PEOPLE


Sanford-Burnham Medical Research Institute

Perry Nisen, MD, PhD, was named CEO of the Sanford-Burnham Medical Research Institute in La Jolla, CA, replacing interim CEO Kristiina Vuori, MD, PhD, effective September 15. Nisen previously worked as senior vice president of science and innovation at GlaxoSmithKline. Prior to that, he was a professor of neuro-oncology at The University of Texas Southwestern Medical Center in Dallas. In his new role, Nisen will oversee the execution of Sanford-Burnham's strategic vision to more quickly translate basic research discoveries into novel treatments for a variety of conditions.

George J. Weiner, MD, will begin a 2-year term as the president of the Association of American Cancer Institutes (AACI) at the organization's annual meeting in late October. The AACI represents 95 academic and freestanding U.S. cancer research centers and supports their efforts to eradicate cancer. Weiner directs the Holden Comprehensive Cancer Center at the University of Iowa and is a faculty member in the university's Interdisciplinary Graduate Program in Immunology. His research focuses on understanding the mechanisms of action of anticancer monoclonal antibodies and the development of immunotherapies for lymphoma.


ESMO

The European Society for Medical Oncology (ESMO) bestowed its ESMO Award upon **Carsten Bokemeyer, MD,** at its annual meeting in September in Madrid, Spain, in recognition of his outstanding contributions to medical oncology. The director of Germany's University Cancer Center Hamburg, Bokemeyer is a world leader in the pathogenesis and biology of malignant germ cell tumors.

Proteogenomics Sheds Light on Tumors

In the first integrated proteogenomic analysis of human cancer, a team of researchers analyzed proteomes of colorectal tumors and identified protein signatures of genetic mutations, potentially leading to advances in diagnosis and treatment.

The Clinical Proteomic Tumor Analysis Consortium, led by researchers at Vanderbilt University in Nashville, TN, used mass spectrometry to gather proteomic data on 95 colorectal tumor samples previously characterized by The Cancer Genome Atlas (TCGA). They found that abnormalities in the genes and messenger RNA of tumor samples did not necessarily correlate with abnormal proteins (Nature 2014 July 20 [Epub ahead of print]).

"People have analyzed messenger RNA expression patterns as signatures of cancer biology and different subtypes of cancer," says the study's senior author, Daniel Liebler, PhD, director of the Jim Ayers Institute for Precancer Detection and Diagnosis at the Vanderbilt-Ingram Cancer Center. "But what we found is that the messenger RNA actually doesn't predict what the protein will do across a collection of tumors, suggesting that protein-level expression might be a better way of characterizing subtypes of tumors."

Liebler's team found five proteomic subtypes of colorectal cancer by analyzing protein levels in the TCGA samples. Significantly, one of the TCGA subtypes split into two proteomic subtypes, only one of which was associated with poor prognosis.

"These proteomic subtypes have very different driving biology," explains Liebler. "Although we need another study to prove the association with poor outcomes, this finding shows that protein-level subtyping of tumors is going to be at least as valuable as messenger RNA transcription subtyping."

Protein-level analysis could also lead to new diagnostic tests to identify subsets of colorectal cancer, he adds.

"Protein-level measurements are already quite compatible with what is currently done to measure certain types of biomarkers and proteins associated with breast cancer, such as HER2 and estrogen receptor," notes Liebler. "Protein data that identify biologically or clinically useful subtypes have the potential to translate directly to clinical diagnostics in a way that has proven to be more difficult for RNA-based measurements."

The research team discovered that 17 chromosomal regions of significant focal amplification identified by TCGA were not necessarily associated with protein abundance, as had been assumed.

"We were very surprised to find that the proteins expressed from these loci were only elevated in four of the 17 cases and had strong effects on the expression of other genes," says Liebler. The finding suggests that proteomic measurements may help researchers zero in on the most impactful genetic abnormalities as potential therapeutic targets.

"Proteomics guides us to a subset of these amplified regions," says Liebler. "It helps us prioritize among many genomic alterations to identify the ones that look like they will have the biggest effects because they manifest very strongly at the protein level." ■

Four Subtypes of Gastric Cancer Identified

Gastric adenocarcinoma, which comprises the majority of stomach cancers, is often treated as a single disease, but it is actually multifaceted. Investigators from The Cancer Genome Atlas (TCGA) have uncovered 4 subtypes, each with distinct molecular aberrations (Nature 2014 July 23 [Epub ahead of print]).

The researchers performed 6 types of molecular characterization, including DNA methylation profiling, Epstein-Barr virus (EBV) status, whole-exome sequencing, and somatic copy-number analysis on gastric adenocarcinoma tissue from 295 untreated patients. Samples were also examined for microsatellite instability (MSI).

"We wanted to develop a robust classification system for gastric adenocarcinoma that's feasible in the real world," says corresponding author Adam Bass, MD, director of Dana-Farber Cancer Institute's Center for Esophageal and