknowledgments

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NIVA acknowledges funding from the Research Council of Norway (project number 329046).

Removal of cell free antibiotic resistance genes from water by membrane filtration and from concentrate by 265 nm UV-LED

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Keywords: AMR, environment, interventions, membrane filtration, UV disinfection

Introduction

- Antimicrobial resistance (AMR) is a global public health threat recognized by WHO, UN and EU.
- Wastewater treatment plants (WWTPs), not designed to remove antibiotic resistance genes (ARGs), contribute to AMR spread in the environment.
- Effective water and wastewater treatment methods are needed to mitigate the release of ARB and ARGs from WWTPs.
- Membrane filtration is widely used in water treatment and reuse, but ARGs removal was not studied extensively.

Objectives

The study focused on mitigation of ARGs emissions to aquatic environment and the aim was:

- To understand whether and to what extent ARGs can be removed by different membrane filtration processes,
- To assess the potential of UV-LED at 265 nm for the treatment of the ARG-rich membrane concentrate.

Methods

- Ultrapure water spiked with *E. coli* cell free DNA, containing the plasmid pCR®II-TOPO encoding kanamycin and ampicillin resistance genes.
- DNA-spiked water used for the rejection experiments in bench-scale membrane test unit (Figure 1).
- 9 commercial ultrafiltration (UF), nanofiltration (NF), reverse osmosis (RO) membranes.
- Concentrate treated by lab-scale UV-LED unit (Figure 1).

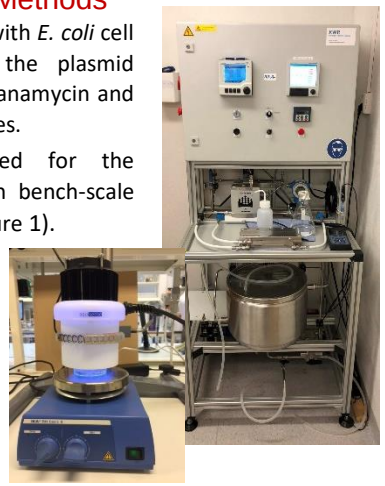

Figure 1. NIVA's membrane and UV-LED units

Analyses

- Plasmid removal was assessed by qPCR (Figure 2).
- CFX96 Touch™ thermocycler (BioRad, Hercules) with SsoFast™ EvaGreen® mastermix (Bio-Rad).
- No DNA extraction, samples directly to qPCR.

Figure 2. qPCR instrument

Results

- More than 99% plasmid removal was achieved by membranes with 1 kDa molecular weight cut off (MWCO).
- Membranes with lower MWCO showed complete removal under the specific experimental conditions, reaching a maximum log reduction value (LRV) above 6.6 (Figure 3).
- UV irradiation can damage and inactivate ARGs in the membrane concentrate.
- The required fluence for 1 log damage was between 23-73 mJ/cm^2 depending on size of target bp segment.

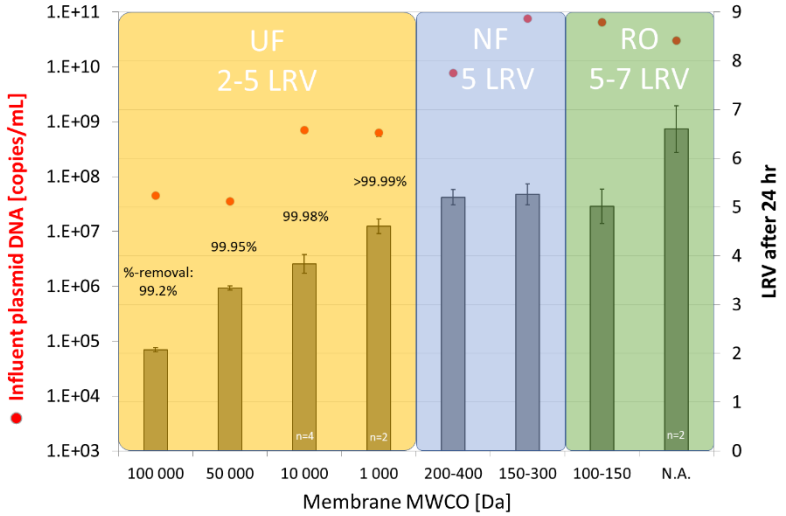

Figure 3. LRV and DNA concentration in the permeate of the membranes with different MWCO

Conclusions

- DNA plasmid rejection varied between 2 and 7 LRV.
- Removal effectivity of DNA plasmid correlated with MWCO of the membranes.
- Membrane filtration, combined with UV-LED treatment of the concentrate, can be an effective measure to remove and inactivate ARGs from water to prevent spreading of AMR in the environment.

Future work

- Confirmation for more complex water matrices and environmentally relevant samples.
- Factors impacting ARGs removal (membrane material, water matrix, operating conditions).

References

1. Krzeminski, P., Feys, E., d'Auriac, M.A., Wennberg, A.C., Umar, M., Schwermer, C.U., Uhl, W. (2020) Combined membrane filtration and 265 nm UV irradiation for effective removal of cell free antibiotic resistance genes from feed water and concentrate, Journal of Membrane Science 598C, 117676
2. Schwermer, C., Krzeminski, P., Wennberg, A, Vogelsang, C., Uhl, W. (2018) Removal of antibiotic resistant E. coli in two Norwegian wastewater treatment plants and by nano- and ultra-filtration processes, Water Science and Technology 77(4), pp. 1115-1126
3. Krzeminski, P., Tomei, M.C., Karaolia, P., Langenhoff, A., Almeida M.C., Felis, E., Gritten, F., Andersen, H.R., Fernandes, T., Manaia, C.M., Rizzo, L., Fatta-Kassinos, D. (2019) Performance of secondary wastewater treatment methods for the removal of contaminants of emerging concern implicated in crop uptake and antibiotic resistance spread: A review, Science of the Total Environment 648C, pp. 1052-1081

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