2049. *Pneumocystis jiroveci* Detection by Nested PCR in HIV-Infected Peruvian Patients

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Session: 230. Diagnostics: Mycology
Saturday, October 6, 2018: 12:30 PM

Background. *Pneumocystis jiroveci* (PJ) is considered a common cause of pneumonia in HIV-AIDS patients. PJ detection now is facilitated by molecular techniques using non-invasive samples; however, there are few PJ colonization studies in HIV population using these techniques. The study aim was to evaluate the frequency and factors related to PJ colonization among HIV-patients with CD4 account <500 cells/mm^3.

Methods. We performed a cross-sectional study evaluating HIV patients older than 18 years old with or without respiratory symptoms with CD4 account <500 cells/mm^3 who attended Hospital Cayetano Heredia in Lima, Peru during May 2017–March 2018. After patients signed an inform consent, clinical information was obtained from the medical chart and a non-induced sputum sample was collected. If patient did not have cough, an oral wash sample using saline was obtained. PJ detection was based on the amplification of the mitochondrial large subunit ribosomal RNA (mtLSU rRNA) in two stages. First, single round PCR was done using external primers (pAZ102E and pAZ102H); then, PCR products were amplified (nested PCR) using internal primers (pAZ102X and pAZ102Y). If the single round PCR was positive in a patient with respiratory symptoms, it was considered a PJ infection. If only the nested PCR was positive, this was considered as PJ colonization.

Results. A total of 177 patients were included, 75 (42.4%) with respiratory symptoms. Three cases were considered PJ infections. A total of 15 cases (8.6%) were colonized by PJ, 7/72 (9.7%) cases with respiratory symptoms and 8/102 (7.8%) among asymptomatic patients. A higher proportion of colonization was seen in patients in whom an oral wash was obtained (14/156, 9.0%) compared with those in whom a non-induced sputum was analyzed (1/18, 5.5%). The frequency of PJ colonization based on CD4 account was 6.5 and 10.3% among patients with ≤200 and >200 cells/mm^3, respectively.

Conclusion. PJ colonization was seen in 8.6% of HIV patients. The proportion of PJ detection was higher when oral wash was analyzed compared with non-induced sputum. Patients with lower CD4 account did not show a higher proportion of colonization.

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

2050. Plasma Next-Generation Sequencing for Pathogen Detection in Pediatric Patients at Risk for Invasive Fungal Infection

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Session: 230. Diagnostics: Mycology
Saturday, October 6, 2018: 12:30 PM

Background. Invasive fungal infection (IFI) is a major cause of mortality and morbidity among immunocompromised patients. Microbiologic culture of biopsy samples remains the diagnostic gold standard. Noninvasive biomarker testing can provide clinically useful information, but does not give species-level identification. Next-generation sequencing (NGS) of cell-free plasma is a noninvasive approach for species-level identification of pathogens, and may guide specific treatment. We sought to describe the diagnostic utility of plasma NGS in high-risk immunocompromised pediatric patients, correlating results with standard microbiology studies.

Methods. Plasma from at-risk immunocompromised patients with suspected IFI was tested using cell-free plasma NGS (Karius, Redwood City, CA). Human reads were removed, and remaining sequences aligned to a curated database including >1,000 pathogens. Organisms present above a predefined significance threshold were reported.

Results. Forty evaluable patients were enrolled, the majority of whom had underlying oncologic diagnoses. Risk for IFI included prolonged febrile neutropenia (FN) in 22 patients, recrudescent FN in 7, concern for IFI on imaging in 8, and concern for IFI based solely on other clinical findings in 3. Six patients met established criteria for proven IFI, 1 for probable IFI, and 13 for possible IFI. NGS plasma testing identified a pathogen which was cultured from infected tissue or blood in 4 of 6 proven cases; one patient with localized cutaneous *Rhizopus* had negative NGS results. A patient with probable IFI (positive β-D-glucan) had *P. jirovecii* identified by NGS. Among 33 patients without proven or probable IFI, NGS testing identified a fungus in one (*C. glabrata*), no organism in 11, and potential alternative sources of fever in 16.

Conclusion. Plasma NGS testing can detect IFI from blood. The test identified fungi from proven IFI, and detected other pathogens in both probable and possible IFI cases. Many patients at risk received prolonged courses of antifungals despite negative testing, suggesting a possible future role for NGS testing in ruling out IFI. Future studies should more definitively evaluate the positive and negative predictive value for NGS testing in patients at risk of IFI.

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2051. Detection of *Candida auris* Among Previously Unidentified Yeasts Isolated from Ear Discharge Specimens in Japan

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Session: 230. Diagnostics: Mycology
Saturday, October 6, 2018: 12:30 PM

Background. *Candida auris* has not been detected since first[1] report in Japan, despite worldwide reports. We recently reported a second isolate of *C. auris* (TWCC 58191) from ear discharge in Japan. We re-analyzed unidentified yeast strains.

Methods. Over 2,000 clinical yeast samples were available. Among these, 16 yeast strains isolated from the ear discharge were not identified using conventional method. *C. auris* was identified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry and internal transcribed spacer and D1/D2 region sequencing. To determine the minimum inhibitory concentration (MIC), the Clinical and Laboratory Standards Institute broth microdilution method was used. Whole genome sequencing, assembly and error correction was performed (Japanese strains). Average nucleotide identity (ANI) among two Japanese strains and four other strains (India, Pakistan, South Africa) was determined. Our 6 strains and previously reported strains (n = 126) were mapped to JCM15448 and single nucleotide variants (SNVs) were detected. An SNV-based phylogenetic tree was constructed.

Results. Five were identified as *C. auris*. Our strains exhibited relatively low MICs (Table 1). Japanese strains had susceptibility to nearly all agents. Because all strains were obtained from chronic otitis media, the susceptibility may be explained by a lack of exposure to antifungal agents. JCM15448 was assembled based on 11 contigs. All ANIs were over 99%; therefore, all of these strains are *C. auris*. A total of 168,810 SNVs were detected in 133 strains. The SNV-based phylogenetic tree is shown Figure 1. Since independent clusters were observed from strains from each area, it is possible that *C. auris* emerged independently in different regions worldwide. The SNV-based phylogenetic tree was more effective for the identification of Japanese strains (Figure 2).

Conclusion. Despite a general lack of reports, *C. auris* exists in Japan. Clinicians must consider the potential for *C. auris* detection from otorrhea samples.

A phylogenic analysis separates native strains from each area. During an outbreak, an SNV-based phylogenic tree is suitable for analysis owing to its good identification ability.

Table 1. Characteristics of our *C. auris* Strains

Strain No	Specimen	Date isolated	MIC (mg/L)						
TWCC			MCFG	CPFG	AMB	5-FC	FLCZ	ITCZ	VRCZ
13846	Otorrhea	2003	0.03	0.25	0.25	≤0.125	4	0.03	≤0.015
13847	Otorrhea	2003	0.03	0.25	0.25	≤0.125	1	≤0.015	≤0.015
13878	Otorrhea	1997	0.06	0.5	0.25	0.5	16	0.125	0.125
50952	Otorrhea	2008	0.03	0.25	≤0.03	≤0.125	2	0.03	0.03
58191	Otorrhea	2017	0.06	0.5	0.25	0.25	4	0.06	0.03
58362	Otorrhea	2008	0.125	>16	0.25	0.5	>64	0.25	2
		break point	4	2	2	128	32		2

Figure 1. Phylogenic tree based on SNVs

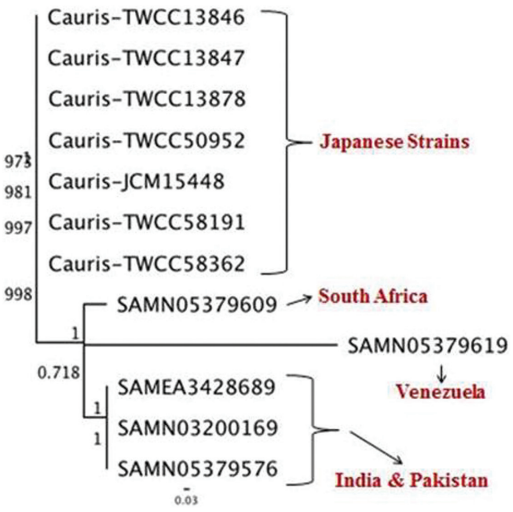
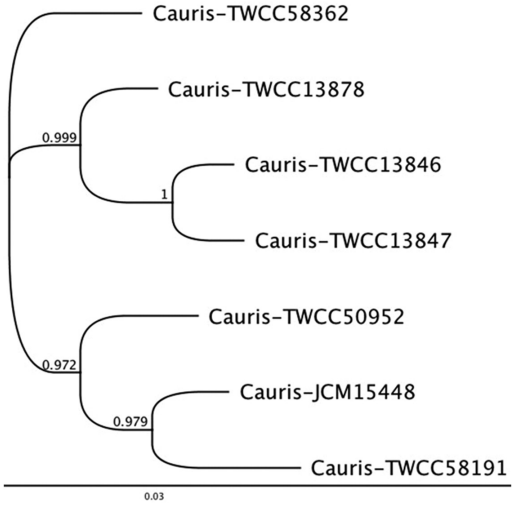


Figure 2. Phylogenic tree of SNVs (only Japanese strains)



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

2052. Performance of the Biofire Filmarray Meningitis/Encephalitis Panel in Cryptococcal Meningitis Diagnosis

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Session: 230. Diagnostics: Mycology
Saturday, October 6, 2018: 12:30 PM

Background. Diagnosing meningitis and encephalitis is challenging in the immunosuppressed population. Cerebrospinal fluid (CSF) culture is the gold standard diagnostic test for cryptococcal meningitis (CM), but is time intensive and requires a high index of suspicion. The BioFire FilmArray Meningitis/Encephalitis (ME) panel offers an option for rapid diagnostic testing. Recent studies suggest similar performance of the ME panel compared with CSF culture in the initial diagnosis and relapse of CM. We investigated the performance of the ME panel in the diagnosis of cryptococcal disease in patients presenting with meningitis.

Methods. A retrospective observational study was performed at an 800 bed regional medical center between June 1, 2016 and March 1, 2018. Laboratory results for all patients admitted with CSF or serum cryptococcal testing were reviewed. We abstracted the results from 14 distinct hospitalizations involving 12 patients (Figure 1) with CM who had an ME panel and CSF culture. Diagnostic performance was determined by comparison of ME panel to CSF culture.

Results. The ME panel demonstrated a 71.43% (95% CI: 29.04–96.33) sensitivity and 100% (95% CI: 59.04–100) specificity for diagnosing CM for the population described in Table 1. ME panel detected all four patients with an initial diagnosis of CM and one of three patients with culture positive relapse.

Conclusion. Our findings suggest that a negative cryptococcal result on the ME panel should not be used to rule out cryptococcal disease, particularly in patients with a previous diagnosis of CM. Additional testing may increase cost, but until larger studies validate the use of rapid diagnostics, fungal culture remains the gold standard for the diagnosis of CM and should not be eliminated from routine evaluation.

Demographics		
Male, % (no.)	86	[12/14]
Age (years), mean	44	
HIV, % (no.)	86	[12/14]
CD4 cell count/μL, median [IQR]	58	[26-121]
History of CM, % (no.)	71	[10/14]
Relapse, % (no.)	30	[3/10]
IRIS, % (no.)	70	[7/10]
CSF results		
WBC count/μL, median [IQR]	52.5	[6-179]
Opening pressure cmH_2O, mean (n=12)[1]	21	

[1] Two patients with no recorded opening pressure.

Table 1. ME and culture results of 14 CSF cryptococcal antigen positive specimens.

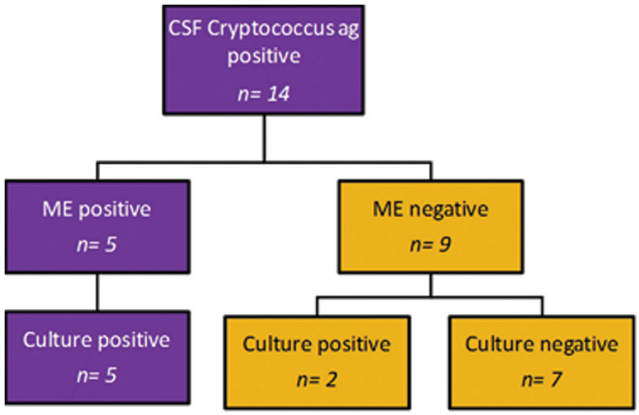

Figure 1: Demographics and description of CSF specimens.

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

2053. Tissue-Based Molecular Diagnostics: A Sensitive and Specific Way for the Identification of Invasive Fungal Infections in the Combat-Related Setting

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Session: 230. Diagnostics: Mycology
Saturday, October 6, 2018: 12:30 PM

Background. Combat-associated invasive fungal infections (IFI) of the deep skin and soft tissue are an infectious disease. Reliance on conventional techniques to diagnose IFIs has limitations as culture is insensitive and time-delayed and histopathology cannot provide a species-level or even a genus-level identification (ID). Molecular-based methods are rapid, provide species-level ID, and have been studied to a limited extent in the trauma setting although they may prove overly sensitive as soil (thereby fungal) contamination is common. In this study, we examined the performance characteristics of a panfungal PCR for the diagnosis of IFI among subjects injured in Afghanistan operations.

Methods. Formalin-fixed paraffin-embedded (FFPE) tissue samples obtained during debridement from IFI cases with angioinvasion (AI) and controls (combat-injured with negative histopathology) were evaluated with a panfungal PCR targeting the internal transcribed spacer (ITS 1 and ITS 2) of the fungal genome.

Results. We assessed 41 injury sites where culture, histopathology, and FFPE specimens were available contemporaneously. Fungus was cultured from 32 sites (78%) with the order Mucorales represented in 18 sites (44%, five sites with *Saksenaea* spp.), and *Aspergillus* spp. in six (15%) sites. Using PCR, a fungus was identified from 33 sites (81%) with order Mucorales identified from 28 sites (68%, 20 with *Saksenaea* spp.) and *Aspergillus* spp. from five (12%) sites. When compared with the gold standard (histopathology), the sensitivity, negative, and positive predictive value were 83, 94, and 98%, respectively. Specificity was calculated to be 99.2% based upon the identification of one false-positive among 118 controls.

Conclusion. Concerns about PCR being overly sensitive for the diagnosis of trauma-related IFI are not upheld. The PCR-based method was sensitive, specific, and had a high negative predictive value for the diagnosis of AI IFI. Re-demonstrated is the inability of culture to identify fungi of the order Mucorales and the need for antifungal coverage targeting fungi of the order Mucorales and Aspergillus in AI IFI. As *Saksenaea* is the dominant fungus identified in this setting, study of the virulence characteristics and antifungal susceptibility is warranted.

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2054. Physician Responses to Positive Rapid Diagnostic Tests for Candida Fungemia in the Absence of Concomitant Positive Blood Cultures

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