PEOPLE

Mary-Claire King, PhD, professor of genetics and medicine at the University of Washington in Seattle, won the 2014 Lasker-Koshland Special Achievement Award in Medical Science for her contributions to medical research and human rights. Bestowed by the Albert and Mary Lasker Foundation, the annual Lasker Awards "recognize the contributions of scientists, clinicians, and public servants who have made major advances in the understanding, diagnosis, treatment, cure, or prevention of human disease" and carry a $250,000 honorarium.

In 1974, King began a meticulous analysis of more than 1,500 families of women with breast cancer, concluding that a single gene was responsible for breast cancers in some families. After analyzing DNA from hundreds of participating relatives, she reported in 1990 that a section of chromosome 17 was responsible for early-onset breast and/or ovarian cancer in some of the families. She named the gene locus *BRCA1*. She also developed DNA-based analysis to help families prove genetic relationships and reunite kidnapped and once-missing children with their biologic families.

In September, **Louis J. DeGennaro, PhD,** was named president and CEO of The Leukemia & Lymphoma Society (LLS), roles he has held on an interim basis since February; he joined the organization in 2005.

DeGennaro has more than 25 years of research, drug development, and management experience in academia and the private sector, including positions at the Max Planck Institute in Munich, Germany, and Wyeth Pharmaceuticals in Princeton, NJ.

Headquartered in White Plains, NY, LLS funds cancer research, supports educational and public-policy efforts, sponsors scientific conferences, and provides financial assistance to patients.

Guiding Genomics Use in Cancer Care

Five major cancer organizations are combining forces to propose standards for applying next-generation sequencing to clinical practice.

The Actionable Genome Consortium (AGC) was founded by Dana-Farber Cancer Institute (Boston, MA), Fred Hutchinson Cancer Research Center (Seattle, WA), The University of Texas MD Anderson Cancer Center (Houston), Memorial Sloan Kettering Cancer Center (New York, NY), and the genome-sequencing company Illumina (San Diego, CA). The group plans to define what constitutes an "actionable event" in individual tumors and to recommend best practices for biopsy, sample storage and transport, and DNA extraction; technical performance standards for DNA sequencing; standards for variant identification, annotation, and interpretation used in whole-genome sequencing; and guidelines for the format and content of clinical reports.

"We want to come up with a panel of therapeutic targets that make sense in terms of medical implications and cost," says Barrett Rollins, MD, PhD, chief scientific officer at Dana-Farber. "We're focusing on the baseline things that an oncologist would want to know about every patient's tumor to order tests that have direct clinical applicability or are very likely to."

For example, the standards might be used to justify testing for specific genetic alterations in non–small cell lung cancers, such as *EGFR* mutations or *ALK* rearrangements, that could be targeted with FDA-approved drugs, he says. Insurance companies would use the standards to determine coverage for tests that may improve clinical outcomes.

Knowing the genetic composition of a tumor may also help oncologists match patients to appropriate clinical trials, says Illumina's Robert Cohen, MBA, director of the AGC.

"In the future, the signature of a tumor will be measured or attempted to be measured in every cancer patient, and that signature should be one way that patients are matched to clinical trials," he says. "Enrollment of all appropriate patients in clinical trials would become the standard of care."

A research arm of the consortium will pursue collaborative projects tackling major issues in molecular oncology, says Cohen. One area of focus will be the potential clinical utility of circulating nucleic acids—for example, whether they could be used as a surrogate for tumor biopsies when tissue-based diagnosis is not possible, such as in patients with bone-only metastases.

The AGC plans to publish its recommendations in early 2015, says Cohen. The group will then work with national cancer organizations to develop official guidelines based on the recommendations.

"The time is right to create uniform standards for the molecular analysis of tumors," says Eric Holland, MD, PhD, director of solid tumor translational research at Fred Hutchinson. "We're going from a phase of scientific discovery to implementation and what it really means to society." ■

CTC Clusters More Likely to Cause Metastasis

Scientists know that circulating tumor cells (CTC) can clump together in groups of two to 50, but how these so-called CTC clusters form and their functional significance has remained unclear.

Now, new research shows that CTC clusters are tumor fragments, held together by the cell junction protein plakoglobin, that break off into the bloodstream. In breast cancers, these clusters are 23 to 50 times more likely to cause metastasis than single CTCs. These findings suggest that targeting pathways involving plakoglobin expression could be beneficial in reducing tumor dissemination (Cell 2014;158:1110–22).

"What kills patients is the metastasis," says co–senior author Shyamala Maheswaran, PhD, an associate professor at the Center for Cancer Research at Massachusetts General Hospital Cancer Center in Boston. "We now have better insight into a mechanism that increases the efficiency of the metastatic process."