



*"The best prevention,  
is Early Detection"*

# EDRN Today

May 2019

CANCER BIOMARKERS RESEARCH GROUP

IN THIS ISSUE

## Early Detection Research Network (EDRN)

by Felicia Evans Long, MBA and Isabel Zaru-Roque, MPH

### EDRN is on the MOVE!

The Cancer Biomarkers Research Group (CBRG) has expertly led the extramural biomarker research. As the result of continuing proactive initiatives and discussions the group has taken several steps to involve key stakeholders in further developing the field of biomarkers in cancer risk assessment and early detection.

CBRG is increasing its social media presence! Tweets and Instagram updates will be sent out weekly to the NCI pages. NCI Blog updates will be forwarded on a monthly basis. Please forward all topics or ideas to Isabel Zaru-Roque.

### Program Director of the Month Dr. Sharmistha Ghosh-Janjigian Cancer Biomarkers Research Group (CBRG)



Dr. Ghosh-Janjigian earned her undergraduate and graduate degrees from Presidency College/University of Calcutta and Jawaharlal Nehru University in India, and conducted postgraduate research at the Beth Israel Deaconess Medical Center/Harvard Medical School in Boston. She is trained in molecular biology and immunology. Prior to joining the NCI, she served as a Scientific Editor for *Biochimica et Biophysica Acta* and a Senior Editor for *Journal of the National Cancer Institute*. Dr. Ghosh-Janjigian is responsible for management, coordination and programmatic leadership for the Pancreatic Cancer Detection Consortium (PCDC), the PreCancer Atlas (PCA) Research Centers (part of the Human Tumor Atlas Network; developed under the auspices of the Cancer MoonshotSM), the Early Detection Research Network (EDRN) and the Molecular and Cellular Characterization of Screen-Detected Lesions (MCL) Consortium.



## Investigator Spotlight, Dr. Sandy Markowitz

**Sanford Markowitz** of Case Western Reserve University, is the contact PI for the 'Biomarkers for Reducing Mortality of Cancers of the Colon and Esophagus', a Biomarker Developmental Laboratory (BDL). The MPIs include Krishna Guda of Comprehensive Cancer Center and William Grady of Fred Hutchinson Cancer Research Center.

They have developed, patented, and licensed to Lucid Diagnostics (and its parent company PavMed) the balloon sampling device and methylated DNA assay for detecting Barrett's esophagus.

These are shown on the [PavMed website](#) and will be commercialized under the names of the EsoCheck esophagus sampling device and the EsoGuard methylated DNA assay.



### Screening for Barrett Esophagus to Prevent Esophageal Cancer:

The incidence of esophageal adenocarcinoma (EAC), in the United States has been increasing for the past four decades, particularly among white men. The prognosis for most patients diagnosed with EAC is not good. The 5-year relative survival rate is 17%. Barrett esophagus (BE) is the only established precursor for EAC. BE, a condition that affects an estimated 1%–5% of the general population, is typically diagnosed in individuals with chronic acid reflux symptoms. However, only a minority of patients who develop EAC have a prior history of BE. Less than 1% BE progress to EAC per year; therefore, only infrequent endoscopic monitoring is required to check for disease progression in most people with BE.

Detection of BE currently requires performing esophagogastroduodenoscopy (EGD); however, because of the high cost of EGD and the lack of a randomized controlled trial demonstrating cost-effective reduction in EAC, endoscopy screening for BE has not been routinely recommended.

The presence of the antecedent BE remains undetected and unknown in about 95% of cases of EAC. There is a need for alternative methods for BE detection that are less expensive than EGD and can be readily implemented in an at-risk population. EDRN investigators used an experimental, swallowable, balloon-like sampling device to check esophageal tissue for changes in DNA methylation in two genes, CCNA1 and VIM, each of which they have previously shown is a biomarker for BE. When combined tests of CCNA1 plus VIM DNA methylation detected BE metaplasia with 90.3% sensitivity and 91.7% specificity. They have proposed that this approach could be a cost-effective, sensitive, and well-tolerated way of screening for BE in at risk individuals. They are currently developing biomarkers than can distinguish dysplastic from non-dysplastic BE.

## 7th MCL Steering Committee Meeting

The Molecular and Cellular Characterization of Screen-detected Lesions Consortium held its 7<sup>th</sup> semi-annual Steering Committee meeting in Nashville, Tennessee and was hosted by the MCL investigator, Dr. Pierre Massion of Vanderbilt School of Medicine. To date, extensive data has been acquired and deposited on the MCL interactive databases, including imaging for pathology using multiplex immunostaining, results from pancreatic mouse models, RNA and DNA sequencing procedures and data, development of a precancer atlas protocol that includes studying single-cell sequencing across the Consortium and common data elements that can provide the meta-data needed to organize and understand the results from these studies. The two co-chairs of the MCL Consortium, Drs. Angelo DeMarzo and Anirban Maitra, emphasized that the consortium members have benefited from extensive resources contributed by the collaborating institutions within the program and from leveraging expertise and resources of additional non-MCL collaborators through the MCL Associate Member program. Hence, the impact of the consortium has been very high and indicates the value of bringing together collaborations from population and biological sciences.

The meeting was attended by several invited investigators, including Dr. David Tuveson from Cold Spring Harbor Laboratory, who talked about developing new strategies and tools for the detection of Pancreatic Cancer, and Dr. Anil Sood from MD Anderson Cancer Center, whose presentation focused on the role that platelets play in ovarian cancer progression and response to therapy. Many investigators from the Vanderbilt School of Medicine also attended, some of whom presented their most recent, unpublished results, including Dr. Ken Lau, whose talk focused on ways of looking at early events in colorectal neoplasia and the recently awarded grant by the Moonshot HTAN program to Drs. Coffey and Lau as co-PIs focused on the development of a Pre-cancer Atlas for Colorectal Cancers.

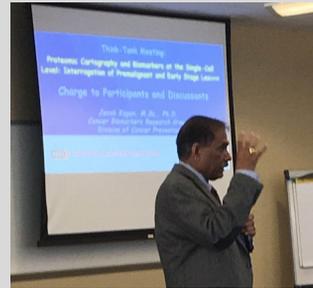


**Molecular and Cellular  
Characterization of Screen-detected  
Lesions Consortium**

# Proteomic Cartography and Biomarkers at the Single Cell Level Think Tank Meeting

The “Proteomic Cartography and Biomarkers at the Single Cell Level Think Tank Meeting” hosted by Dr. Kagan and Dr. Srivastava on April 23<sup>rd</sup> and 24<sup>th</sup> provided a platform for the exchange of groundbreaking ideas.

Single-cell proteomic analyses are pivotal to our understanding of tumor clonal evolution, detection of aberrant structural and functional changes within the tumor microenvironment, improved genotypic and phenotypic characterization of all the cells within the tumor microenvironment, identification of aberrant cellular communications networks, and aberrant protein networks within individual cells, as compared to the to the bulk tumor analysis. Finally, single-cell proteomic data is essential for the establishment of searchable, and scalable (from organ specific tissue to cellular composition to characterization of individual cells and cellular organelles) databases for characterization of human precancer and early stage tumors and the development of new generation of early detection markers.



## Brain Break

Can you solve this month's riddle? Answers will be given out in next month's newsletter. The first one to solve the riddle correctly may go to Felicia's office for the correct answer and a prize.

Turn me on my side and I am everything. Cut me in half and I am nothing. What am I?

### **Shout out to April eNewsletter Winners**

Dr. Ghosh-Janjigian from NCI and Sean Kelly from Jet Propulsion Laboratory, JPL

**The correct answer was 13112221.** Each number describes the previous number. Starting with 1, the second line describes it 11 (one 1). Then the third line describes 11 as 21 (two 1's). Then the fourth line describes 21 as 1211 (one 2, one 1). This is the pattern.