

#### FAIRFAX COUNTY HEALTH DEPARTMENT

# Surprised by Science:

The Role of Whole Genome Sequencing in Multi-Drug Resistant Organism Outbreak Management

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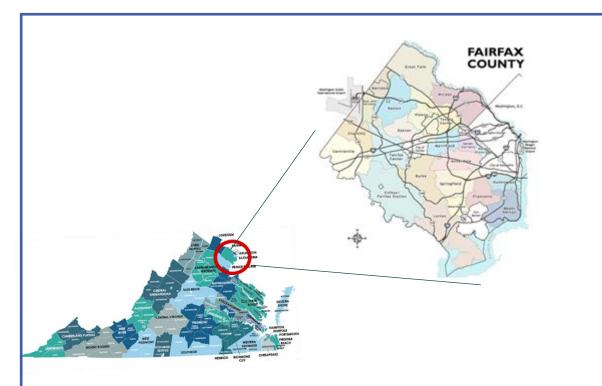
## **Objectives**

- Review the local health department's response to multiple cases of multidrug resistant organisms (MDROs) in high-risk facilities;
- Highlight the value of ongoing collaboration with facility leadership and the infection prevention and control team;
- Discuss the role of whole genome sequencing in MDRO investigations.



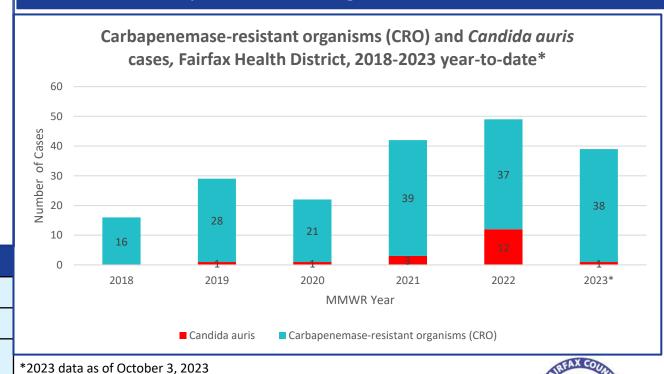


### **Fairfax Health District and MDROs**



Population	1.2 million
Acute Care Hospitals (ACH)	5
Long-term Acute Care Hospital (LTACH)	1
Skilled Nursing Facilities (SNFs)	15

Fairfax County Health Department (FCHD) has documented over a 50% increase in multi-drug resistant organisms (MDROs) since 2018 when these pathogens first became reportable in Virginia





## **Outbreak A: Acute Care Hospital**

- Enterobacter cloacae organism with KPC mechanism
- 126 high-risk contacts from two admissions (49 inpatient, 77 discharged)

KPC mechanism

5 high-risk contacts (2 inpatient, 3 discharged)



"2 Case #3

Case #4

- KPC mechanism
- 54 high-risk contacts (41 inpatient, 13 discharged)

- Enterobacter cloacae organism with KPC mechanism
- 16 high-risk contacts (13 inpatient, 3 discharged)





### **Case Medical Record Review**

High acuity patients

Lengthy hospital admissions

Multiple healthcare visits in months prior

Multiple invasive procedures

Multiple indwelling medical devices





### Investigation facilitated through close collaboration

#### Acute Care Hospital Infection Prevention Team

- Timely notification and quick action by IP staff
- Sharing of contact list
- Discussions with hospital IP staff
- Recommendations provided and actions taken

#### Fairfax Health District Skilled Nursing Facilities

Colonization screening of residents

#### State HAI AR Program

- Consultation and guidance on next steps
- Notification of contacts transferred outside of Fairfax Health District

#### Neighboring Local Health Districts

- Notification and coordination with high-risk facilities
- Public Health Laboratory Partners
  - Coordinating forwarding of specimens and consultation on results





### Whole Genome Sequencing Results

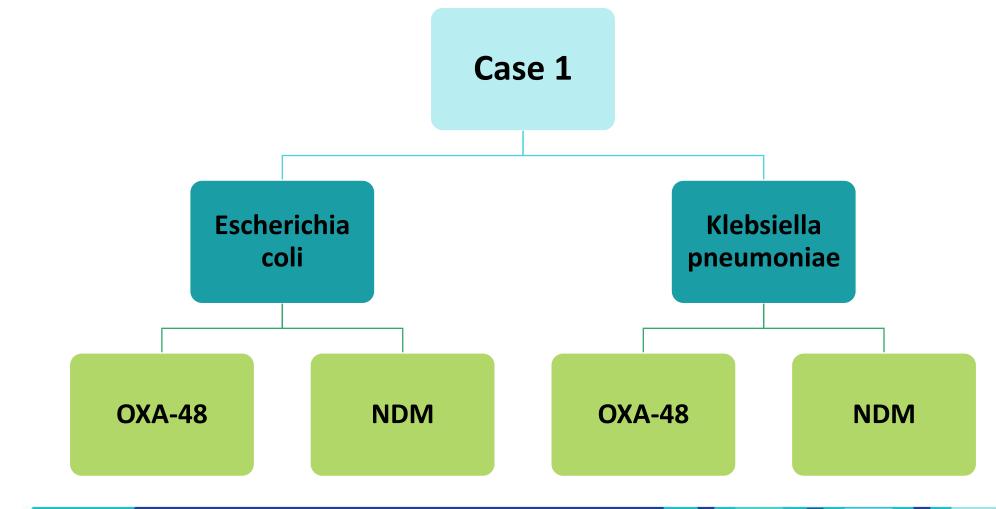
Dryad SNP	CASE 1	CASE 4
CASE 1		22
CASE 4	22	

- DCLS whole genome sequencing was completed on two samples.
  - Case 2 and 3 did not have isolates available for sequencing.
- DCLS Dryad testing results found the isolates to be 22 SNPs apart. Typically, ≤ 10 SNP differences suggest genetic relatedness.
- However, SNP differences greater than 10 can still be significant if isolates are further apart in time or there is an epidemiological link.





# **Outbreak B: Skilled Nursing Facility**



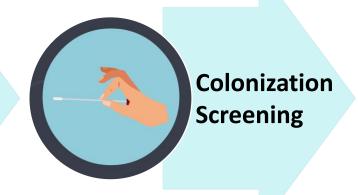




### **Skilled Nursing Facility Action Steps**





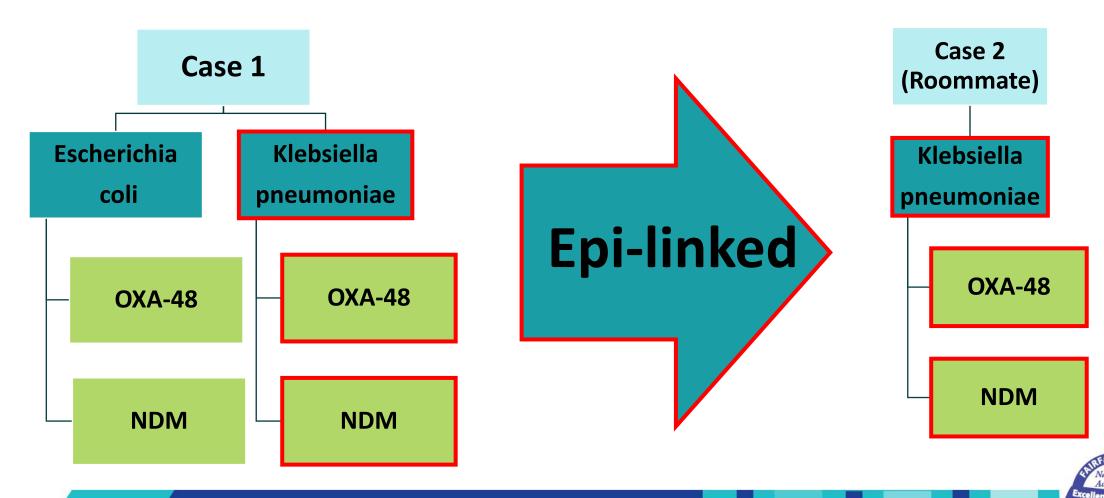


Roommates shared a semi-private room for 7 days.





### **Roommate's Test Results**





#### **SNF Reactive ICAR Recommendations**

PPS

 Point Prevalence Survey of unit: 17 residents consented to colonization screening and 6 residents declined screening

• 3<sup>rd</sup> resident was identified with NDM mechanism

**Nursing** 

Staff

Nursing staff education on hand hygiene and proper PPE donning & doffing

• Staff training on Enhanced Barrier Precautions vs. Contact Precautions

**EVS** 

**Staff** 

VDH Regional IP performed ATP testing of high touch surface areas

• Daily and terminal cleaning and disinfection procedures to EVS staff





## Whole Genome Sequencing Results

Dryad SNP	CASE 1	CASE 2	CASE 3
CASE 1		2	25738
CASE 2	2		25900
CASE 3	25738	25900	

- DCLS performed Single Nucleotide Polymorphism (SNP) comparison analysis
- Typically, ≤ 10 SNP differences suggest genetic relatedness





# **Antimicrobial Resistance Gene Summary**

Case	Specimen Source	Species ID	Resistance Genes
Index Case	Peritoneal Fluid	Klebsiella pneumoniae	OXA-181 (OXA-48-like), NDM-5
Roommate	Urine	Klebsiella pneumoniae	OXA-181 (OXA-48-like), NDM-5
Resident in Same Unit	Colonization Rectal Swab	Klebsiella pneumoniae	NDM-7

Resistance gene testing showed differences in NDM alleles between the two roommates and the colonized resident on the same unit.





#### Conclusion

- Infection Prevention and Control guidance was promptly provided based on information known at the time.
- Whole Genome Sequencing results were available after the outbreak investigations concluded and shed new light on both outbreaks.
  - The Acute Care Hospital results were too variable to confirm relatedness.
  - The Skilled Nursing Facility results decreased the outbreak from 3 to 2 cases.
- Are these results surprising?





## Acknowledgements

- Acute Care Hospital (A) Infection Prevention Team
- Division of Consolidated Laboratory Services (DCLS)
- Fairfax County Health Department
  - Division of Epidemiology and Population Health
  - Public Health Laboratory
- Maryland Antibiotic Resistance Laboratory Network (MD ARLN)
- Skilled Nursing Facility (B) Administration, Director of Nursing, Infection Preventionist, Unit Charge Nurses, Regional Infection Prevention Team
- Virginia Department of Health
  - Healthcare Associated Infections and Antibiotic Resistance (HAI AR) Program
  - Northern Virginia Regional Team







#### FAIRFAX COUNTY HEALTH DEPARTMENT

# Questions?

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