Conclusion: ID is nearly universally involved in the care of patients with DUA-IE, but this patient population requires input from numerous sub-specialties. Multidisciplinary care teams provide a promising framework for DUA-IE to enhance and integrate nuanced decision-making.

Disclosures: Sarah E. Wakeham, MD, Celero Systems (Advisor or Review Panel member/Optum Labs (Grant/Research Support/UpToDate (Other Financial or Material Support, Author)

7.10. Non-invasive Diagnosis of Whipple Endocarditis Using Next-Generation Sequencing for Microbial Cell-free DNA in Plasma

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Session: P-28 Endocarditis

Background: Tropheryma whippelii is a gram-positive bacillus that causes Whipple’s disease, a protozoal multisystem infection classically characterized by arthralgias, chronic diarrhea, malabsorption, and weight loss. T. whippelii infection has a wide spectrum of clinical manifestations including pleuropulmonary disease, skin hyperpigmentation and cardiac infection. Endocarditis has been diagnosed in a small number of patients and may represent an atypical presentation of T. whippelii infection. Diagnosis can be challenging and has typically been accomplished with histopathology on resected valvular tissue or GI tract biopsy. Next-generation sequencing (NGS) of microbial cell-free DNA offer a unique means of pathogen detection, assessment of infection burden and monitoring of response to both medical treatment and surgical debridement/definitive source control in a case of Bartonella quintana endocarditis.

Methods: McDNA was extracted from plasma and NGS was performed by Karius, Inc. (Redwood City, California). Human sequences were removed and remaining sequences were aligned to a curated database of over 1,400 pathogens. Organisms present above a predefined statistical significance threshold were reported and quantified in DNA molecules per microliter (MPM). Chart review was performed for clinical correlation.

Results: A 64-year-old male with history of valve replacement presented with symptoms of cough, dyspnea, fever, chills, and left-sided chest pain. Transesophageal echocardiography showed a paravalvular leak. Bartonella quintana was detected by Karius NGS (in parallel Bartonella henselae serologies were positive). After 4 weeks of parental antibiotics, repeat Karius testing demonstrated a 94% (16-fold) decrease in the Bartonella quintana mDNA signal to 8813 MPM. He underwent surgical valve replacement; twenty-four hours after removal of the infected valve repeat Karius testing showed a rapid decay of the Bartonella quintana mDNA signal to 103 MPM. The patient completed 3 months of oral antibiotics post-operatively, ultimately returning to his former performance status.

Conclusion: Plasma-based next-generation sequencing assays for circulating microbial cell-free DNA offer a unique means of pathogen detection, assessment of infection burden and monitoring of response to both medical treatment and surgical debridement/definitive source control in a case of Bartonella quintana endocarditis.

Disclosures: Asim A. Ahmed, MD, Karius (Employee)

7.12. Risk of Infective Endocarditis after Transcatheter Aortic Valve Replacement in Patients with Bloodstream Infection: A Population-Based Study

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Session: P-28 Endocarditis

Background: Transcatheter aortic valve replacement (TAVR) was initially approved as an alternative to surgery for patients at high surgical risk. However, it is now being considered for patients with intermediate and low surgical risk. This will result in the expansion of patient pool for TAVR; hence it is of interest to ascertain risk factors associated with IE in patients who underwent TAVR and subsequently developed a BSI.

Methods: A population-based study was conducted in 7 counties in southeastern Minnesota using the expanded Rochester Epidemiology Project (E-REP) for adult (≥18 years) patients who underwent TAVR and subsequently developed a BSI. Transcatheter procedures that included replacement of either the aortic or mitral valve were included. Medical records were screened for development of BSI from time of TAVR until May 15, 2020. Patients were classified as having BSI only, BSI with IE at outset, or BSI with subsequent development of new IE. Early IE was defined as that occurring < 12 months following TAVR, with subsequent cases defined as late IE.

Results: A total of 247 patients underwent TAVR during the study period. There were 24 patients with BSI only and 10 (42%) developed IE with an annual incidence of 5 per 1000 patient-years. Median age was 85 ± 4 years. Male gender was affected predominantly (70%). Six developed IE at outset of BSI, while four developed IE subsequent to BSI. The median time to development of IE was 791 days following TAVR. There was an equal number of early and late IE cases (n=5). The most common pathogen causing IE was viridians group streptococci (n=4) followed by enterococci and coagulase-negative staphylococci with 2 patients each. Mean Charlson comorbidity index was 6.6. Two patients with IE died before resolution of infection (20%).

Conclusion: The incidence of BSI and subsequent IE in patients with TAVR was low in our population. Due to the small number of BSI and IE cases, statistical analysis was not feasible. An analysis of all cases seen at Mayo Clinic is planned since the number of cases would be much higher to investigate potential risk factors associated with BSI and IE.

Disclosures: Larry M. Baddour, MD, Boston Scientific (Consultant) M. Rizwan Sohal, MD, Azryo Biologics (Consultant)Medtronic Inc (Consultant, Research Grant or Support)

7.13. The Clinical Impact of Implementation of a Multidisciplinary Endocarditis Team

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Session: P-28 Endocarditis

Background: There are up to 50,000 new cases of infective endocarditis each year in the United States, of which approximately 20% are culture negative endocarditis (CNE). In hospital mortality remains high at 20 to 30%. Despite advances in diagnostic testing, determining the timing of surgery and duration of treatment in CNE are significant challenges for clinicians. Plasma next-generation sequencing (NGS) for circulating microbial cell-free DNA (mCDA) has shown utility in diagnosing and monitoring the response to treatment in endocarditis.

Methods: Serial blood samples were obtained prior to and after aortic valve replacement in a patient with culture negative endocarditis. Microbial cDNA was extracted from plasma and NGS was performed by Karius, Inc. (Redwood City, California). Human sequences were removed and remaining sequences were aligned to a curated database of over 1,400 pathogens. Organisms present above a predefined statistical significance threshold were reported and quantified in DNA molecules per microliter (MPM). Chart review was performed for clinical correlation.

Results: A 53-year old man with history of homelessness, well-controlled HIV infection and a bioprosthetic aortic valve presented with symptomatic severe aortic stenosis and elevated inflammatory markers 3 years following valve surgery. Transesophageal echocardiography showed a paravalvular leak. Bartonella quintana was detected by Karius NGS (in parallel Bartonella henselae serologies were positive). After 4 weeks of parental antibiotics, repeat Karius testing demonstrated a 94% (16-fold) decrease in the Bartonella quintana mDNA signal to 8813 MPM. He underwent surgical valve replacement; twenty-four hours after removal of the infected valve repeat Karius testing showed a rapid decay of the Bartonella quintana mDNA signal to 103 MPM. The patient completed 3 months of oral antibiotics post-operatively, ultimately returning to his former performance status.

Conclusion: Plasma-based next-generation sequencing assays for circulating microbial cell-free DNA offer a unique means of pathogen detection, assessment of infection burden and monitoring of response to both medical treatment and surgical debridement/definitive source control in a case of Bartonella quintana endocarditis.