AMP 2020: Get AMPed!

Updates and Case Studies in Molecular Pathology

Sunday, November 15, 2020

VIRTUAL COURSE

FINAL PROGRAM (as of 10/20/2020)

TIME (eastern)	SESSION	SPEAKER
10:30am	**Welcome and Introductions**	**Yassmine Akkari, PhD** *Legacy Health*
10:35am	**AMP Survey Results of SARS-CoV-2 Molecular Testing Laboratories** Since the beginning of the COVID-19 outbreak, AMP has conducted a series of online surveys of laboratories performing SARS-CoV-2 molecular testing in order to monitor, understand, and collect real-time data on laboratories' efforts and experiences during the COVID-19 pandemic response. The survey results have been instrumental in AMP's advocacy efforts and have been presented at congressional hearings, the CDC, and FDA. In this presentation, I will present the results of these surveys. The surveys covered multiple parameters of SARS-CoV-2 testing, including test demand and capacity, testing methodology and performance, resource and supply chain concerns, test reimbursement, FDA oversight and public health reporting requirements. A survey conducted in April 2020 resulted in a robust data set of 255 total responses with 118 complete responses from US laboratories. A follow-up survey was conducted in August and September of 2020 and another robust data set emerged, with 249 total responses including 113 complete responses from US laboratories. **Learning Objectives:** • Describe the major hurdles that have faced laboratories in implementing SARS-CoV-2 molecular testing in response to the COVID-19 pandemic. • Summarize the current state of US laboratory testing for SARS-CoV-2.	**Karen Weck, MD** AMP President *University of North Carolina*
11:20am	**COVID-19 – Current State of SARS-CoV-2 Testing: Challenges and Triumphs** During this session the speakers will describe their first-hand experiences with testing challenges related to the COVID-19 pandemic including innovative approaches employed to mitigate supply chain issues. They will also discuss impacts on the upcoming "coflu" (COVID/influenza) season. **Learning Objectives**: • Identify supply chain issues and mitigation strategies during the COVID-19 pandemic. • Describe the status of widespread testing for influenza in addition to SARS-CoV-2.	**Erin H. Graf, PhD, D(ABMM)** *Mayo Clinic Arizona* **Gerald A. Capraro, PhD, D(ABMM)** *Carolinas Pathology Group and Atrium Health*
11:55am	**BREAK** (10min)	
12:05pm	**From the Operating room to the Laboratory: Pre-analytic Considerations for Tissues** This session will cover best practices for molecular diagnostic testing on tissue with a focus on pre-analytic factors. The suitability of the tissue used for subsequent molecular testing is impacted by a variety of different factors that start in the operating room or radiology suite when the tissue is being obtained through processing in gross pathology, histology,	**Lauren L. Ritterhouse, MD, PhD** *Massachusetts General Hospital, Center for Integrated Diagnostics*

	and finally in the molecular diagnostic laboratory. We will cover important best practices that include specimen types, multi-disciplinary communication, tissue fixatives and processing, as well as specimen enrichment and adequacy requirements. **Learning Objectives:** • Troubleshoot tissue specimens that fail molecular diagnostics. • Implement best practices for pre-analytic processes.	
12:30pm	**Testing Modalities to Look at Genome Structure: Conventional Cytogenetics, FISH, and Chromosomal Microarray Analysis** This session will describe various testing modalities to assess structural and numerical variations that occur throughout the whole genome. **Learning Objectives:** • Demonstrate the clinical utility of identifying whole genome structural and numerical aberrations in disease workup. • Describe testing modalities that aid in the diagnosis of such genome aberrations. • List the advantages and disadvantages of each modality.	**Yassmine Akkari, PhD**
12:55pm	**Introduction to NGS: Libraries, sequencing chemistries and use in clinical practice** The session will talk about the different platforms and chemistries currently used for NGS along with associated limitations and challenges. Examples of the use of NGS in Clinical Practice will also be presented. **Learning Objectives:** • Distinguish the various chemistries used for NGS. • Apply the knowledge gained to understanding the use of NGS in clinical practice.	**Honey V Reddi, PhD, FACMG** *Medical College of Wisconsin*
1:25pm	**Introduction to Bioinformatics Pipeline & Data Analysis** This session is an introduction to the general bioinformatics pipeline and its three major components - primary analysis, secondary analysis, and tertiary analysis. It describes the main steps in sequence generation, sequence processing, and results interpretation including quality evaluation, read mapping, coverage analysis, variant calling, annotation, and variants filtering. **Learning Objectives:** • Describe the major components of a general bioinformatics pipeline. • Describe the main steps in each component. • Introduce the annotation and interpretation of sequence variants.	**Weiwei Zhang, PhD** *University of Nebraska Medical Center*
1:55pm	**BREAK** (10min)	
2:05pm	**Introduction to the Case Presentations**	**Nathanael G. Bailey, MD** *University of Pittsburgh*
2:10pm	**Interactive Case(s) on Pre-analytic Considerations** This is an interactive session that highlights some of the pre-analytic considerations in molecular testing. Two real cases will be presented. Each case will focus on certain pre-analytic limitations encountered in our daily practice followed by a discussion on how to overcome these limitations and contribute the most to patients' care. **Learning Objectives:** • Discuss rationale for specimen selection for molecular testing.	**Annie T. Garcia, MD** *Baylor College of Medicine*

	• Question and investigate a "negative" test result. • Prioritize the most clinically relevant molecular test in a limited tissue sample.	
2:40pm	**Interactive Case(s) on Testing Modalities to Look at Genome Structure** This session will be an interactive discussion of challenging real cases encountered in the clinical laboratory setting, exemplifying the integration of cytogenetic and molecular testing modalities to look at genome structure in the clinic. **Learning Objectives:** • Identify cases for which cytogenetic and molecular testing of genome structure could be beneficial. • Demonstrate the utility of cytogenetic and molecular testing modalities in deciphering challenging genomic structural rearrangements. • Promote forward thinking to utilize cytogenetic and molecular testing modalities of genome structure to solve challenging clinical questions.	**Cinthya Zepeda-Mendoza, PhD** *ARUP Laboratories*
3:10pm	**BREAK** (5min)	
3:15pm	**Interactive Cases on Bioinformatics** Case 1: Bioinformatics to troubleshoot NGS issues Case 2: Tertiary analysis (Constitutional case) Case 3: Tertiary analysis (Somatic case) **Learning Objectives** • Demonstrate how bioinformatics can be used to troubleshoot experimental issues in NGS tests. • Discuss informatics resources available for tertiary analysis in constitutional and somatic testing. • Illustrate how informatics can be used for variant filtration during tertiary analysis of NGS data.	**Sabah Kadri, PhD** *Ann & Robert H. Lurie Children's Hospital of Chicago; Northwestern University Feinberg School of Medicine*
4:05pm	**Interactive Cases on NGS** NGS provides the opportunity to examine a huge amount of data at once, and the clinical interpretation is often challenging. We present two cases which demonstrate how to thoughtfully review clinical NGS data to support patient care. Case presentations include the identification of a novel virus, and a review of tumor sequencing with both somatic and germline variants identified. **Learning Objectives** • Describe the principles of the virome test (an NGS tool for virus identification); • Explain the predictive value of viral genomics for virus surveillance and identification of novel viruses in the population • Describe the framework for the clinical interpretation of somatic variants • Explain how germline variants may appear in tumor-only sequencing • Discuss the potential risks and benefits of identifying germline variants in tumor sequencing	**Alanna Church, MD** *Boston Children's Hospital; Harvard Medical School* **Roberta Sitnik, MSc, PhD** *Hospital Israelita Albert Einstein*
4:35pm	**Closing Remarks, and Evaluations**	**Nathanael G. Bailey, MD**
4:40pm	**Adjourn**	