



Asuragen to Present at Upcoming Association for Molecular Pathology 17th Annual Meeting

Austin, Texas – November 15, 2011. [Asuragen, Inc.](#), a leader in molecular diagnostic technologies, will present at the upcoming Association for Molecular Pathology (AMP) 17th Annual Meeting, November 16-19, 2011 in Grapevine, TX. Asuragen will have a significant scientific presence at the conference with a podium talk and six posters highlighting Asuragen's development efforts in the areas of oncology, genetic testing, microRNA and next generation sequencing.

Gary Latham, Ph.D., Director of Research and Technology Development at Asuragen, will be joined by Jessica Booker, Ph.D., from University of North Carolina School of Medicine in an early bird session chaired by William Highsmith, Ph.D., from Mayo Clinic, titled "Advancements in *FMR1* Methylation PCR." The session will describe recent progress in the development and evaluation of PCR technologies to address the limitations of currently applied Southern blot analysis of methylation status in expanded *FMR1* alleles.

In addition, the following [poster presentations](#) will be made during the conference by Asuragen and its collaborators:

- "AGG Genotyping Reclassifies Expansion Risk for Equivalently Sized Intermediate and Premutation Fragile X Alleles: Outcomes of a Multicenter Study of 469 Mother-Child Transmissions" (Andrew Hadd, Asuragen; Sarah Nolin, NYS-IBR; Elizabeth Berry-Kravis, Rush; Flora Tassone, UC-Davis; Stephanie Sherman, Emory, Abstract No. G48). This poster summarizes results from a multicenter collaborative study on the effect of interrupting AGGs on stability of CGG repeats. The study shows that the number and position of AGGs affect both the risk and magnitude of CGG repeat expansion. The 3' uninterrupted CGG repeat length may be used to reclassify risk in the 45-69 CGG repeat range.
- "Beyond Southern Blot Analysis: Fragile X Syndrome Case Studies and Analysis of New Sample Types using *FMR1* Methylation PCR" (Ru Cao, Asuragen; Feliciano Ramos, Zaragoza; Rob Willemsen, Rotterdam; Elizabeth Berry-Kravis, Rush; Abstract No. G52). This poster presents the evaluation of a novel PCR-based technology (*FMR1* methylation PCR) to a series of Fragile X case studies for routine CGG sizing, allele-specific methylation assessment and genotype/epitype/phenotype correlations across different sample types.
- "Multi-Site Evaluation of a Multiplex Assay for the Rapid Detection of Leukemia Associated Fusion Transcripts" (Emmanuel Labourier, Asuragen; Christopher Gocke, Johns Hopkins; Michael Griffiths, WMRGL; Abstract No. H16). This poster describes the evaluation of a qualitative multiplex research assay for the detection of fusion transcripts resulting from chromosomal abnormalities associated with AML, ALL & CML. The assay helped resolve complex cytogenetic cases, positively identified the expected fusion transcript in RNA samples from cases with low blast count, and resulted in 99% agreement (196/198)* with standard cytogenetic methods.
- "Two Complementary and Scalable PCR-based Workflows Enable Next Generation Sequencing of Cancer-Associated Genes in FFPE Tumor DNA" (Gary Latham, Asuragen, Abstract No. TT01). This poster describes development of PCR-based target enrichment methods for amplifying dozens to thousands of cancer gene loci in tumor specimens on both Illumina and Ion Torrent NGS platforms. The results of this research study reveal sensitive and accurate identification of actionable mutations in cancer-relevant samples.
- "Development of a miRNA based Classification Model for Differential Diagnosis of Pancreatic Ductal Adenocarcinoma in Fine Needle Aspirates: a Multicentre Study" (Anna Schwarzbach, Asuragen, Abstract No. ST15). This poster describes the development and validation of a miRNA-based laboratory developed-test (miR*Inform*TM Pancreas) to aid in the differential diagnosis of PDAC in pancreatic FNA specimens. When used in conjunction with conventional FNA cytology, this testing service allows identification of PDAC with 92.5% accuracy, as compared to 80.2% for FNA cytology alone. The test also enables resolution of indeterminate FNA cytology with an accuracy of 74.1%.



- “Evaluation of the Prognostic Utility of miRNA and Commonly Proposed Genetic Markers in Stage II Colon Cancer” (Elizabeth Mambo, Asuragen; Karen Rasmussen, Spectrum Medical Group, Abstract No. ST27). This poster describes the utility of clinicopathologic features, histological parameters, and multiple genetic markers and miRNA expression in predicting cancer recurrence in stage IIA colon cancer. The research was performed in retrospectively collected colon cancer samples with known clinical outcomes. Specific miRNA predicted recurrence independent of grade and other clinicopathologic features.

About Asuragen

Asuragen is a fully integrated diagnostic development company and pharmaceutical services provider. The Company’s diagnostic product portfolio consists of the first-ever validated microRNA diagnostic service for [pancreatic cancer](#), quantitative RNA tests for [leukemia gene translocations](#), innovative genetic testing solutions for the [Fragile X mental retardation \(FMR1\) gene](#), [Signature® Oncology](#) products for the qualitative detection of gene translocations and mutations in a variety of hematological and solid tumors, RNA stabilization technologies, and industry-leading controls and standards engineered using its patented [Armored RNA® technology](#). Asuragen is empowered with a high level of scientific expertise and assay development capabilities, CLIA and GLP testing services, and an established cGMP manufacturing facility, which allow it to span the spectrum of discovery, testing, production and commercialization. For more information, visit www.asuragen.com.

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