Conclusion. In a large US inpatient sample, the causative organisms in immunocompromised patients did not differ much from those in immunocompetent patients. CAP pathogens in immunocompromised patients were more likely to involve gram-negative bacilli such as *P.aeruginosa* and *E.coli,* than gram-positive cocci. These findings may have implications when deciding on empiric therapy in these patients.

Disclosures. Abhishek Deshpande, MD, PhD, Ferring Pharmaceuticals (Advisor or Review Panel member)Merck (Consultant)

1485. Mobile Bedside Ultrasound (mBSUS) and Use of an Artificial Intelligence Algorithm for Diagnosis of Pediatric Pneumonia in Limited Resource Settings

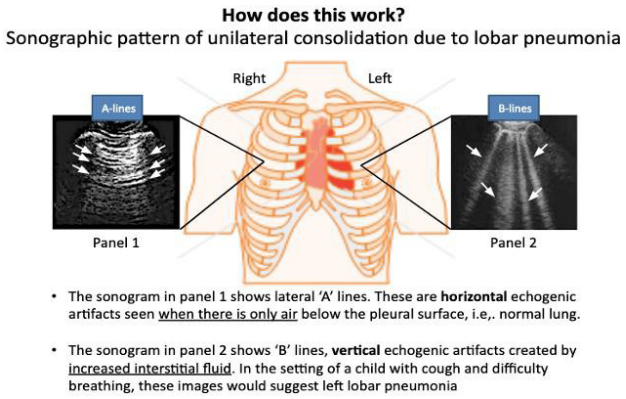
ingrid Y. Camelo, MD, MPH[1]; Christopher Gill, MD MS[2]; Rachel Pieciak, MPH[3]; [1]BMC, Boston, MA; [2]Boston U. School of Public Health, Boston, MA; [3]MPH, Boston, Massachusetts

Session: P-67. Respiratory Infections - Bacterial

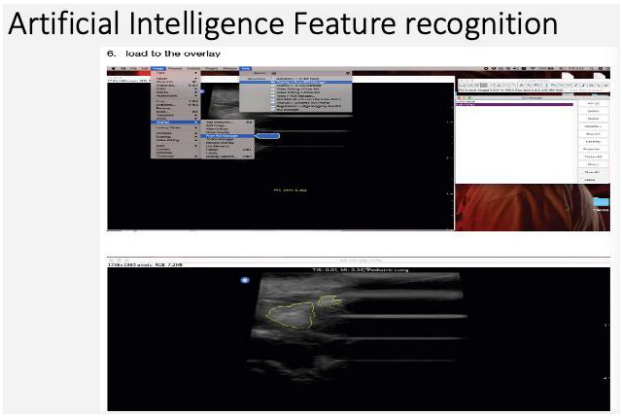
Background. In low and middle-income countries (LMICs) pneumonia is by far the leading cause of death among children < 5 years of age. A key factor is the challenge of pneumonia diagnosis. Chest X-Ray is the gold standard for pneumonia diagnoses but exposes children to ionizing radiation and is mainly restricted to hospital settings.

advances in artificial intelligence (AI) render possible the automated interpretation of mobile bedside US (mBSUS) images on a smartphone, obviating the need for a radiologist.

Ultraspund findings in pneumonia



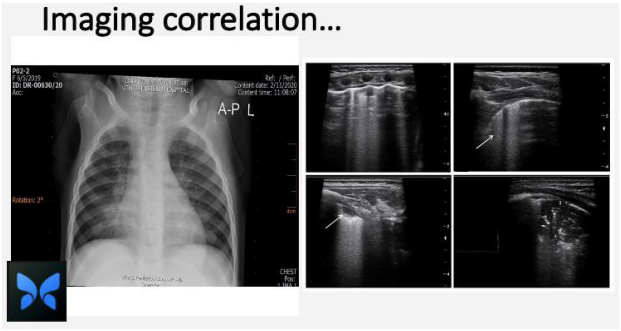
Artificial intelligence feature recognition



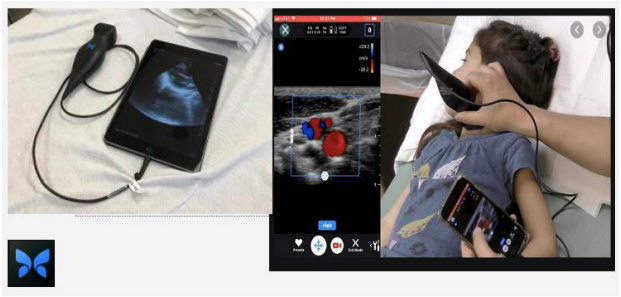
Methods. We measured the accuracy of mBSUS for the diagnosis of pneumonia using chest X-Ray as the gold standard. Children 1-59 mo presenting at the University Teaching Hospital in Lusaka, Zambia with ages ranging from aged 1-59 months and meeting WHO criteria for severe/very severe pneumonia were enrolled. Clinical data is collected in RedCap. Digital X-Rays were done at the University Teaching Hospital and saved as JPEG images. Pulmonary mBSUS images are taken using a butterfly, a mobile device system, and stored in the butterfly iCloud of the Butterfly app and transmitted to an iOS phone or tablet. Images are stored locally and saved to a secured/encrypted cloud platform for remote viewing with a HIPAA (Health Insurance Portability and Accountability Act) compliant secure cloud.

Images are currently extracted from the clips stored in the butterfly icloud, radiologists annotate the images that have abnormal findings and they are then sent to the AI lab where they are analyzed and organized to build a platform of similar images that could be recognized by the machine learning system.

Imaging correlation CXR Vs mobile bedside ultrasound mBSUS

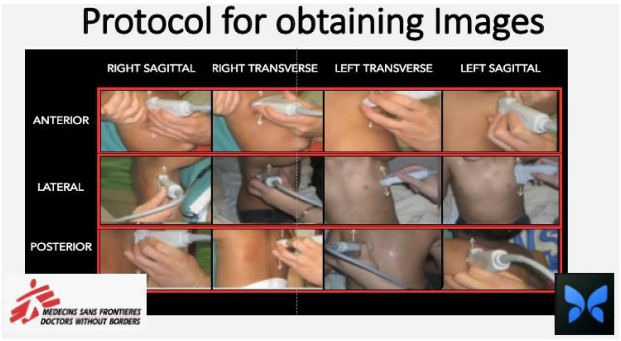


Butterfly ultrasound system



Results. Of the 11 patients enrolled so far, ll have been having ultrasound images that correlated with chest x-ray findings. In three of those patients, the ultrasound has shown pulmonary findings not recognized or hardly seen on chest x-ray. The artificial intelligence lab is developing a pull of images that will be used to recognize patterns of consolidation from mBSUS images.

Protocol fro obtaining images



Conclusion. Mobile pulmonary ultrasound mBSUS is a feasible, non radiation technique that could be used in limited-resource settings to diagnose pneumonia in children. Images obtained from mBSUS can be used to build a pattern of recognition based on consolidation findings.

Disclosures. **All Authors**: No reported disclosures

1486. Phylogenetic and alpha toxin variant analyses of *Staphylococcus aureus* strains isolated from patients during the SAATELLITE study

David E. Tabor, PhD[1]; Christine Tkaczyk, PhD[2]; Andrey Tovchigrechko, PhD[1]; Bret R. Sellman, PhD[1]; Michael McCarthy, n/a[1]; Pin Ren, PhD[1]; Kathryn Shoemaker, MS[1]; Hasan S. Jafri, MD, FAAP[1]; Bruno François, Physician[3]; Mark T. Esser, PhD[1]; Jasmine Coppens, Dr.[4]; Leen Timbermont, PhD[4]; Basil Xavier, PhD[4]; Christine Lammens, Bcs[5]; Herman Goossens, PhD[6]; Surbhi Malhotra-Kumar, PhD[7]; Alexey Ruzin, PhD[1]; [1]AstraZeneca, South San Francisco, California; [2]AstraZeneca BioPharmaceuticals R&D, Gaithersburg, Maryland; [3]CHU Limoges, Limoges, Limousin, France; [4]University of Antwerp, Wilrijk, Antwerpen, Belgium; [5]University Antwerp, Department of Medical Microbiology, Antwerp, Antwerpen, Belgium; [6]University of Antwerp, Antwerp, Antwerpen, Belgium, Antwerp, Antwerpen, Belgium; [7]Universiteit Antwerpen, Wilrijk, Antwerpen, Belgium

COMBACTE-SAATELLITE Study Group

Session: P-67. Respiratory Infections - Bacterial

Background. Suvratoxumab is a human monoclonal antibody that neutralizes *S. aureus* (SA) alpha toxin (AT). SAATELLITE, a phase 2 study of the safety and efficacy of suvratoxumab for reducing the incidence of SA pneumonia

(NCT02296320), was conducted within the consortium for Combatting Bacterial Resistance in Europe.

Methods. A total of 304 SA isolates (baseline, onset and last available isolates from suspected serious bacterial infections, SSBIs) collected from the lower respiratory tract samples from 165 subjects during SAATELLITE were subjected to whole genome sequencing.

AT gene (*hla*) sequences were translated and amino acid variation was identified in comparison to the reference SA USA300 FPR3757. Phylogenetic analysis, genomic annotation and ST analysis were performed.

AT expression in SA culture supernatants was performed by ELISA. Representative isolates with novel AT subtypes that had not been identified in previous studies were tested for hemolytic activity and suvratoxumab neutralizing activity.

Wilcoxon rank sum test and Fisher's exact test were performed, respectively: a) to compare difference in baseline AT expression in relation to SA pneumonia incidence; b) to evaluate the association between occurrence of AT stop codons and incidence of SA pneumonia at baseline, as well as the association between occurrence of AT stop codons and treatment arms at post baseline.

Results. We identified a total of 44 sequence types (STs) and 21 unique AT subtypes, 7 of which have not been described previously. No substitutions were located in the suvratoxumab binding region and all novel AT subtypes displaying lytic activity were neutralized by suvratoxumab.

We detected stop codons Q113B and W205B in AT sequences in 53 and 2 SA isolates, respectively. We uncovered no significant associations of: 1) baseline AT expression with SA pneumonia incidence [p=0.967]; 2) occurrence of AT gene stop codon with either SA pneumonia incidence [p >0.999] or suvratoxumab treatment [p=0.103; lower frequency of stop codons in suvratoxumab arm versus placebo].

Conclusion. Our data indicated that: 1) suvratoxumab target region in (AT) remains conserved; 2) suvratoxumab is active against all AT variants identified to date; 3) suvratoxumab did not exert pressure on SA clinical isolates for selection of escape mutants.

Disclosures. David E. Tabor, PhD, AstraZeneca (Employee, Shareholder) Andrey Tovchigrechko, PhD, AstraZeneca (Employee, Shareholder)KitePharma, a Gilead company (Employee, Shareholder) Bret R. Sellman, PhD, AstraZeneca (Employee, Shareholder) Michael McCarthy, n/a, AstraZeneca (Employee) Kathryn Shoemaker, MS, AstraZeneca (Employee) Hasan S. Jafri, MD, FAAP, AstraZeneca (Employee) Mark T. Esser, PhD, AstraZeneca (Employee) Alexey Ruzin, PhD, AstraZeneca (Employee, Shareholder)

1487. Pneumonia due to Co-Infection in the ICU: Detection and Clinical Significance

Casey S. Zelus, MD[1]; Michael Blaha[1]; Kaeli Samsom, MA, MPH[1]; Jasmine R. Marcelin, MD[1]; Trevor C. Van Schooneveld, MD, FACP[1]; Andre C. Kalil, MD, MPH[1]; Kelly Cawcutt, MD, MS[1]; [1]University of Nebraska Medical Center, Omaha, Nebraska

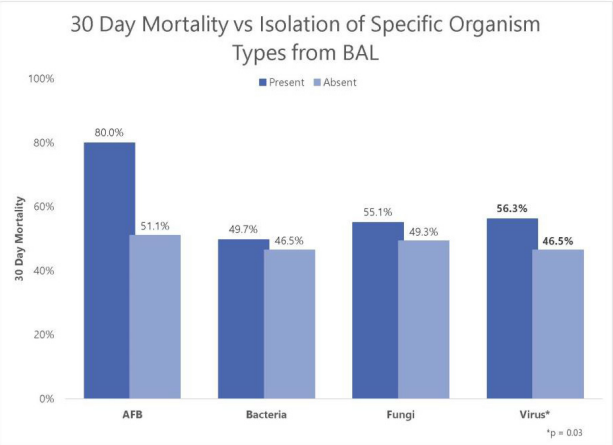
Session: P-67. Respiratory Infections - Bacterial

Background. Pneumonia is a significant cause of morbidity and mortality, with increasing interest in the detection and clinical significance of co-infection. However, the impact of methodology to obtain lower respiratory samples along with the utility of various microbiological diagnostic testing remains unclear.

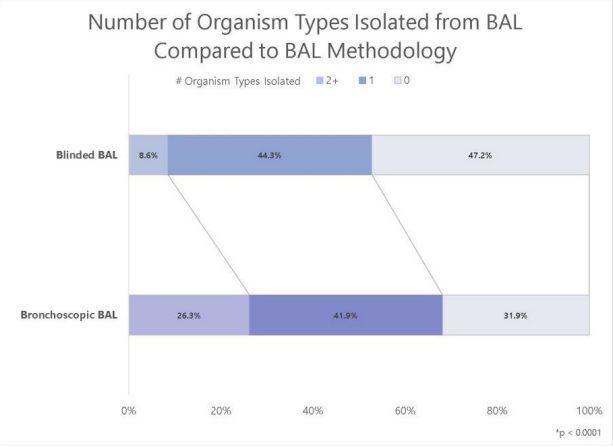
Methods. A single-center retrospective analysis was performed on bronchoalveolar lavage (BAL) samples obtained from mechanically ventilated adults treated in critical care units from August 2012 to December 2017. BAL methodology (bronchoscopic vs blinded), microbiological diagnostic testing, and outcomes measures were obtained. Associations between categorical variables were assessed using Chi-Square or Fisher's exact tests. Kruskal Wallace tests analyzed differences in distributions of measures between categories based on number of organism types detected. SAS software version 9.4 (SAS Institute Inc., Cary, NC).

Results. Analysis of the 803 samples that met inclusion criteria found a significant linear association between mortality and number of organism types detected by BAL, with 30 day mortality rates of 43.0%, 47.8%, and 58.3% among those with zero, one, and two or more organisms respectively (p = 0.003). Comparing BALs with at least one organism isolated, the detection of viruses specifically was associated with increased mortality, with the presence and absence of viral organisms corresponding to 56.3% and 46.5% mortality at thirty days (p = 0.03). No association was found between mortality and isolation of acid-fast bacilli, bacteria, or fungi. Co-infection was detected more frequently among bronchoscopic BALs than blinded BALs (26.3% vs 8.6%, p < 0.0001), with more viruses detected bronchoscopic BALs (41.9% vs 13.1%, p < 0.0001), and more bacteria in blinded BALs (41.8% vs 33.0%, p = 0.01).

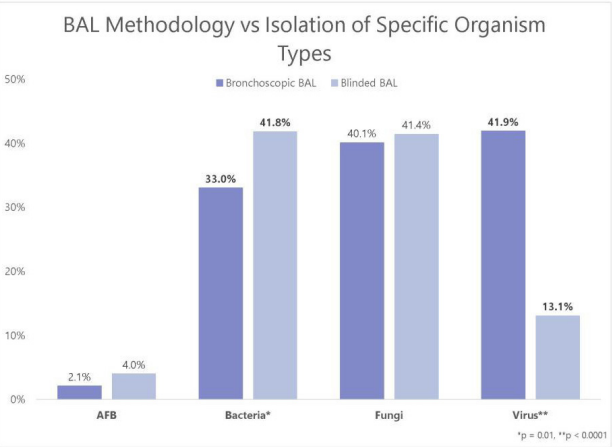
30 Day Mortality vs Isolation of Specific Organism Types from BAL



Number of Organism Types Isolated from BAL Compared to BAL Methodology



BAL Methodology vs Isolation of Specific Organism Types



Conclusion: Co-infection in mechanically ventilated adult patients with pneumonia appears to be a significant risk factor for mortality, with the detection of viral organisms potentially playing an independent role. Within this population, bronchoscopic BALs may have a valuable diagnostic and prognostic methodology.

Disclosures. **All Authors**: No reported disclosures