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Fall 2017

The Path Report Volume 1 Issue 2

Pathology Department, New York Medical College

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Recommended Citation

Pathology Department, New York Medical College. (2017). The Path Report Volume 1 Issue 2. Retrieved from https://touroscholar.touro.edu/nymc_arch_news/2

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WHO ARE WE?

Our Faculty consists of:

• Clinical: 16 FT and 4 PT

Research: I4 FT

Teaching: 2 FT

• Active Retired: 3

In addition, we have:

- Residents: 12 AP/CP
- Four 2017 graduates with Fellowships at NYU, Manhattan MEs, UCLA, NIH

WHERE ARE WE?

Our facilities include:

- Hospitals:
 WMC, MHRH, HA
 (3), BSCH (3)
- Outreach:
 Bradhurst and
 White Plains
 clinics, physician
 offices, specialty
 groups/hospitals

The Path Report

VOLUME I, ISSUE 2

FAII 2017

Spotlight on Research: Meet our Eggspert!

The main focus of our research group is identification and assessment of chemical hazard. For this purpose we use novel model, In Ovo Genotoxicity Assay which was developed as an alternative mechanistic tool for the screening of genotoxic potential of various compounds to reduce the use of animal assays. This unique, alternative model is intermediate between in vitro and in vivo models, and utilizes metabolically competent livers of the chicken or turkey fetuses (Chicken or Turkey Egg Genotoxicity Assay (CEGA or TEGA), respectively). Since the termination of avian fetuses according to the CEGA / TEGA protocol occurs several days before hatching, in compliance with Animals (Scientific Procedures) Act 1986, the assay is not considered to be



Dr. Tetyana Kobets with egg incubators

an animal model.

The CEGA and TEGA can be used for the evaluation of multiple endpoints, including genotoxicity, histopathologic evaluation and genomic profiling which contributes to elucidation of the mechanisms on molecular and

morphological levels by which chemicals can cause cancer. For the assessment of genotoxic potential of tested compounds two assays are used 32P-nucleotide postlabeling assay which detects DNA adducts, and comet assay which detects presence of DNA strand breaks, both assays being appropriate and widely used for evaluation of chemical-induced DNA damage in vivo. The model can be also enhanced by evaluation of the histopathological changes, and, for the chicken, microarray analysis which investigates chemical -induced changes in gene expression. It is important to mention that CEGA is the first alternative model that allows enhanced analysis of tissue-specific gene expression analysis, since it utilizes the whole organism as opposed to other in vitro methods.

Recent Publications

Xu D, Dai W, Li C.

Polo-like kinase 3, hypoxic responses, and tumorigenesis.

Cell Cycle. 2017 Aug 31:0. doi: 10.1080/15384101.2017.1373224. [Epub ahead of print]

Li C, Park S, Zhang X, Eisenberg LM, Zhao H, Darzynkiewicz Z, Xu D. Nuclear Gene 33/Mig6 Regulates the DNA Damage Response through an ATM-dependent Mechanism.

J Biol Chem. 2017 Aug 25. pii: jbc.M117.803338. doi: 10.1074/jbc.M117.803338. [Epub ahead of print]





Commitment to Education

STAR Program

We were pleased to participate in this summer's STAR Program: Summer Trainees in Academic Research. Twenty-one students from high school, college, and medical school participated. Led by our own Weihua Huang and supported by Philips Healthcare, the students utilized an Amazon virtual server and learned to assemble/circularize, align/map, and correct/validate whole bacterial genomes

from sequenced Illumina short-reads and PacBio long-reads. In total, more than 70 whole genomes were achieved. In addition, two high school students are going to participate in science competitions using the genomic data they analyzed. One student, Nick Casieri, made a point to tell us that "the experience with using the IGV bioinformatics software, as well as editing and completing complete genomes, will prove invaluable as I continue my studies in Biochemistry at Boston College". In addition to educating students about bioinformatics, these whole genome sequences are from various clinical isolates with multidrug resistance and are a great resource for future research.



Dr. Weihua Huang alongside the Genomics Core Laboratory poster.

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