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.

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710. 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 whipplei* is a gram-positive bacillus that causes Whipple's disease, a protean multisystemic syndrome classically characterized by arthralgias, chronic diarrhea, malabsorption, and weight loss. *T. whipplei* 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. whipplei* 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 (mcfDNA) in plasma offers a rapid, non-invasive means of diagnosis of this rare cause of culture-negative endocarditis and challenging clinical entity.

Methods: McfDNA analysis was performed in a patient with culture negative endocarditis. 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 significant deterioration of the mitral valve. An exhaustive infectious workup including blood cultures was negative. Karius testing detected *T. whipplei* at 766 MPM within two days of sample receipt. The normal range for *T. whipplei* is 0 MPM based on a cohort of 684 healthy individuals. Blood PCR for *T. whipplei* was confirmatory.

Table 1: Clinical Parameters of Case

Clinical Parameters of Case of *T. whipplei* infection diagnosed by NGS of mcfDNA from plasma:	
Age	64
Male	Male
Presenting symptoms	Exertional dyspnea
Antecedent symptoms	None
Tmax/Fever at presentation	99.8 was Tmax. Otherwise afebrile
Hgb/Hct	8.3/27.5
WBC with %N	8.7 with 83%
Platelets	188,000
PT/PTT	INR 3.3 PT 33.2 No PTT
ESR mm per hr/CRP md per dL	ESR 49 CRP not done
Albumin	3.8
Blood culture result(s)	9 sets all negative
Sites/organ systems involved:	
Joint	none
Diarrhea/abdominal pain/malabsorption/weight loss	none
Central nervous system/ocular	none
Heart	mitral valve degeneration/regurgitation
Skin	none
Pulmonary	none
Systemic	none
Imaging results	CT chest/abd/pelvis showed pulmonary edema and was otherwise negative
Empiric antibiotics	
Antibiotic pretreatment duration prior to Karius Test	vancomycin/ceftriaxone for 4 days
Choice of antibiotics after Karius Test	ceftriaxone/moxifloxacin
Karius Test result	*Tropheryma whipplei* 766 MPM RR (0 MPM)
Karius Test turnaround time from sample receipt	46 hours
Other infectious disease testing, result and turnaround time:	
***T. whipplei* blood PCR (ARUP)**	Positive, turnaround time 37 days
***Histoplasma* and *Blastomyces* antigens, CF and ID antibodies, Fungitell assay, *Coxiella* serology, *Bartonella quintana* PCR, *Brucella* antibodies, *Legionella* antibody, *Rickettsia* antibodies, Blood PCR for CMV, EBV and BKV**	All negative

MPM – molecules of microbial cell-free DNA/microliter
RR – reference range based on the 97.5th %ile in a cohort of healthy individuals

Conclusion: NGS for mcfDNA in plasma offers a rapid, non-invasive method for identifying *T. whipplei* and, to our knowledge, the first diagnosis of Whipple disease using NGS of plasma mcfDNA.

Disclosures: Christiaan R. de Vries, MD, PhD, Karius (Consultant, Independent Contractor)Stanford University (Employee) Ann Macintyre, DO, Karius (Employee)

711. Rapid, non-invasive detection and monitoring of *Bartonella quintana* endocarditis by plasma-based next-generation sequencing of microbial cell-free DNA

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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 (mcfDNA) 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 cfDNA 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 parenteral antibiotics, repeat Karius testing demonstrated a 94% (16-fold) decrease in the *Bartonella quintana* mcfDNA 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* mcfDNA 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)

712. 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 of blood stream infection (BSI) and infective endocarditis (IE) following TAVR. We aim to study the incidence, epidemiology and 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 all adult (≥18 years) patients who underwent TAVR from January 1st, 2010 to December 31st, 2018. 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 15th, 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 of BSI and 10 (42%) developed IE with an annual incidence of 5 per 1000 persons-years. Median age for patients who developed IE was 85.4 years. Male gender was affected predominantly (70%). Six developed IE at outset of BSI, while four developed IE subsequent to IE. 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.

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

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