

POSTER P3293

AMR surveillance in wastewater and clinical isolates from a tertiary hospital: Preliminary results



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BACKGROUND

AMR (meta)genomic surveillance can assess the spread of AMR genes in the environment and detect their potential reservoirs.

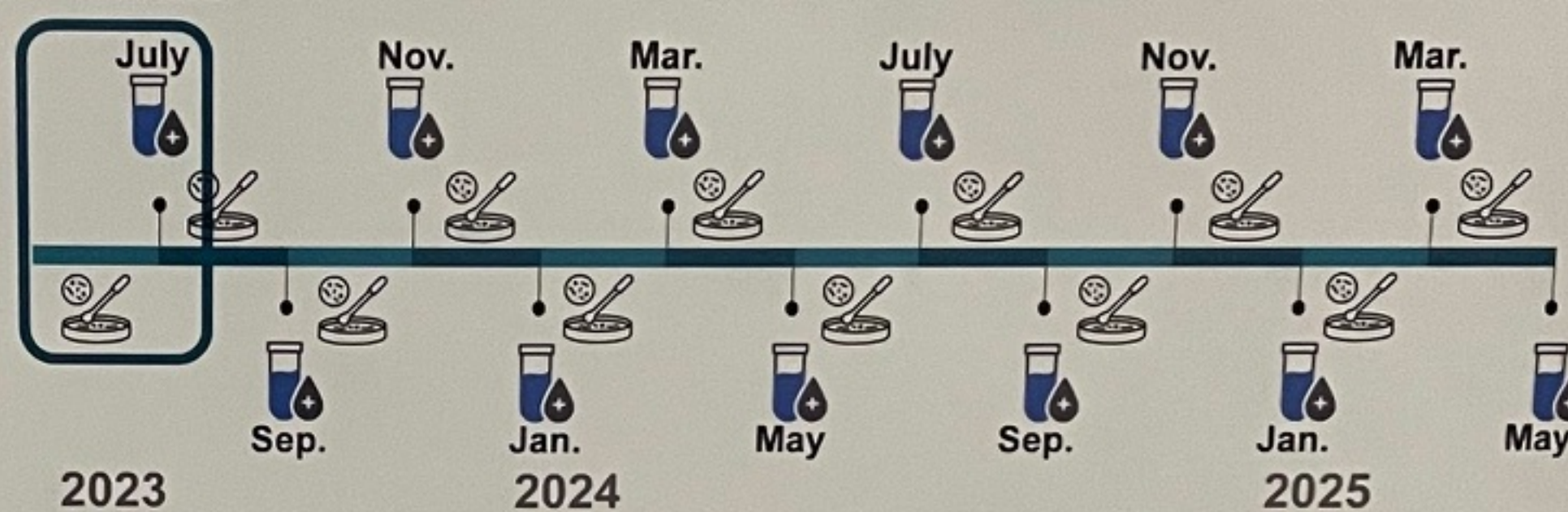
This study aims to evaluate the presence of AMR genes in clinical isolates and their spread through hospital wastewater.

We present the preliminary results of a study that will last over 2 years.

METHODS

1st results

Chronogram



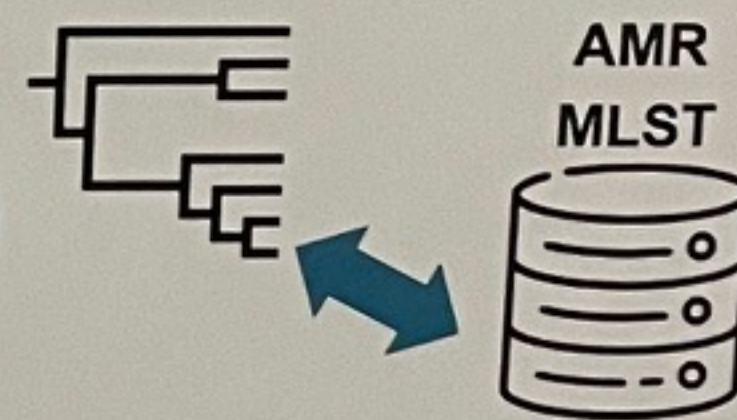
Workflow



Clinical/water sampling



Genome/metagenome HTS, QC & assembly

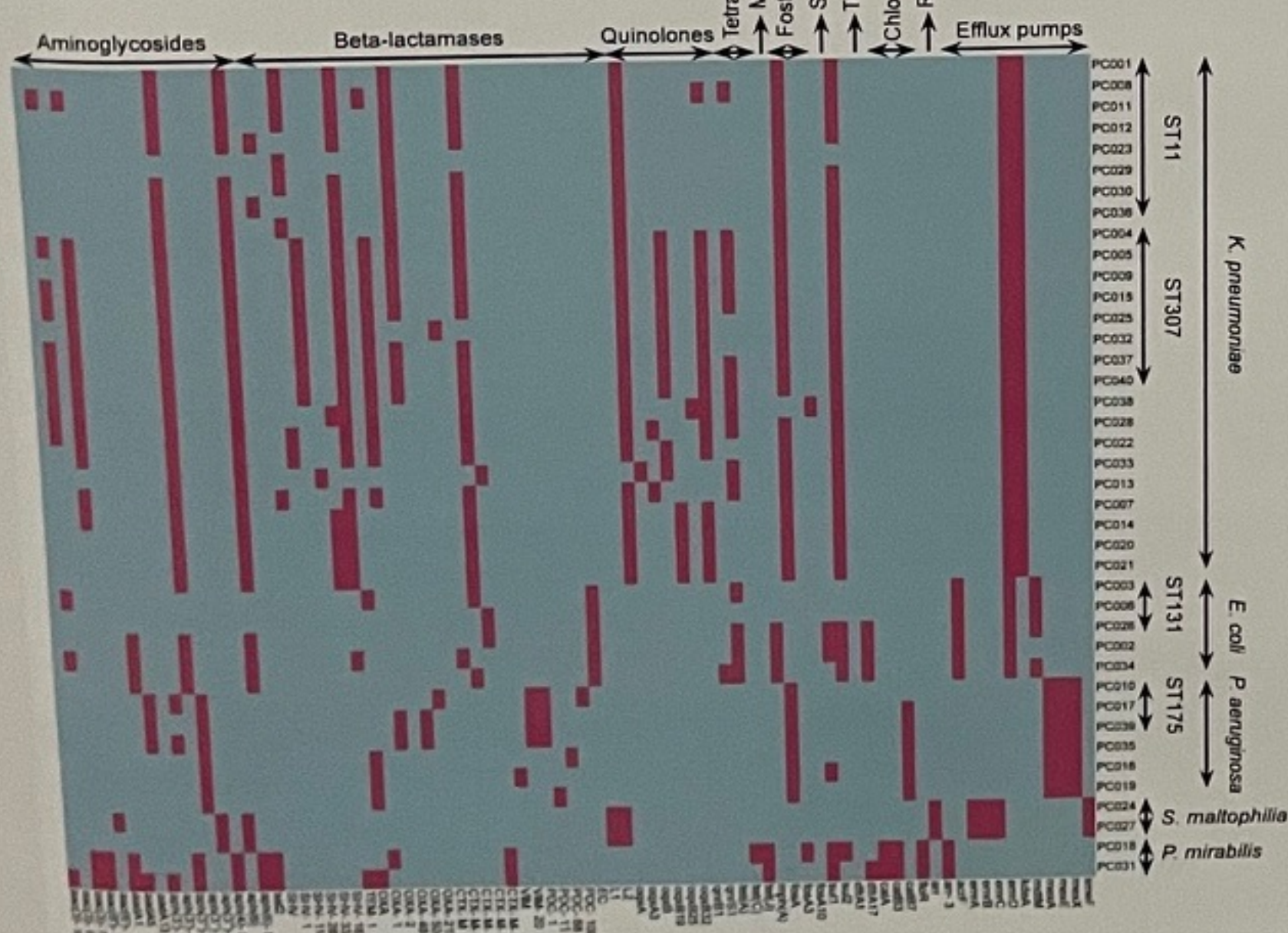


Taxonomy & annotation

RESULTS & CONCLUSIONS

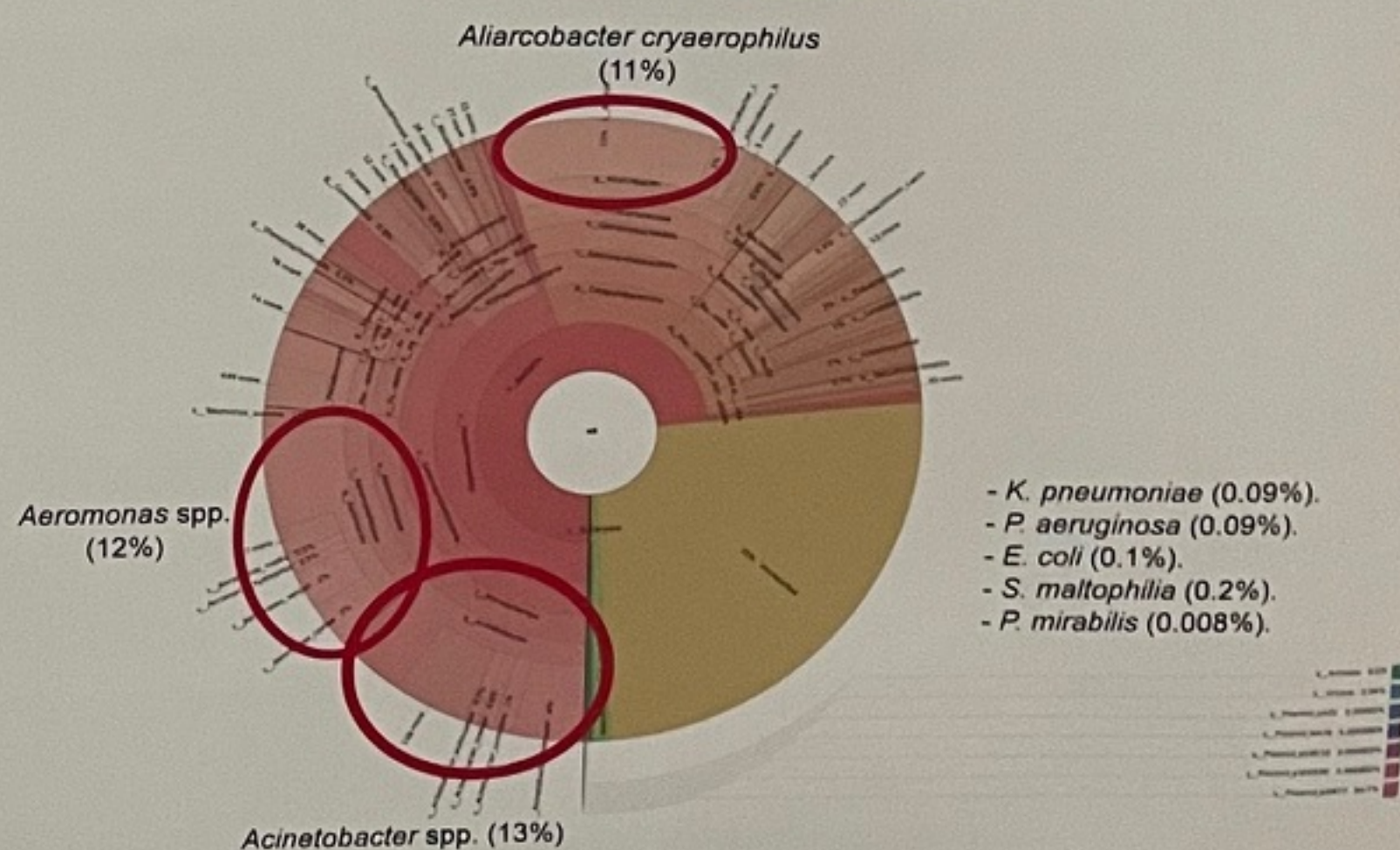
Clinical isolates

Wastewater



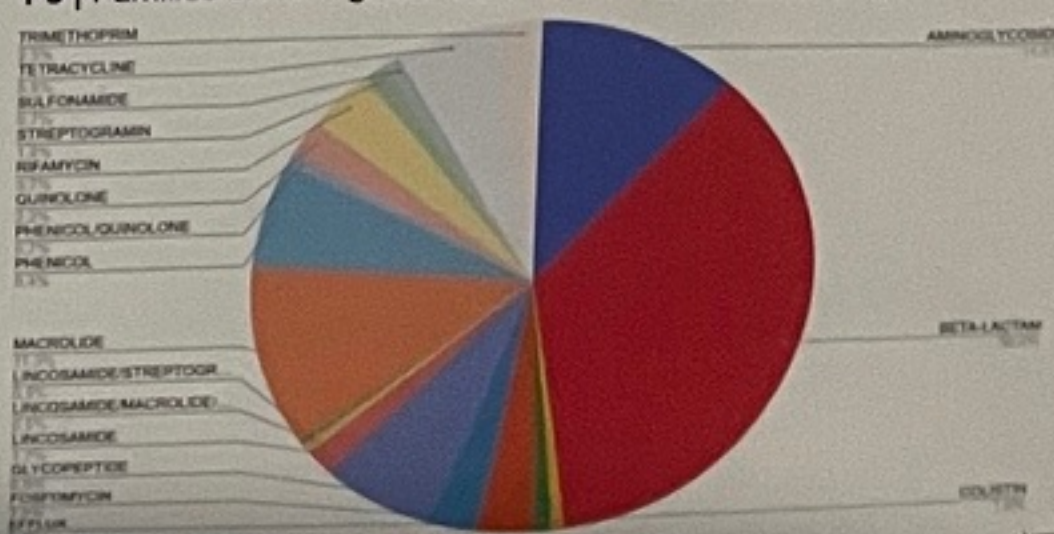
F1 | AMR genes detected (pink) in clinical isolates. The species and the main STs are highlighted in the right side, and the antibiotic families on the top.

- Hospital wastewater surveillance is powerful to detect AMR bacteria from both clinical and environmental sources.
- There were AMR bacteria from other sources (healthy people, biofilms...) in the water sample.
- Beta-lactamases were dominant both in clinical and environmental samples.
- As the project progresses, we will be able to depict the evolution and spreading of AMR.



F2 | Microbial taxonomy in the wastewater sample. The three top species and/or genera are highlighted. The percentage of the clinical species included in the dataset are also reported.

F3 | Families of AMR genes found in the wastewater sample.



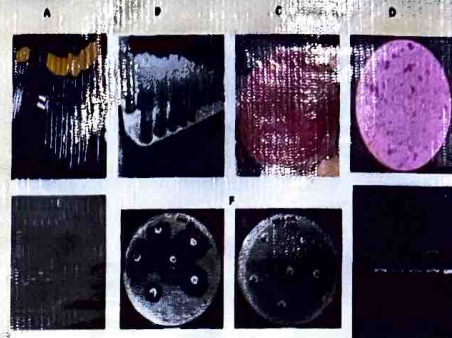
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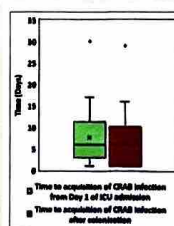
- All adult patients admitted to the interdisciplinary ICU had swabs sampled from the oral cavity, axilla, antecubital fossa and inguinal folds at regular intervals throughout the ICU stay.
- High-touch environmental surfaces (HITES) were randomly sampled around the patient's vicinity.
- Colonisation proportion, colonisation pressure, and incidence densities were recorded.
- The clonal relatedness of CRAB recovered from surveillance cultures and subsequent infection was determined by random amplified polymorphic DNA (RAPD) PCR assay using M13 universal primers.
- Sequence-based typing (SBT) of the blaOXA-51-like gene was performed on a subset of strains.



- A- Surveillance samples collected using viscose swabs.
- B- Inoculation of swabs into enrichment broth for increased recovery of colonizers.
- C- Isolation of bacteria from the surveillance cultures on MacConkey Agar.
- D- Preliminary identification by Gram Staining method.
- E- Molecular identification of *Acinetobacter* species.
- F- Antimicrobial susceptibility testing by Kirby-Bauer's Disk diffusion method for *A. baumannii*.
- G- RAPD PCR analysis showing DNA fingerprints of multiple *A. baumannii* strains.

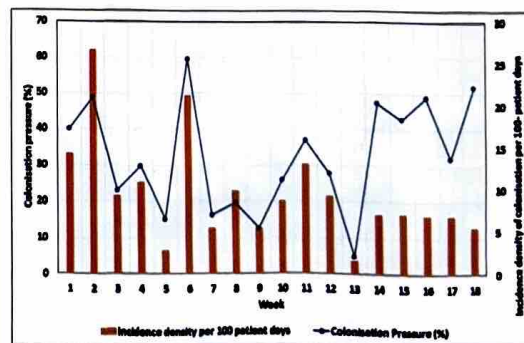
CHARTS AND FIGURES

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- ```
graph TD; A[235 patients
Study cohort] --> B[93 patients (39.57%)
Colonised by
A. baumannii]; B --> C[72 patients (77.41%)
Imported Carriers]; B --> D[21 patients (22.58%)
Acquired carriers]; C --> E[23 patients (31.94%)
Acquired A.
baumannii infection]; C --> F[49 patients (67.97%)
Not infected]; D --> G[3 patients (14.28%)
Acquired A.
baumannii infection]; D --> H[18 patients (85.71%)
Not infected]
```
- 235 patients**  
**Study cohort**
- 93 patients (39.57%)**  
**Colonised by**  
***A. baumannii***
- 72 patients (77.41%)**  
**Imported Carriers**
- 21 patients (22.58%)**  
**Acquired carriers**
- 23 patients (31.94%)**  
**Acquired *A.***  
***baumannii* infection**
- 49 patients (67.97%)**  
**Not infected**
- 3 patients (14.28%)**  
**Acquired *A.***  
***baumannii* infection**
- 18 patients (85.71%)**  
**Not infected**



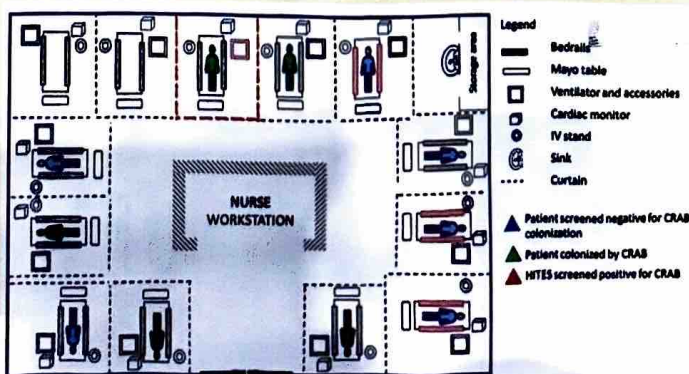
**Colonization proportion of *A. baumannii* on various body sites**

| Body Site         | Colonization Proportion (%) |
|-------------------|-----------------------------|
| Inguinal folds    | 3.94                        |
| Antecubital fossa | 13.15                       |
| Axilla            | 7.89                        |
| Oral Cavity       | 18.5                        |



- Oral colonization of *A. baumannii* is a growing concern in ICUs; the morbidity and mortality of infections caused by them are high. <sup>34</sup>
- High colonization pressure by CRAB calls for an extensive approach towards infection control and prevention measures.
- Due to the dynamics of pathogen dissemination, interventions to control CRAB may need to be expanded beyond a single unit and may require a more comprehensive evaluation of other units.
- Future work should be focused on translating clinical and epidemiological data in conjunction with genomics to better understand the short-term dynamics of *A. baumannii* transmission within the hospital.

**Schematic representation of the ICU illustrating the patients and the HITES screened for CRAB**



We are grateful to the Lady Tata Memorial Trust, Mumbai for providing Ph.D. fellowship to MT.

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# Post-antibiotic risk for recurrent lower respiratory tract infection during prolonged hospitalization

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## Background

- Hospital-acquired pneumonia (HAP) and ventilator-associated pneumonia (VAP) are common complications of hospitalization that cause significant morbidity and mortality<sup>1,2</sup>.
- HAP treatment failure, typically defined by lack for clinical response to initial antibiotic therapy, has been reported in as many as 20% of cases<sup>3</sup>.

## Knowledge Gap

- Late, post-antibiotic HAP/VAP recurrences may have increased risk for multidrug-resistant organisms (MDROs), but their incidence and features are not well defined.
- We sought to define the temporal patterns and risk factors for recurrent, post-antibiotic HAP/VAP, in order to inform targeted infection prevention interventions.

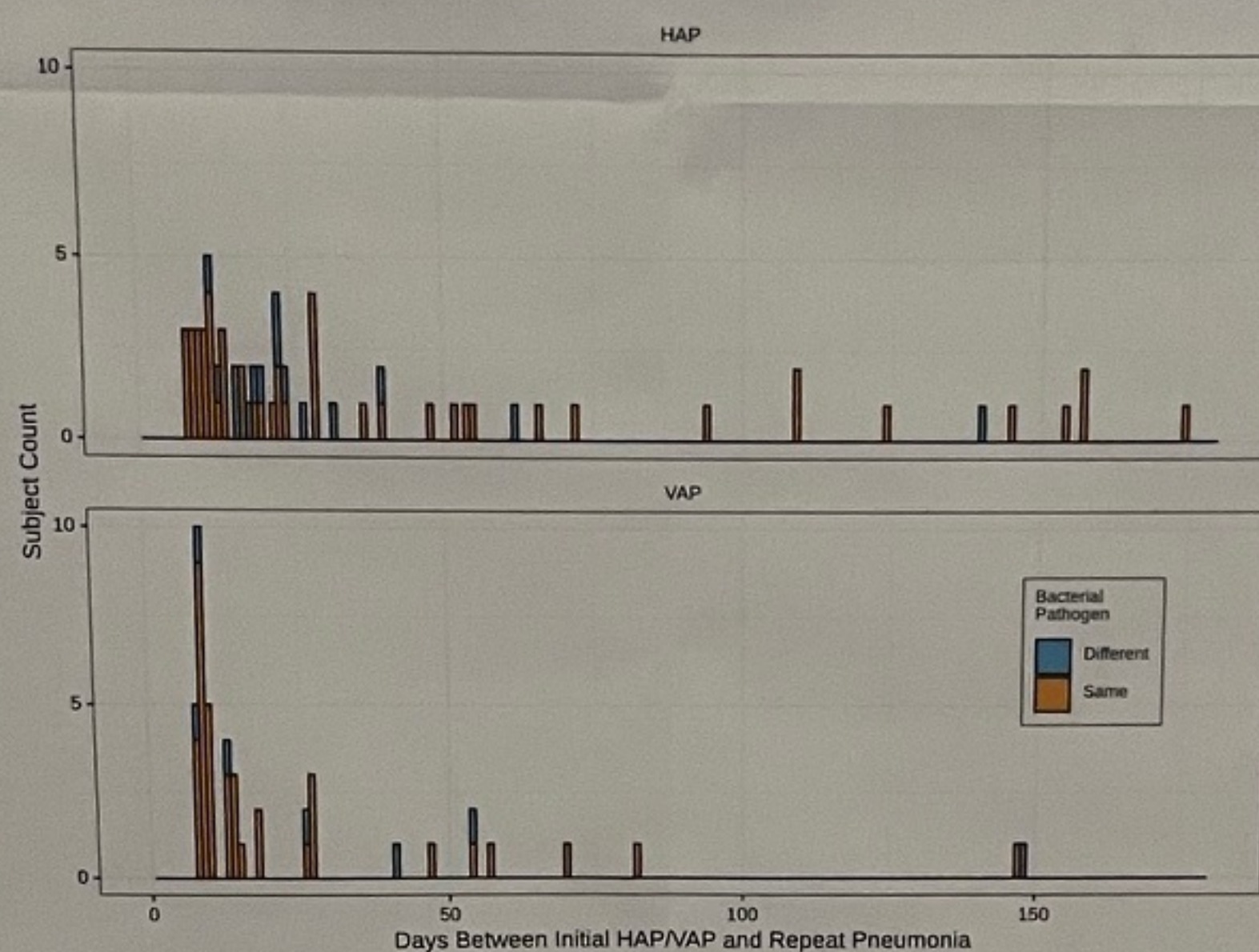
## Methods

- We performed a retrospective cohort study at the Hospital of the University of Pennsylvania in Philadelphia, PA, USA (IRB #850502). We identified a source cohort at high risk for HAP/VAP on the basis of their admission diagnoses and bed location.
- We obtained demographic, medical history, medication (including antibiotic), and microbiology data from all subjects, drawing on a comprehensive electronic health record. HAP/VAP events were adjudicated on the basis of clinical documentation and microbiology.
- Data were organized using R statistical software version 4.3.2 and plots generated using the "ggplot2" package. Hierarchical generalized additive (hGAM) models were fit using Stan Hamiltonian Monte Carlo (HMC) version 2.34.1, via "cmdstanr" and "brms".

## Study Population

- We identified 7002 high-risk patients admitted to the Hospital of the University of Pennsylvania over a five-year study period, among whom we found 515 HAP/VAP cases. 351 subjects had culture-positive HAP, and 164 subjects had culture-positive VAP.
- From these index HAP/VAP cases, we identified 108 recurrent HAP/VAP cases (20%) between 7 and 180 days after index HAP/VAP diagnosis.

## Results: New & Persistent HAP/VAP Pathogens

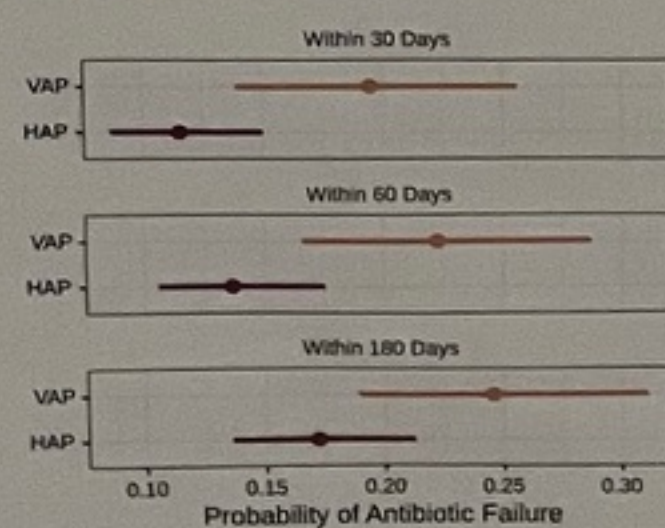


- Of 108 observed late HAP/VAP recurrences, 86 (79.6%) were attributed to the same bacterial pathogen, and 22 (20.4%) were attributed to a different bacterial pathogen.

## Conclusions

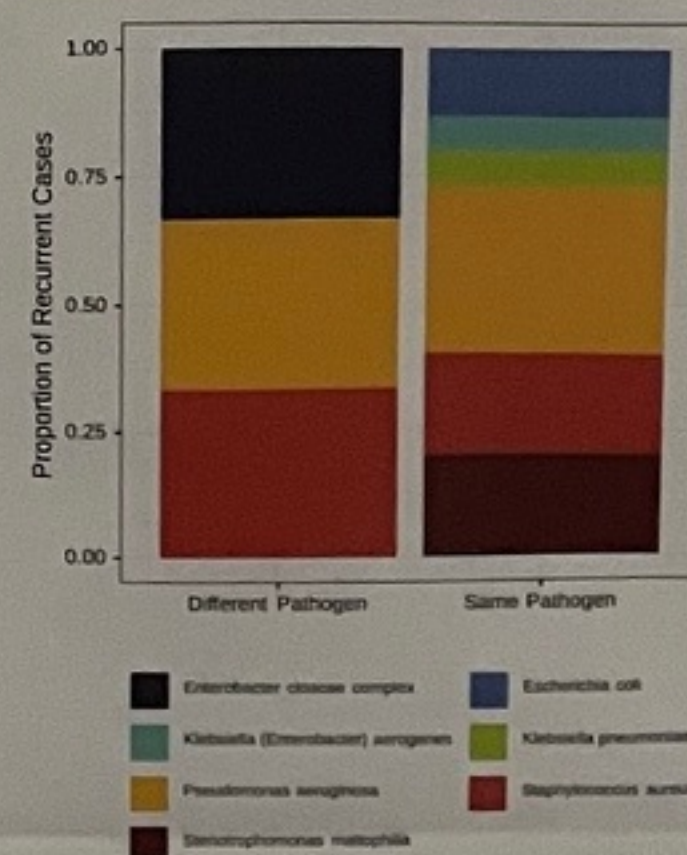
- In a high-risk cohort with prolonged hospitalization, we observed a late HAP/VAP recurrence rate of 20%, with 79.6% of late HAP/VAP recurrences attributed to the same bacterial pathogen.
- Pseudomonas aeruginosa* accounted for the largest proportion of same-pathogen recurrences and matched other bacteria in its association with different-pathogen HAP/VAP episodes. *Pseudomonas aeruginosa* was also observed to recur over the largest time window, likely reflecting its capacity for persistent colonization in high-risk populations.
- The observed late recurrences of HAP/VAP point to the need to better understand post-antibiotic respiratory microbiome changes that may contribute to pathogen persistence and/or new bacterial pathogen colonization. Temporal analysis of HAP/VAP recurrence may point to high-risk periods that could benefit from targeted infection prevention interventions.

## Results: Time & Risk of HAP/VAP Recurrence



- We evaluated the effect of time post index HAP/VAP on the binomial probability of recurrent infection, identifying greater risk of recurrent VAP than HAP at 30-, 60- and 180 days.
- VAP recurrence risk was 19.5% (95% CrI 13.9% to 25.6%), 22.2% (95% CrI 16.6% to 28.7%), and 24.6% (95% CrI 18.9% to 21.1%) at 30-, 60-, and 90-days respectively.
- HAP recurrence risk was 11.6% (95% CrI 8.7% to 15.0%), 13.7% (95% CrI 10.6% to 17.5%), and 17.2% (95% CrI 13.6% to 21.3%) at 30-, 60-, and 90-days respectively.
- In our cohort, the greatest risk of late recurrent HAP/VAP was observed around 33 days (95% CrI 20 to 49 days) after index HAP/VAP diagnosis. The gap between HAP/VAP episodes was not significantly different between same-pathogen and different-pathogen groups.

## Results: Pathogen Features & Late HAP/VAP Recurrence



- We observed recurrent HAP/VAP cases attributable to *Pseudomonas aeruginosa* (33.3%), *Staphylococcus aureus* (20%), *Stenotrophomonas maltophilia* (20%), *Escherichia coli* (13.3%), *Klebsiella pneumoniae* (6.7%), and *Klebsiella (Enterobacter) aerogenes* (6.7%). Time to recurrent infection did not differ significantly across index pathogens in this cohort; *Pseudomonas aeruginosa* recurrence was observed across the widest time range (median 14 days, 95% CrI 9.3 to 54.7 days).
- The cases of late recurrent HAP/VAP that were attributed to a pathogen different from the index HAP/VAP pathogen were attributed to *Pseudomonas aeruginosa*, *Staphylococcus aureus*, or *Enterobacter cloacae* complex.

## References

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microbiome  
transmission  
lab

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# Aircraft lavatory wastewater surveillance for SARS-CoV-2 and other coronaviruses by using family-wide RT-PCR, Thailand, October – November 2023

LB076



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## Background

- Establishing a globally equitable aircraft-based wastewater genomic surveillance system is imperative to effectively monitor the dissemination of the SARS-CoV-2 variant and other pathogens such as enteric viruses; Coronaviruses (CoV), Enteroviruses, Adenovirus, Caliciviruses and Rotaviruses etc.
- We conducted the surveillance of lavatory wastewater in aircrafts to identify other coronaviruses beyond SARS-CoV-2.

## Methods

- We collected lavatory wastewater from aircraft by port health officers between October and November 2023 at BKK Suvarnabhumi Airport.
- Lavatory wastewater samples were stored at 4 degrees Celsius and sent to lab centre within 48 hours.
- Three PCR protocols, including SARS-CoV-2 Real-time PCR and two pan-CoV PCR protocols, including Quan pan-CoV vs Xui pan-CoV PCR protocols, were used to compare sensitivity and specificity.
- We aimed to test 4 common human CoVs (229E, NL63, OC43, and HKU1) and 3 emerging CoVs (MERS-CoV, SARS-CoV, and SARS-CoV-2) in one PCR tube using family-wide PCR concept.

## Results

- A total of 40 lavatory wastewater samples from 20 flights were collected.
- The flights were from 19 cities in 17 countries.
- There were from the Middle East (2), Africa (1), Australia (1), Asia (8), and Europe (8).
- Thirteen (13) of 40 samples (32.5%) were SARS-CoV-2 positive tested by real-time PCR.
- Which four of them (10%) positive by Xui's pan-CoVPCR, but not by Quan's pan-CoV PCR protocol.
- However, 5 samples were positive for HCoV 229E and 2 samples were positive HCoV OC43 by Quan's protocol.
- Multiple pathogens were detected in 5 samples.
- Xui's pan-CoV PCR protocol is more sensitive than Quan's protocol for the detection of SARS-CoV-2, but Quan's protocol showed better sensitivity for the detection of HCoV 229E and OC43.



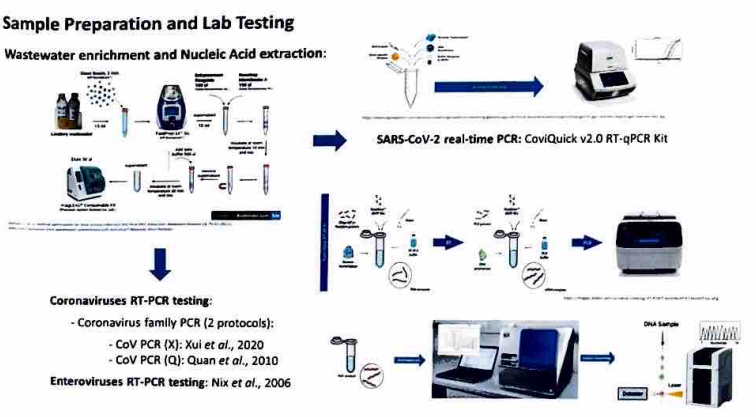
| Table 1. Consensus PCR results by Xui-CoV and Quan-CoV of aircraft lavatory wastewater samples from each departure city |               |                  |                                    |                           |                          |               |
|-------------------------------------------------------------------------------------------------------------------------|---------------|------------------|------------------------------------|---------------------------|--------------------------|---------------|
| Original country                                                                                                        | No. of flight | Tested specimens | SARS-CoV-2 Real-time PCR (no. / %) | Quan's protocol (no. / %) | Xui's protocol (no. / %) | Protocol      |
| Addis Ababa, Ethiopia                                                                                                   | 278           | 2                | Not detected                       |                           |                          |               |
| Singapore, Singapore                                                                                                    | 278           | 2                | Not detected                       |                           |                          |               |
| Seoul, South Korea                                                                                                      | 338           | 2                | Not detected                       |                           |                          |               |
| Xiamen, China                                                                                                           | 172           | 2                | Not detected                       |                           |                          |               |
| Taipei, China                                                                                                           | 263           | 2                | Not detected                       |                           |                          |               |
| Kuala Lumpur, Malaysia                                                                                                  | 264           | 2                | Detected (2)                       |                           |                          | SARS-CoV-2    |
| Tokyo, Japan                                                                                                            | 294           | 2                | Not detected                       |                           |                          |               |
| Hanoi, Vietnam                                                                                                          | 348           | 2                | Not detected                       |                           |                          |               |
| Sydney, Australia                                                                                                       | 287           | 2                | Detected (2)                       |                           |                          | HCoV 229E (1) |
| London, United Kingdom                                                                                                  | 348           | 2                | Not detected                       |                           |                          |               |
| Amsterdam, Netherlands                                                                                                  | 370           | 2                | Not detected                       |                           |                          |               |
| Paris, France                                                                                                           | 286           | 2                | Not detected                       |                           |                          |               |
| Moscow, Russia                                                                                                          | 286           | 2                | Detected (2)                       |                           |                          | HCoV OC43 (2) |
| Frankfurt, Germany                                                                                                      | 314           | 2                | Detected (2)                       |                           |                          | HCoV 229E (1) |
| Zurich, Switzerland                                                                                                     | 365           | 2                | Detected (2)                       |                           |                          | HCoV 229E (1) |
| Kuwait City, Kuwait                                                                                                     | 258           | 2                | Not detected                       |                           |                          |               |

## Conclusions

- Not only was SARS-CoV-2 detectable in aircraft lavatory wastewater samples, but there was successfully identified other coronaviruses such as HCoV 229E and HCoV OC43 by using family and genus-specific PCR.
- It plays a crucial role in implementing surveillance of novel coronavirus pandemics in the future, particularly MERS coronavirus.
- Family- and genus-specific PCR concept is also the alternative approach for detecting multiple viruses in one assay from aircraft wastewater.

## Acknowledgements

- We thank you all Port Health officers and airlines staff to assist the working.
- We also thank iPHAC-IDC programme led by EIDCC TRC, Chulalongkorn University to support the funding for working and travel funds.





# Transmission of Multidrug-Resistant Organisms (MDROs) during Physical and Occupational Therapy Appointments at 3 Veteran Affairs (VA) Nursing Homes (NHs)

P3281

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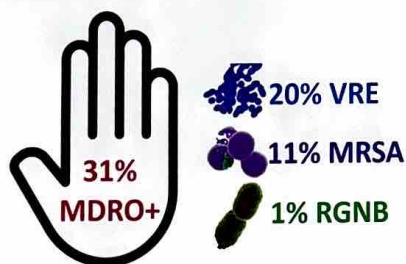
## Background

Older adults frequently require post-hospital rehabilitation at nursing home (NH) facilities. We characterize multidrug-resistant organism (MDRO) transmission on patient hands and equipment used during physical therapy (PT) and occupational therapy (OT) appointments.

## Methods

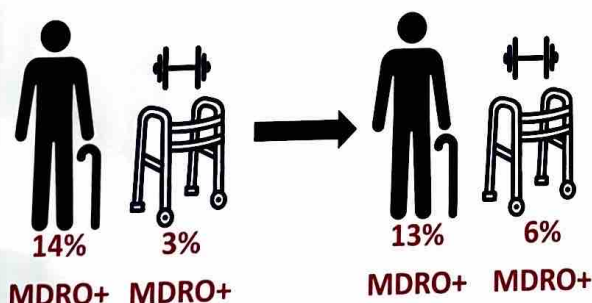
- 3 VA nursing homes (April '21-Sept '23)
- 2003 surveillance swabs collected during PT/OT appointments (n=105 patients)
- Tested for methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant *Enterococcus* (VRE), and resistant gram-negative bacteria (R-GNB)

Figure 1. Patient hand colonization during PT/OT



31% of NH patients had at least one MDRO on their hand during PT/OT.

Figure 2. MDRO contamination at appointment start (left) vs. appointment end (right)



Twice as many surfaces were MDRO-positive at end of PT/OT compared to the session start (6% vs 3%,  $p < 0.001$ ).

Figure 3a. Patient hand and surface contamination during PT/OT sessions in the patient's room/hallway

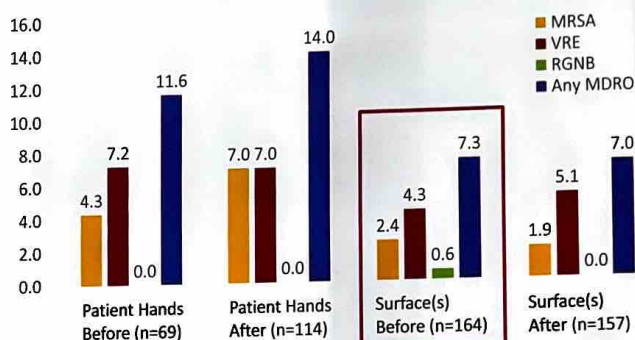
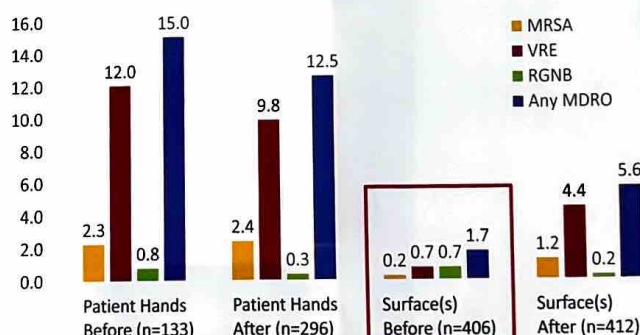


Figure 3b. Patient hand and surface contamination during PT/OT sessions in the therapy gym



MDRO contamination on surfaces is high when PT/OT occurs in patient's rooms compared to off-unit gym (7% vs 2%,  $p < 0.001$ ).

- Nursing home patients often arrived to therapy with MDRO-colonized hands.
- Portable equipment was more commonly contaminated than stationary equipment.
- Interventions to reduce patient hand contamination can reduce MDRO transmission.

**Limitations:** Lack of generalizability (3 VAs out of 132 across the U.S.); Uneven recruitment and visit frequencies across 3 sites; Cleaning of equipment not recorded.

34th **ECCMID** EUROPEAN CONGRESS OF CLINICAL MICROBIOLOGY AND INFECTIOUS DISEASES

Barcelona, Spain  
27 – 30 April 2024



# Enhancing feedback and implementation of infection risk scan (IRIS) findings among healthcare workers in nursing homes.

P3456

Amphia

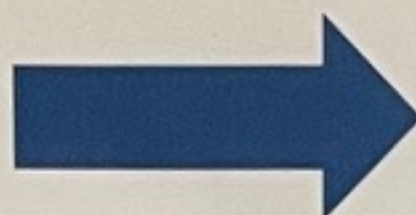
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## KEY FINDINGS

- Utilization of visual representation
- Engagement of Visual representation
- Sustained improvement
- Transparency and motivation



This study demonstrate that the IRIS method is a valuable tool for enhancing the quality of infection prevention in nursing homes, The key finding is that the feedback from the spider plot does not yield the desired results in the workplace, but simplifying the layout does provide clarity.

## Background

The Infection Risk Scan (IRIS) evaluates infection prevention programs in nursing homes, focusing on key parameters such as spread of Enterobacteriales ESBL, environmental contamination, hygiene protocols, and more. It was initially used mainly by management, limiting its impact on actual improvements.

## Objective

Does changing the visualization of the IRIS results make health professionals more actively involved in their role? Does an adapted way in which the findings of the IRIS scan are presented result in a higher level of involvement and participation of healthcare professionals?

## Methods

In an effort to boost improvement efforts, the presentation of IRIS findings now includes visually appealing posters with color-coded results (red, orange and green) alongside accompanying photos that highlight areas for improvement, in addition to the standard feedback from the spider plot, as shown in Figure 1.

## Results

While reports were discussed at management levels, posters with visual results were shared and discussed with healthcare teams (on care floors). These areas for improvement, figure 2, displayed prominently, effectively identified improvement areas. A follow-up of the improvement areas after six months showed proactive efforts by healthcare teams in addressing identified shortcomings.

## Conclusions

A clear and concise feedback loop is essential for healthcare workers to effectively engage with IRIS scan data. This enables them to comprehend the information and feel empowered to take action. With improved feedback, individuals are more motivated to make enhancements, leading to active participation in quality improvement efforts. This ultimately enhances patient care and organizational performance.

Figure 1:

an example of the conventional presentation of IRIS findings used to provide feedback to nursing homes

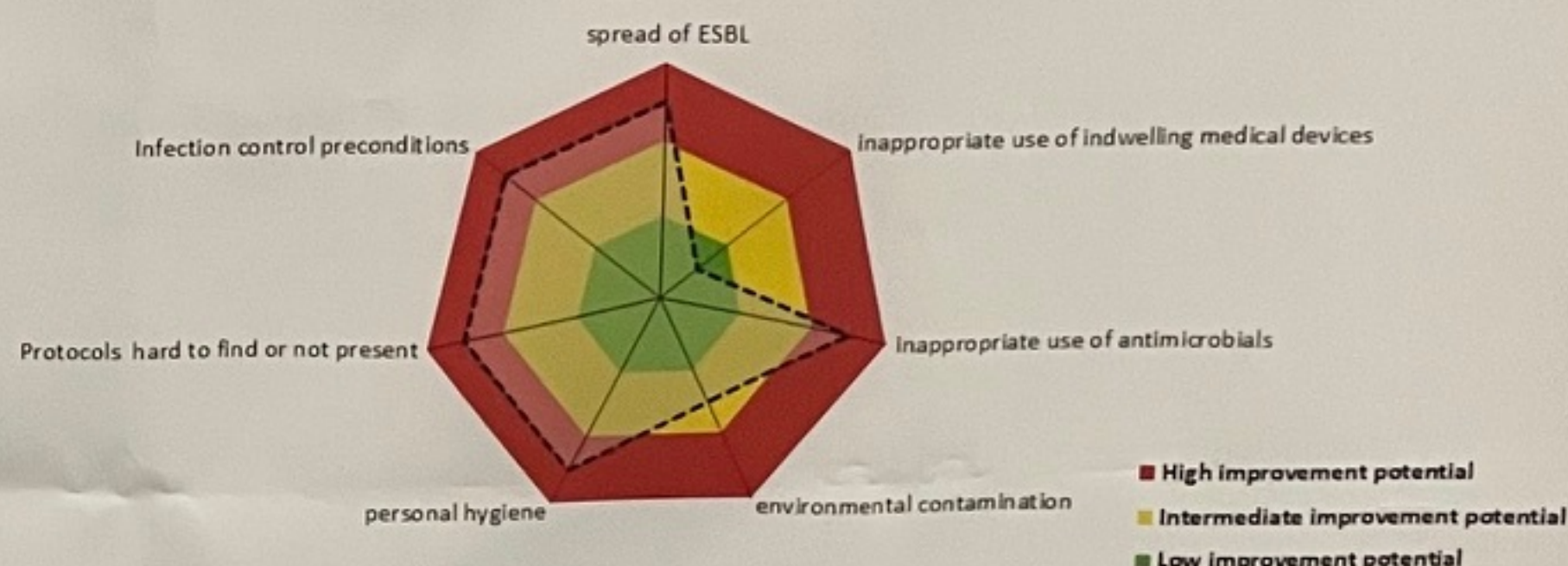


Figure 2:

an example of a customized poster for the healthcare teams on the care floor



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Barcelona, Spain  
27 – 30 April 2024



# Proper glove use: a multicentre before-after regional de-implementation study

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on behalf of the "Goed Gebruik Handschoenen" study group of the Infection Prevention and Antimicrobial Resistance Care Network South-western Netherlands

## Background

In healthcare, a substantial number of **disposable non-sterile gloves** are used. However, their use is often inappropriate or incorrect. This poses several risks: firstly, there is an increased potential for spreading microorganisms, secondly, it can cause dermatological problems, and thirdly, it produces unnecessary waste and costs.

## Results

The modified version of the **COM-B** questionnaire was filled out by 1,111 participants across 13 healthcare centres (8 different hospitals and 5 different nursing homes), between December 2021 and June 2022. Most of the participants were nurses (53%). **Opportunity** scored lowest, and **behaviour** scored highest (Figure). This did not differ between hospitals and nursing homes.

**1550** pre-intervention **observations** (between December 2021 and September 2022) were performed by 15 healthcare centres (10 hospitals and 5 nursing homes), **940** post-intervention observations (between December 2021 and December 2022) were performed by 6 healthcare centres (5 hospitals and 1 nursing home) (Table), showing a significant decrease in unnecessary glove use by HCW (*P* value 0.017).



Procurement glove statistics from 2019 and 2022 were compared for 3 healthcare centres, resulting in a significant decrease in one (*P* value <0.001). Procurement statistics from 2020 and 2021 were not reliable due to the COVID-19 pandemic.

## Aim

1. Gain insights into healthcare workers (HCW) **perspectives** on glove use and misuse.
2. Evaluate if a **behaviour change** was achieved through an intervention, shown as a reduction in inappropriate and incorrect glove use.
3. If the introduction of the intervention resulted in a **reduced use of gloves**.

## Key findings

Preliminary results indicate the **need for targeted interventions** to address issues related to the opportunity to correctly wear gloves.

While incorrect use is notably high, it is noteworthy that after the intervention incorrect use of gloves was significantly decreased.

Figure. Results of the COM-B questionnaire; n=1,111 healthcare workers.

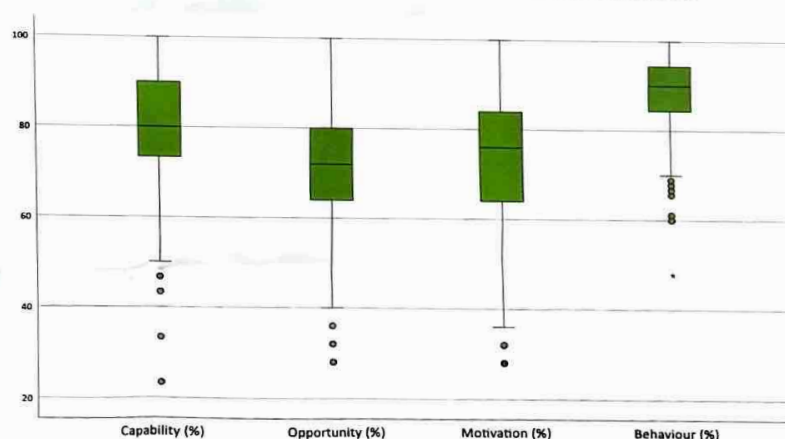


Table. Results of the observations of healthcare workers before and after the introduction of the intervention.

|                            | Before<br>n=1550 (%) | After<br>n=940 (%) |
|----------------------------|----------------------|--------------------|
| HCW should wear gloves     | 818                  | 445 <sup>1</sup>   |
| HCW wears gloves           | 755 (92.3)           | 416 (93.5)         |
| HCW does not wear gloves   | 63 (7.7)             | 29 (6.5)           |
| HCW should not wear gloves | 732                  | 492 <sup>1</sup>   |
| HCW wears gloves           | 310 (42.3)           | 175 (35.6)*        |
| HCW does not wear gloves   | 422 (57.7)           | 317 (64.4)         |
| HCW wears gloves           | 1057                 | 590 <sup>2</sup>   |
| Correct                    | 409 (38.7)           | 243 (41.2)         |
| Incorrect                  | 648 (61.3)           | 347 (58.8)         |

Abbreviations: HCW; healthcare worker, n; number. <sup>1</sup>For 3 HCW information about whether the HCW should wear gloves was missing. <sup>2</sup>For four HCW information about correct use was missing. \*statistically significant, *P* value 0.017

## Methods

- A **multicentre before-after study** was conducted in the South-western region of the Netherlands.
- Healthcare centres could express interest in participation through a kick-off meeting in March 2021.
- A regional policy about glove use was formulated.
- Pre-intervention, a modified version of the **COM-B questionnaire** was distributed to HCW.
  - The **percentage** was calculated by dividing the score of a subscale by the maximum score that could be achieved for that subscale.
- The **intervention** comprised a toolbox sent to the participating healthcare centres. Participants could select fitting tools for implementation.
  - The toolbox included a.o. a videogame quiz, stickers for gloveboxes, and posters.
- The intervention also encompassed **HCW observations** regarding glove use; before and after the implementation of the selected tools.
- Procurement statistics** of gloves from 2019 to 2023 were gathered from participating healthcare centres.

