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Spring 2019

The Path Report Volume 2 Issue 4

Pathology Department, New York Medical College

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Pathology Department, New York Medical College. (2019). The Path Report Volume 2 Issue 4. Retrieved from https://touroscholar.touro.edu/nymc_arch_news/9

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The Path Report

VOLUME II, ISSUE IV

SPRING 2019

Spotlight on Research:

Gary Williams, MD

It is with greatest pleasure that we would like to congratulate our very own Dr. Gary Williams for receiving an Excellence in Science Award from the Genetic Toxicology Association at this year's Annual Meeting at the University of Delaware. The Excellence in Science Award is the highest award in the Genetic Toxicology Association that is awarded to a member for their outstanding contribution to the field of genetic toxicology.

Dr. Williams has been a major contributor to the study of the genetic effects of chemicals. He developed proliferating cultures of rat liver epithelial cell lines which were used for investigation of the processes of cell transformation and mutagenesis. Also, he developed primary cultures of hepatocytes and demonstrated their utility for measurement of DNA repair as a screening method. These advances were recognized for their potential to reduce animal use by the Society of Toxicology with the Enhancement of Animal Welfare Award in 2002. In the course of this work, he developed the William's Medium E, an extensively used liver cell culture media.

Recently, he developed the use of avian eggs for assessment of chemical genotoxicity using measurement of liver DNA strand breaks and adducts. These unique models, named the Chicken and Turkey Egg Genotoxicity Assays, allow monitoring of changes in gene expression and histopathology in addition to genetic effects.

Dr. Williams has authored or coauthored over 500 publications. His publications have been cited more than 23,000 times as recorded by Google Scholar. In 2006 he was awarded the Dean's Distinguished Research Award by New York Medical College.



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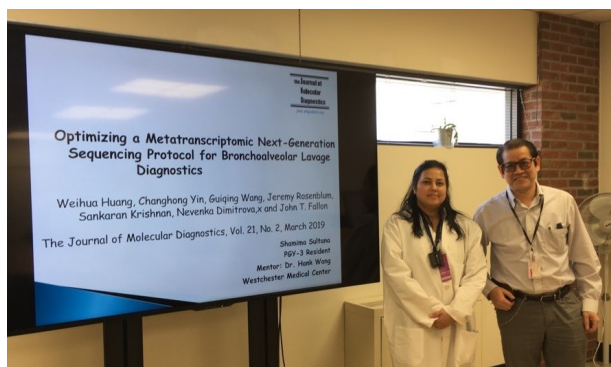
G Williams, MD

R Zachrau, MD

Journal Club Highlight:

Shamina Sultana, PGY-3 Resident, and Mentor, Dr. Hank Wang (right)

Congratulations
to first author
Weihua Huang!



Optimizing a Metatranscriptomic Next-Generation Sequencing Protocol for Bronchoalveolar Lavage Diagnostics

Huang W, Yin C, Wang G, Rosenblum J, Krishnan S, Dimitrova N, Fallon JT.

Compared with conventional serologic, culture-based, and molecular-based diagnostic tests, next-generation sequencing (NGS) provides sequence-evidenced detection of various microbes, without prior knowledge, and thus is becoming a novel diagnostic approach. Herein we describe an RNA-based metatranscriptomic NGS (mtNGS) protocol for culture-independent detection of potential infectious pathogens, using clinical bronchoalveolar lavage specimens as an example. We present both an optimized workflow for experimental sequence data collection and a simplified pipeline for bioinformatics sequence data processing. As shown, the whole protocol takes approximately 24 to 36 hours to detect a wide range of Gram-positive and -negative bacteria and possibly other viral and/or fungal pathogens. In particular, we introduce a spike-in RNA mix as an internal control, which plays a critical role in mitigating false-positive and false-negative results of clinical diagnostic tests. Moreover, our mtNGS method can detect antibiotic resistance genes and virulence factors; although it may not be comprehensive, such information is imperative and helpful for the clinician to make better treatment decisions. Results from our preliminary testing suggest that the mtNGS approach is a useful alternative in diagnostic detection of emerging infectious pathogens in clinical laboratories. However, further improvements are needed to achieve better sensitivity and accuracy.

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