Background

- Mycobacterium avium Complex (MAC) are ubiquitous in the environment and are thought to be acquired by inhalation or ingestion.
- MAC presence in nature makes determining where an individual acquired his or her disease difficult to ascertain. It also may contain clinical cultures and may complicate clinical diagnosis.

Methods

- A retrospective case review of all patients with MAC cultures from two clusters (October – December 2016, March – May 2017) was conducted. Patient demographics, comorbidities, radiographic images and clinical details were analyzed.
- Microbiology laboratory practices were reviewed, including AFB smear, culture preparation and genetic probe identification.
- Reagents, stains and water sources were cultured and local laboratory and reagent manufacturers were contacted.

Results

- Only positive AFB growth is referred to the laboratory. No increase was seen in reference cultures, suggesting a contamination at culture set up rather than amplification processes.
- A cluster was identified with 22 isolates from October to December 2016.
- All AFB processing took place under one hood (culture and amplification).
- Positive cultures were sent for species identification by rpob gene sequencing.
- 59% of isolates were M.michaele following M.senegalense with 27%.
- Culture of PANTA™ reagent grew M. chimaera.
- A review of AFB cultures from past years showed a surge of cases during the months of October to November 2016, from the typical 1-3 cases per month as illustrated in figure 1 prompting an in-depth investigation of a possible pseudo-outbreak of MAC.

Conclusions

- Increased MAC cultures above baseline incidence should prompt an internal evaluation and audit of infection control practices.
- Early detection is essential for outbreak control and the early identification of possibly contaminated medical equipment or instruments. This improves patient management and aids public health responses.

- The pseudo-outbreak did not have clinical implication as patients that lacked clinical signs and symptoms were not treated. Additionally those with a clinical syndrome that might be consistent with MAC, were not functionally impaired and did not require treatment.
- The poly-microbial nature of the 2nd cluster of MAC cultures indicates water contamination as a possible source.
- Separation of amplification and culture preparation tasks both spatially and temporally were recommended to decrease cross contamination, but implemented after the second cluster.
- Identifying MAC to species level assisted in evaluating clinical significance and suggesting common sources.
- Additional studies are required to evaluate variability of M.chimaera in the region in regards to geographic sameness versus point source.
- Environmental cultures may aid in trying to determine true outbreak and emerging clinical pathology versus infection control lapses leading to a pseudo-outbreak.

References

(1) David E. Griffith, Timothy Aksamit Et Al ; An Official ATS/IDSA Statement: Diagnosis, Treatment, and Prevention of Nontuberculous Mycobacterial Diseases, AJCC 2007
(2) Salvatore D'Asto and Daniele Orsini, Et Al ; Non tuberculous mycobacteria (NTM) contamination in a hospital water supply network: Association with pulmonary infection in respiratory, ERJ 2015
(3) Ramil Sommerstein, Christian Rößger Et Al ; Transmission of Mycobacterium Chimaera From Heater–Cooler Units during Cardiac Surgery despite an Ultrasound Air Ventilation System , ERJ2016

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