ASSOCIATION FOR MOLECULAR PATHOLOGY
Education. Innovation & Improved Patient Care. Advocacy.
9650 Rockville Pike. Bethesda, Maryland 20814
Tel: 301-634-7939 | Fax: 301-634-7995 | amp@amp.org | www.amp.org

AMP 2017 Molecular Pathology Outreach Course

AMPlicons: A Practical Molecular Toolkit and Case Studies

Wednesday, November 15, 2017

Salt Lake Marriott Downtown at City Creek, Salt Lake City, UT

Detailed Agenda

TIME	SESSION	SPEAKER	CE hours
7:30am	**Registration and Continental Breakfast**		
8:30am	**Welcome and Introductions**	***Annette S. Kim, MD, PhD*** *Brigham & Women's Hospital*	
8:35am	**Contemporary Topics in Molecular Diagnostics**	***Federico A. Monzon, MD*** *Castle Biosciences*	
9:25am	**Break (SEW leaves)**		
9:30am	**Molecular Testing Landscape – Pre-Analytical Considerations: Everything Starts With the Sample** This presentation will provide an overview of major clinically used molecular diagnostic tests emphasizing the importance of quantitative and qualitative sample requirements as a prerequisite for successful testing. A growing menu of molecular tests may require adjustment of sample triage and processing algorithms to optimize the use of materials. Pathologists play a crucial role in selecting appropriate specimens and ensuring its adequacy, particularly in solid tumor testing. • Compare main types of samples submitted for molecular testing highlighting key criteria for specimen selection. • Assess requirements for the sample adequacy in relation to the test performance characteristics.	***Anna Yemelyanova, MD*** *University of Texas MD Anderson Cancer Center*	**0.5**
CASE STUDIES: Non-Template Amp ("Prête-à-Utilizer")			
10:00am	**Cleavase Probe Amplification for the Factor V (F5) and Prothrombin (F2) Genes** Mutations in the Factor V and prothrombin genes have been implicated in deep vein thrombosis. A case presentation will illustrate the application of the cleavase probe amplification method in the detection of these mutations and their clinical implications. • Explain the mechanism of the cleavase probe signal amplification methodology. • Describe the application of testing for genes involved in thrombophilia.	***Cynthia Jackson, PhD*** *Rhode Island Hospital*	**1.0**
	Finding What's Lost: Multiplex Ligation-Dependent Probe Amplification (MLPA) for Detection of Large Deletions in Cystic Fibrosis This case will cover the basics of the MLPA method for detection of copy number variants. A brief review of Cystic Fibrosis (CF) and CF carrier screening will be presented with a specific case to illustrate how MLPA can be clinically applied in challenging cases to reach an appropriate diagnosis. • Describe the principles of Multiplex Ligation-dependent Probe Amplification (MLPA) for copy number detection. • Evaluate Cystic Fibrosis carrier screening data and select cases where MLPA is an important adjunct to routine methods.	***Mark Ewalt, MD*** *University of Colorado*	

ASSOCIATION FOR MOLECULAR PATHOLOGY
Education. Innovation & Improved Patient Care. Advocacy.
9650 Rockville Pike. Bethesda, Maryland 20814
Tel: 301-634-7939 | Fax: 301-634-7995 | amp@amp.org | www.amp.org

10:25am	**HPV Genotyping Using Transcription-Mediated Amplification (TMA)** This presentation will use HPV genotyping in a case of an abnormal pap test using TMA. It will include a discussion of how to design primers, the enzymes involved in TMA, and how it differs from PCR. • Describe the steps of transcription-mediated amplification including which enzymes catalyze each step. • Identify the distinctions between TMA from PCR, and determine how that changes primer design and interpretation of results.	***Jeffrey Gagan, MD, PhD*** *Brigham & Women's Hospital*	
	Oligo Hybridization-Based Methodology: Microarray in the Infectious Diseases Diagnostic Laboratory The case will cover the methodology behind oligo hybridization-based microarray assay, discuss an example of a microarray assay used in the infectious diseases diagnostic laboratory, and describe its impact on patient care. • Review the basic concepts of microarray methodology. • Describe the application of microarray methodology in the infectious diseases diagnostic laboratory.	***Sophie Arbefeville, MD*** *University of Minnesota Medical Center*	
10:50am	**Break**		
	CASE STUDIES: Specialized PCR Methods		
11:05am	**Triplet Repeat-Primed PCR for Detection of Trinucleotide Repeat Expansion** This case will provide an overview of PCR-based sizing analysis for the diagnosis of trinucleotide repeat disorders such as Huntington disease and Fragile X. Relative advantages and disadvantages of the method in comparison with historic approaches will be discussed. • Describe the principles underlying triplet repeat-primed PCR for trinucleotide repeat sizing and compare with other sizing methodologies. • Discuss the advantages and disadvantages of triplet repeat-primed PCR.	***Kristy Crooks, PhD*** *University of Colorado, Denver*	**1.0**
	BCR-ABL1 Testing in CML This case will discuss the clinical context, methods, interpretation, and clinical implications of BCR-ABL1 fusion detection in the setting of chronic myelogenous leukemia. Reverse transcriptase real time PCR will be discussed in detail. • Describe how amplicon specificity is achieved using real time RT-PCR. • Explain the purpose of an international scale value in interpretation of BCR-ABL1 quantitative results.	***Anthony N. Snow, MD*** *University of Iowa Hospitals & Clinics*	
	One-Step Wonders: Sample to Answer PCR in Infectious Diseases This case will describe the changing landscape of PCR for infectious disease diagnostics emphasizing the potential and pitfalls of sample to answer testing. • Develop awareness of the role of sample to answer testing. • Describe pitfalls associated with sample to answer testing.	***Kevin Alby, PhD*** *Hospital of the University of Pennsylvania*	
	1 in 160 Billion? So You are Saying There is a Chance… This case will illustrate the clinical applications of short tandem repeat analysis for identity testing as well as discuss the technical caveats of this assay that may limit the analytical sensitivity of this assay in some cases. • List the clinical applications for identity testing by STR analysis. • Describe the technical caveats with STR analysis.	***Annette S. Kim, MD, PhD*** *Brigham & Women's Hospital*	
12:00pm	**LUNCH**		

ASSOCIATION FOR MOLECULAR PATHOLOGY
Education. Innovation & Improved Patient Care. Advocacy.
9650 Rockville Pike. Bethesda, Maryland 20814
Tel: 301-634-7939 | Fax: 301-634-7995 | amp@amp.org | www.amp.org

CASE STUDIES: Basic SNV Detection by NGS			
1:15pm	**Next-Generation Sequencing in AML** This case will review the use of next-generation sequencing to detect single nucleotide variants in acute myeloid leukemia (AML) and how genomic data is integrated in prognostication and sub classification of AML. • Describe the prognostic significance of commonly mutated genes in acute myeloid leukemia. • Describe the mechanism, advantages, and limitations of Ion Torrent next-generation sequencing.	***Jennifer Dunlap, MD*** *Oregon Health & Science University*	**0.5**
	Difficult to Sequence Areas of the Genome Next-generation sequencing technologies are now commonly used to clinically interrogate the entire genome or targeted regions of the genome. However, the underlying genome architecture poses significant challenges in the sequencing and analysis of genomic data which results in "holes" in the genome and cannot be addressed due to technical limitations of the current technologies. This case will present an overview of the current challenges and alternative techniques to address medically important but technically challenging regions of the genome. • Describe the typical areas of the genome that present challenges with NGS based capture, sequencing and/or analysis. • Identify the appropriate alternative applications to address such challenges.	***Avni Santani, PhD*** *Children's Hospital of Philadelphia*	
CASE STUDIES: Detection of Fusions			
1:45pm	**Case Studies of Genomic Rearrangements Detected by DNA Next-Generation Sequencing: Modern Day ALKemy** Case studies involving genomic rearrangement of the ALK locus will be presented to illustrate the sequencing and bioinformatic challenges in detecting genomic rearrangements by direct next-generation sequencing (NGS) of DNA. The advantages and disadvantages of DNA-NGS, RNA-Seq, IHC, and FISH testing will be specifically addressed. The FDA-approved companion diagnostic FISH assay for crizotinib will be included in the discussion. • Identify the pitfalls and challenges in identifying and interpreting genomic rearrangements from DNA NGS data. • Compare and contrast the available techniques for identifying genomic rearrangements involving the ALK locus	***Jason Rosenbaum, MD*** *Hospital of the University of Pennsylvania*	**0.5**
	Multiplex Fusion Detection Using RNA Anchored Multiplex PCR (AMP) for Solid Tumors This case will discuss clinical context, conceptual method details, advantages, and interpretation of anchored multiplex PCR for multiplex fusion detection in the context of a clinical case. • Describe advantages of anchored multiplex PCR over previous methods including fluorescent *in situ* hybridization. • Describe the uses of a molecular barcode and unique start sites as applied in anchored multiplex PCR.	***Anthony N. Snow, MD*** *University of Iowa Hospitals & Clinics*	
2:15pm	**Break**		

ASSOCIATION FOR MOLECULAR PATHOLOGY
Education. Innovation & Improved Patient Care. Advocacy.
9650 Rockville Pike. Bethesda, Maryland 20814
Tel: 301-634-7939 | Fax: 301-634-7995 | amp@amp.org | www.amp.org

CASE STUDIES: Copy Number Assessments			
2:30pm	**Copy-Number Determination in Cancer Samples Using Next-Generation Sequencing Assays** This case will provide background, methods and practical examples of copy-number variation (CNV) detection as a part of next-generation sequencing (NGS) oncology profiling. Pros and cons of this methodology for CNV detection compared with other methodologies (e.g. FISH) will be discussed. • Describe how NGS data from cancer specimens may be utilized to produce clinically applicable copy-number information. • Compare the pros and cons of NGS oncology copy-number results in comparison with other methods, especially FISH.	***Jeremy Segal, MD, PhD*** *University of Chicago*	**0.5**
	Single-Nucleotide Polymorphism (SNP) Arrays and Array Comparative Genomic Hybridization for the Detection of Copy-Number and Copy-Neutral Genetic Abnormalities This case will compare the utilization, advantages, and disadvantages of SNP arrays and aCGH for detecting copy-number abnormalities (e.g., duplication, deletion) and copy-neutral abnormalities (e.g., loss of heterozygosity, uniparental disomy). • Describe the principles underlying SNP array and aCGH methodologies. • Compare the relative advantages and disadvantages of the two methodologies in different genetic or clinical scenarios.	***Kristy Crooks, PhD*** *University of Colorado*	
CASE STUDIES: Non-Invasive or Cell Free DNA Testing			
3:00pm	**Liquid Biopsies- Just Go With the Flow** This case will highlight a common clinical application and one methodology for liquid biopsies. The case will include a discussion of some of the terminology, pre-analytic, analytic, and post-analytic issues surrounding liquid biopsies. • List the appropriate clinical scenarios in which liquid biopsies are currently used and potential future applications. • Describe the specimen limitations that are inherent to liquid biopsies.	***Annette S. Kim, MD, PhD*** *Brigham & Women's Hospital*	**0.5**
	Molecular Weapons to Avoid Invasive Testing: NIPT This case will demonstrate the usefulness of non-invasive prenatal testing (NIPT) using cell- free DNA in the clinical laboratory. The case will also discuss the technical procedures as well as the clinical utility and pitfalls of the test. • Explain the procedures involved in NIPT. • Evaluate the usefulness and pitfalls of the technique.	***Roberta Sitnik, PhD*** *Hospital Israelita Albert Einstein*	
3:30pm	**Closing Remarks and Questions**	***Annette S. Kim, MD, PhD***	
3:45pm	**Adjourn**		