850. External Validation of the Methicillin-Resistant Staphylococcus aureus Bacteremia Score
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Session: P-37. HAI: Gram-positives (MRSA, MSSA, VRE)

Background. Predictive scoring systems, such as the Pitt Bacteremia Score (PBS) and Acute Physiology and Chronic Health Evaluation II (APACHE-II), can optimize clinical decisions and provide adjustment for confounding among patients with Methicillin-Resistant Staphylococcus aureus bacteremia (MRSA). The recently introduced MRSAB score demonstrated superior discriminatory ability in mortality prediction compared to APACHE-II and PBS, however external validation is lacking.

Methods. Single center, retrospective cohort study of adult patients admitted to University of Colorado Hospital from 2013–2020 with initial episode of MRSA were included. Patients transferred from an outside hospital, left against medical advice, or died/pursued comfort care within 24 hours of index culture were excluded. The primary outcome was discrimination of 30-day all-cause mortality. The discriminatory abilities of APACHE-II, PBS and MRSAB were compared using receiver operating characteristic (ROC) analysis. The sensitivity, specificity, positive predictive value (PPV), and negative predictive value (NPV) were analyzed, and optimal MRSAB score was identified by Youden Index.

Results. Overall, 170 patients met study inclusion. The median (IQR) age was 57 (47-66) years, 69% were male, and 19% were in an ICU during blood culture collection. The most common infection sites were skin and soft tissue (41%), musculoskeletal (23%), and line-related (19%), whereas endovascular (14%) infections were less common. The median (IQR) PBS, APACHE-II and MRSAB scores were 2 (0-4), 17 (12-23), and 6.5 (3-11), respectively. Thirty-day all-cause mortality was 12.9%. ROC curve analysis revealed an area (95% CI) for the APACHE-II, PBS, and MRSAB scores of 0.84 (0.77-0.92), 0.71 (0.57-0.85), 0.79 (0.68-0.90), respectively. A threshold MRSAB score of ≥10 identified patients with 96% (95% CI 0.92-0.99) specificity and 94% sensitivity (0.86-0.98). The positive and negative predictive values for mortality were 0.99 (0.97-1.00) and 0.99 (0.97-1.00), respectively.

Receiver operator characteristic (ROC) curves for the prediction of 30-day mortality

Conclusion. The MRSAB score is a useful predictive scoring model, with discriminatory ability comparable to APACHE-II, and excellent NPV at ≥10. Our findings support routine clinical and research application.

Disclosures. Matthew Miller, PharmD. Allergan (Speaker's Bureau)/Tetraphase (Speaker's Bureau)

851. Compliance with Guidelines for Management of Staphylococcus aureus Bacteremia and its Effect on Mortality
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Session: P-37. HAI: Gram-positives (MRSA, MSSA, VRE)

Background. In the US, Staphylococcus aureus bacteremia (SAB) occurs in about 19.7 /100,000 people. A recent increase in methicillin-resistant Staphylococcus aureus (MRSA) bacteremia infections rate and mortality has led to more infectious diseases (ID) consultations. We assessed if an infectious diseases consultation within 7 days of initial blood culture results was associated to greater compliance with Infectious Diseases Society of America (IDSA) guidelines for managing Staphylococcus aureus bacteremia and a decrease in all-cause mortality and relapse within 90 days.

Methods. A retrospective cohort of patients admitted to two community hospitals from January 2014 to June 2016 with a positive blood culture for methicillin-resistant Staphylococcus aureus (MRSA) bacteremia and a decrease in all-cause mortality and relapse within 90 days.

Results. A total of 331 patients were included in the analysis. A significantly higher proportion of patients with complicated SAB had an ID consult (61% vs. 17.5%, p < .0001) and for uncomplicated SAB the reverse was true (39% vs 79%, P < .0001). An ID consult was associated with increased compliance with IDSA guidelines (75% vs. 5%, p < .0001). Patients with an ID consult had a significantly higher duration of antibiotic treatment [30(14-42) vs. 5(1.5-12), p<.0001], an earlier start of treatment in number of days [0(0-7) vs. 0(0-12), p=.0036] and a lower mortality within 90 days of blood culture (61% vs. 17.5%, p < .0001). Logistic regression model showed that an ID consult reduced 90-day mortality by 69%, OR 0.313 [CI 95 % (0.313-0.154), p=0.001] and tracheosophageal echocardiography by 78%, OR 0.228 [CI 95 % (0.228-0.052), p<0.05].

Conclusion. ID consultation in the setting of SAB has been shown to increase compliance with IDSA guidelines and reduce 90-day mortality.

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852. Genomic Clusters of Methicillin-Resistant Staphylococcus aureus (MRSA) Causing Bloodstream Infections (BSIs) in Hospitalized Adults, 2018-19
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Session: P-37. HAI: Gram-positives (MRSA, MSSA, VRE)

Background. MRSA BSIs have 15-50% mortality and are commonly diagnosed in US hospitals. However, the frequency of hospital transmission of MRSA causing BSI is unknown.

Methods. We performed Illumina shotgun whole genome sequencing (WGS) of 106 sequential MRSA isolates from different adults with a BSI at two Philadelphia academic hospitals in a single health system in July 2018-June 2019. We abstracted clinical data from the electronic medical record. Genomic data were analyzed preliminarily using the Staphopia Analysis Pipeline.

Results. Among 106 subjects, 51.9% were male, 47.2% were white, 46.2% were black, 23.6% were < 40 years of age, and mean age was 53.1 years (s.d. 17 years). One isolate had WGS data that were inadequate for analysis. Of 105 genomes, 52 (99.0%) had SNP data. The mating status for the remaining 53 isolates was determined. Of 105 strains, 94 (89.5%) were USA300 and 11 (10.5%) were USA500. There were 6 clusters (i.e., < 35 SNP differences in the core genome) among the remaining 94 strains. Of USA300 strains, 44 were USA300 and 6 were USA500. There were 6 clusters (i.e., < 35 SNP differences in the core genome) among the 105 isolates. Four clusters were CC5 and two were CC8 strains. One cluster of CC5 strains involved 3 subjects, and 5 clusters involved 2 subjects. One cluster of ST8/USA300 strains were separated by only 1 SNP (Fig a). This and two other clustered pairs were from subjects who had overlapping hospital stays. Two of these paired subjects had an overlap in the same unit while the third pair was in the hospital together on a number of occasions (total of 40 days overlap) but never simultaneously in the same unit. The other three clustered pairs did not have temporally overlapping hospital stays, suggesting transmission via a hospital reservoir. One of these three pairs had hospitalizations overlapping in time, one at each study hospital, before each of them had infections with the related MRSA strains. There was not a clear-cut clustering of SNP distances among the isolate genomes into transmission and non-transmission groups, with some pairs of patient isolates separated by 40-80 SNPs (Fig b).