Translational Epidemiology: Targeting Lung Cancer Screening

by Shelia Hoar Zahm, Sc.D.

Tenure-track investigators Hormuzd A. Katki, Ph.D., and Anil K. Chaturvedi, Ph.D., share a passion for applying epidemiologic discoveries to improve public health. Using their expertise in risk-based screening, the investigators demonstrated that the benefits and harms of low-dose computed tomography (LDCT) screening strongly depended on an individual’s pre-screening risk of lung cancer death, as detailed in their recent publication* in the New England Journal of Medicine. This finding is a proof-of-principle that targeting lung cancer screening efforts based on an individual’s risk of lung cancer death, rather than on coarse age/smoking criteria, could improve the efficiency of LDCT screening programs, resulting in more cases identified and fewer false positives.

The investigators’ interest in this issue began in 2011, when NCI reported the results of the National Lung Screening Trial (NLST). The results showed that screening with LDCT resulted in 20 percent lower lung cancer mortality compared to screening with chest radiography. This landmark finding led to a recommendation by the U.S. Preventive Services Task Force (USPSTF) for LDCT screening of persons aged 55 to 74 years who meet the NLST entry criteria for smoking: having a minimum of 30 pack-years smoking history and, if former smokers, had quit no more than 15 years before screening. Other expert bodies recommended LDCT screening programs using similar combinations of criteria.

However, LDCT screening of the millions of eligible U.S. smokers would entail a dramatic increase in use of LDCT resources, and many more smokers would endure further scans, invasive testing, and/or surgery as a result of false-positive findings. Drs. Katki and Chaturvedi recognized an opportunity to show that risk-based screening could be used to refine the selection criteria and thereby improve the efficiency of LDCT lung screening.

In collaboration with Dr. Katki’s postdoctoral fellow Stephanie Kovalchik, Ph.D. (now at the RAND Corporation in Santa Monica, California), the investigators used epidemiologic data to identify the persons at highest risk of lung cancer death among the already high-risk trial participants. The researchers categorized the NLST participants into risk quintiles using a lung cancer death risk calculator that they developed and validated with data from the NCI Prostate, Lung, Colorectal and Ovarian Screening Trial. The risk model included age, body mass index, family history of lung cancer, pack-years of smoking, years since smoking cessation, and emphysema diagnosis.
The authors reported that in the NLST, 88 percent of the prevented lung cancer deaths occurred in the 60 percent of participants in the top three quintiles of risk. These participants accounted for 64 percent of the false-positive screens. In contrast, only 1 percent of the prevented lung cancer deaths occurred in the 20 percent of participants in the lowest risk quintile.

“Screening only those with the best benefit-to-harm profile might result in preventing nearly all of the preventable cancer deaths with considerable cost savings, as well as reductions in complications from clinical work-ups of smokers whose findings turn out to be negative,” Dr. Katki said.

The new USPSTF lung screening recommendations cited this paper, as did the accompanying editorial by Dr. Peter Bach of the Memorial Sloan Kettering Cancer Center, who cited data from it to opine that screening guidelines should focus on screening only those people at sufficiently high risk of lung cancer death.

Work is ongoing to validate the risk model in additional study populations, including the NIH-AARP Diet and Health Study, the American Cancer Society Cancer Prevention Study II, and the Centers for Disease Control and Prevention National Health Interview Study. Once validated, the model will be made publicly available on the NCI web site. Drs. Chaturvedi and Katki are also evaluating whether biomarkers associated with lung cancer risk provide additional risk stratification.

“In earlier work, we identified circulating immune/inflammation markers that predict risk of lung cancer,” Dr. Chaturvedi explained. “We plan to evaluate if incorporating these biomarkers into eligibility criteria will aid in identifying smokers most likely to benefit and less likely to be harmed from LDCT screening.”

Ideally, lung cancer screening guidelines would reflect the principle of “equal management of people at equal risk of disease,” akin to that used in cervical cancer screening guidelines (discussed in the July 2013 issue of Linkage). Doing so would ensure simplified and consistent management of people with equal risk of lung cancer death, regardless of the specific combinations of factors leading to that risk.

“Many of the organizations who issue cancer screening guidelines have encouraged establishment of screening registries, which are needed to provide the data we would use to develop risk-based clinical management guidelines in the future,” Dr. Katki noted.

As exciting as the prospect of lung cancer screening is, however, “the most important thing for smokers to do to lower their risk of lung cancer, and all other tobacco-related diseases, is to quit smoking,” Drs. Chaturvedi and Katki stated.

Lisa Mirabello, Ph.D., M.S., and Steven C. Moore, Ph.D., M.P.H., have been selected as NIH Earl Stadtman Investigators. Named after a noted biochemist at the National Heart, Lung, and Blood Institute, the Stadtman program is a trans-NIH recruitment initiative designed to attract the most talented early career scientists to NIH.

Dr. Mirabello joined DCEG in 2007 as a postdoctoral fellow in the Clinical Genetics Branch (CGB) and became a research fellow in 2010. Dr. Mirabello is interested in understanding the contribution of genomic and epigenomic alterations to cancer etiology. She has received a number of awards for her work in this area, including a DCEG Fellowship Achievement Award as well as DCEG and NIH Fellowship Awards for Research Excellence.

Dr. Mirabello’s childhood dream was to become a veterinarian, but her priorities changed once she worked in an animal clinic after studying animal science at Cornell University. “I became more interested in understanding why the animals were sick, what caused the underlying disease,” she said. “That’s what steered me to get a master’s in experimental pathology and ultimately a Ph.D. in infectious disease and population genetics.”

During her doctoral work at the State University of New York in Albany, School of Public Health, Dr. Mirabello studied mosquito population genetics to understand the epidemiology of malaria in humans. “That work inspired my interest in public health,” she said. “It eventually led me to think about cancer epidemiology and ways that I could apply my unique background in population genetics to understand why people get cancer. That’s when I met Dr. Savage and realized that DCEG was a perfect fit.”

As a tenure-track investigator in the Genetic Epidemiology Branch, Dr. Mirabello is focused on three major areas of study: osteosarcoma, Diamond-Blackfan anemia (DBA), and human papillomavirus (HPV) methylation and genomics.

Dr. Mirabello, Sharon A. Savage, M.D., Chief of CGB, and colleagues are using genome-wide association studies and exome sequencing to better understand the genetic etiology of osteosarcoma, a rare bone cancer. In addition, Dr. Mirabello is examining how genetic variation affects patient outcomes, such as metastasis, survival, and response to chemotherapy. “The end goal is to find something that could be a novel marker of disease or clinical outcome,” she explained.

Dr. Mirabello became interested in DBA, a cancer predisposition syndrome, through her work on osteosarcoma. DBA patients have a high incidence of osteosarcoma, and she has been leading the hunt for new disease-causing mutations.

In addition, Dr. Mirabello is collaborating with Mark Schiffman, M.D., M.P.H., Nicolas Wentzensen, M.D., Ph.D., M.S., and colleagues on HPV methylation and genomics. This research is aimed at understanding the unique, highly carcinogenic nature of HPV type 16 and identifying markers to distinguish the common benign from the rare carcinogenic infections. They have initiated new projects to study the genome-wide genetic variation and methylation of the carcinogenic HPV types, starting with HPV 16.
“We are currently working on the largest study to compare all the carcinogenic HPV types, and variants within types, to try to pin down which genetic variants are linked to carcinogenicity,” she said.

Dr. Moore, also selected as an NIH Earl Stadtman Investigator, joined the Nutritional Epidemiology Branch (NEB) in 2005 through the Yale-NCI Cooperative Graduate Training Program in Cancer Epidemiology and became a research fellow in 2009. His research focuses on the role of physical activity and obesity in the development of cancer. Dr. Moore has received a number of awards for his work in this area, including a DCEG Fellowship Achievement Award and the Karen Hornbostel Memorial Award from the American College of Sports Medicine.

An avid runner since the age of 15, Dr. Moore credits this health-oriented passion and his experience working at the AIDS Division in the Connecticut Department of Public Health for inspiring his initial interest in public health. “There was a community health side to that job, but there was also a focus on data that I found very intriguing,” he said.

Dr. Moore went on to receive his M.P.H. and Ph.D. in cancer epidemiology from the Yale School of Public Health, where he discovered the emerging field of energy balance. He also developed an early interest in studying the molecular and mechanistic mediators of cancer.

As a tenure-track investigator in NEB, Dr. Moore studies the role of obesity-related factors on cancer risk, including waist circumference, sedentary behavior, and physical activity. With Charles E. Matthews, Ph.D., and other collaborators, he is exploring these questions in large population-based studies.

“Right now, we’re working on the largest study to date of physical activity and cancer using pooled data from the NCI Cohort Consortium,” he said. “This study is unique in that it’s the first Cohort Consortium study to examine a single exposure across all individual cancer types. By providing definitive data on physical activity and cancer risk, this study could help to inform or refine public health guidelines for physical activity.”

Dr. Moore is also a pioneer in the field of metabolomics, which applies novel high-throughput technology to analyze small-molecule metabolites in biospecimens like blood or urine as a way to understand how molecular pathways may influence cancer risk. In studying the metabolomics of energy balance, Dr. Moore, Joshua Sampson, Ph.D., Rashmi Sinha, Ph.D., Deputy Chief of NEB, and colleagues have been instrumental in uncovering biomarkers for body mass index and diet.

“As a group, we were some of the very first people to examine how metabolomics can help predict future cancer,” Dr. Moore said. “It’s been exciting to see this collaboration come together.”

As DCEG investigators, Drs. Mirabello and Moore enjoy the independence and intellectual freedom of academic research. Their motivation stems from a passion for discovery and a desire to make a lasting impact on the field of public health.

“I hope that one day my discoveries may be translated into tools to improve cancer screening or management, and ultimately improve human health,” Dr. Mirabello said. “That is my goal.”

“The most exciting thing for me is finding something new,” Dr. Moore said, “finding something that nobody has ever seen before. And sometimes making observations that in one light are not striking but in another light—when you think about them again—are a big deal.”
Sharon Savage Appointed Chief of the Clinical Genetics Branch

Sharon A. Savage, M.D., was named the new Chief of the Clinical Genetics Branch (CGB). She takes over from Mark H. Greene, M.D., who directed the Branch since its creation in 1999. Dr. Greene will stay on in CGB as a senior investigator.

Dr. Savage joined CGB in 2006 as a tenure-track investigator and was promoted to senior investigator with tenure in 2012. Her research has focused on the genetic and molecular epidemiology of telomere biology, pediatric cancer etiology, and inherited cancer predisposition syndromes, including dyskeratosis congenita and Li-Fraumeni syndrome. Dr. Savage currently leads an international effort focused on the genetic etiology of osteosarcoma, and serves as the NCI Liaison to the American Academy of Pediatrics Council on Environmental Health. She was recently elected to the American Society of Clinical Investigation in honor of her scholarly achievements in biomedical research.

Sam Mbulaiteye Awarded Scientific Tenure

Sam M. Mbulaiteye, M.D., of the Infections and Immunoepidemiology Branch (IIB), has been awarded scientific tenure by the NIH. His research focuses on unraveling the role of infections, immunity, and genetic factors in the etiology of Burkitt lymphoma (BL) and Kaposi sarcoma. Both of these malignancies are endemic in Africa and their risk is substantially increased in the setting of HIV/AIDS.

Dr. Mbulaiteye received his primary medical degree in 1990 from Makerere University in Kampala, Uganda. He earned an M.Phil. in epidemiology and biostatistics in 1994 from the University of Cambridge in the United Kingdom (U.K.), and received specialization in internal medicine (M. Med.) from Makerere University in 1996.

After working at the Uganda Cancer Institute and the Uganda Virus Research Institute, Dr. Mbulaiteye joined IIB as a research fellow in 2000. He is a principal investigator of the Epidemiology of Burkitt Lymphoma in East-African Children and Minors (EMBLEM) study, a multicountry and multiyear case-control study of childhood BL in Uganda, Tanzania and Kenya. The study is providing the opportunity to explore whether genetic resistance to malaria lowers risk of BL, among other questions.

Dr. Mbulaiteye is a member of the Editorial Board for the International Journal of Cancer, Frontiers in Cancer Epidemiology and Prevention, and Co-Editor-in-Chief for Infectious Agents and Cancer. At NCI, he currently serves on the DCEG Genotyping Review Committee and the NIH Tenure-Track Investigators Committee.

Dr. Mbulaiteye is a recipient of the DCEG Outstanding Paper by a Fellow (2003), the NCI Directors Investigator Innovation Award (2008), and the NIH Award of Merit (2008), and was featured in an NCI Special Report: A Journey to Discovery, Journal of Minority Medical Students (2009).
Highlights from the 2014 NCI Intramural Scientific Retreat

In January, DCEG scientists participated in the annual NCI Intramural Scientific Investigators Retreat. Three DCEG tenure-track investigators were invited to give presentations highlighting their research.

Sam Mbulaiteye, M.D., spoke on “Burkitt lymphoma: Use of new tools to answer old questions”; Nicolas Wentzensen, M.D., Ph.D., discussed “Methylation biomarkers in the etiology and prevention of gynecologic malignancies”; and Xiaohong Rose Yang, Ph.D., M.P.H., presented “Identifying novel high-risk susceptibility genes for familial chordoma and melanoma.”

During the retreat, Neil E. Caporaso, M.D., received the 2014 NCI Women Scientist Advisors Mentoring and Leadership Award.

In addition, Douglas Lowy, M.D., NCI Deputy Director, presented the 2014 NCI Director’s Innovation Awards, which are designed to support the development of novel approaches and technologies for accelerating cancer research. These include Principal Investigator (PI) Awards, which are given to tenure-track or recently tenured PIs (within five years of tenure), with an upper limit of $50,000, and Career Development Awards, which are given to postdoctoral fellows, staff scientists, staff clinicians, and senior scientists, with an upper limit of $10,000. Fourteen DCEG scientists received awards, as listed below:

**Principal Investigator Awards**

Laura Beane-Freeman, Ph.D., and Melissa C. Friesen, Ph.D.
“Lung cancer-related inflammatory markers associated with endotoxin and other bioaerosol exposures in agricultural settings”

Kevin M. Brown, Ph.D.
“A genome-scale functional screen to identify genes mediating melanocyte bypass of oncogene-induced senescence and melanoma risk”

Ludmila Prokunina-Olsson, Ph.D.
“Development of total and allele-specific in situ mRNA detection of the prostate stem cell antigen (PSCA) in several tumor types”

Douglas R. Stewart, M.D.
“Characterization of the spectrum of localized rearrangements in neurofibromatosis type 1-associated tumors”

**Career Development Awards**

Maria Constanza Camargo, Ph.D., M.S., M.H.A.
“Comparison of *Helicobacter pylori* strains associated with gastric cancer”

Shahinaz M. Gadalla, M.D., Ph.D.
“Transcriptomic profiling in the cancer predisposition syndrome dyskeratosis congenita”
Lauren C. Houghton, Ph.D.
“A study of endocrine disruptors and breast cancer risk in migrants”

Paula Hyland, Ph.D., M.P.H.
“Characterizing the methylome diversity of gastric cancer from a high risk Chinese population”

Rena Jones, Ph.D., M.S.
“Environmental exposures and cancer risks from concentrated animal feeding operations in the Agricultural Health Study”

Troy Kemp, Ph.D. (contractor)
“T follicular helper cells: Role in HPV vaccine immunogenicity”

Olusegun Onabajo, Ph.D.
“Development of an IFNL4-inducible cell line for high throughput screening of small molecule inhibitors”

Anand Pathak, M.D., Ph.D., M.P.H.
“Elucidating molecular mechanisms in familial hairy cell leukemia using methylation array analysis”

Qian Xiao, Ph.D., M.P.H.
“Inequalities in colorectal cancer: The influence of built environment and change in neighborhood”

DCEG Hosts Dame Valerie Beral, 2014 NCI Rosalind Franklin Award Recipient

In January, DCEG hosted Dame Valerie Beral, Professor of Epidemiology and Director of the Cancer Epidemiology Unit at the University of Oxford, for a two-day visit.

Dame Valerie is the 2014 recipient of the NCI Rosalind Franklin Award. She was presented with the award at the NCI Intramural Scientific Investigators Retreat, where she spoke on “Rosalind Franklin and Cancer in Women.”

After the retreat, Dame Valerie visited DCEG as a Distinguished Lecturer. She shared the story of Rosalind Franklin with DCEG staff and joined a vibrant discussion on career development issues, work-life balance, and modern challenges in the workplace. The event was hosted by Amy Berrington de González, D.Phil., Patricia Hartge, Sc.D., and Katherine McGlynn, Ph.D., Deputy Chief of the Hormonal and Reproductive Epidemiology Branch.

Dame Valerie is an eminent epidemiologist with research interests in hormonal, reproductive, and infectious causes of cancer. After studying medicine at Sydney University, she undertook clinical work in Australia, New Guinea, and the United Kingdom and spent almost 20 years working in the Department of Epidemiology at the London School of Hygiene and Tropical Medicine. Dame Valerie is principal investigator for the Million Women Study on the effects of women’s lifestyles on health, with a particular focus on the effects of hormone replacement therapy. She also leads international collaborative studies of breast, ovarian and endometrial cancer.
Staff Recognized at DCEG Town Hall Meeting

In February, DCEG held a Town Hall Meeting to recognize the accomplishments of Division members during the past year. Stephen J. Chanock, M.D., Director of DCEG, welcomed staff and gave an update on Division activities. In addition, he paid special tribute to those who have made a substantial impact with their scientific contributions and service to the Division and Institute in 2013.

Fellowship Achievement Awards honored fellows who excelled during the past year and included stipend increases at the next appointment renewal. Recipients were Paige Maas, Hilary Robbins, M.S.P.H., Sarah Nyante, Ph.D., Sara Karami, Ph.D., Arash Etemadi, M.D., M.P.H., Ph.D., and Mitchell Machiela, Sc.D.

Awards were also given for DCEG Outstanding Research Papers of 2013 in recognition of exceptional publications from fellows and staff scientists or clinicians. The Division's Senior Advisory Group judged the competition based on the papers' impact, innovation, and clarity of thought and language. Five fellows received awards:

Peter Aka, Ph.D.
“Endemic Burkitt lymphoma is associated with strength and diversity of Plasmodium falciparum malaria stage-specific antigen antibody response,” Blood

Bari Ballew, Ph.D.
“A recessive founder mutation in Regulator of Telomere Elongation Helicase 1, RTEL1, underlies severe immunodeficiency and features of Hoyeraal Hreidarsson Syndrome,” PLoS Genetics

Indu Kohaar, Ph.D. (former DCEG fellow)
“Genetic variant as a selection marker for anti-prostate stem cell antigen immunotherapy of bladder cancer,” Journal of the National Cancer Institute

Stephanie Kovalchik, Ph.D. (former DCEG fellow)
“Targeting of low-dose CT screening according to the risk of lung-cancer death,” New England Journal of Medicine

Meredith Shiels, Ph.D.
“Circulating inflammation markers and prospective risk of lung cancer,” Journal of the National Cancer Institute

The recipient in the staff scientist or clinician category was:

Hannah P. Yang, Ph.D.
Each year, the Division recognizes staff members who have gone above and beyond the regular call of duty and provided a tremendous service to their Office, Branch, or the Division as a whole. DCEG Special Appreciation Awards were given to Casey Dagnall, for her critical work involving multiple process implementations, improvements, and cost savings initiatives for the Cancer Genomics Research Laboratory (CGR); Joseph Boland, M.S., for his outstanding leadership as the Director of CGR’s Research and Development group; Charlotte Mercanti, for her instrumental role in coordinating DCEG’s move from Executive Plaza to the Shady Grove building; and Mindy Kaufman, for her tireless work providing support to the Division Director for the past 12 years.

Michael Cook, Ph.D., and Laura Beane Freeman, Ph.D., received DCEG Outstanding Mentor Awards in recognition of their exceptional commitment to the growth and productivity of junior scientists. In the nomination by fellows, Dr. Cook was praised for “personalizing his mentoring for different projects and adeptly wearing and switching between the hats of teacher, coach, and sponsor.” Dr. Beane Freeman was recognized for her “characteristic unselfishness and collegiality, a reason why all those who have benefitted from her mentorship consider her a valuable resource.”

A DCEG Exemplary Service Award was given to Mark H. Greene, M.D., in honor of his exemplary service in the creation and growth of an outstanding intramural program in clinical cancer genetics in DCEG and for his service to DCEG, NCI, and NIH over the past 15 years. Dr. Greene has been a key member of multiple working groups within the Division, NCI, and NIH and has served on 26 highly influential intramural and extramural committees. Nearly all of Dr. Greene’s acts of service have been generously given during his term as Chief of the Clinical Genetics Branch (CGB) and also while conducting his own highly successful research program, with more than 200 publications to his credit. In addition, Dr. Greene has mentored 23 individuals who have all gone on to extraordinary careers, and worked tirelessly to help trainees and recruit the best scientific staff to the CGB and to the Division.

Winners of the 2014 DCEG Fellows Award for Research Excellence, which had been announced earlier in the year, also received recognition at the Town Meeting. The event was coordinated by Alyssa Voss, M.P.H., Office of Communications and Special Initiatives.
DCEG Honorees at NCI Director’s Award Ceremony

At the NCI Director’s Awards ceremony in November, several DCEG staff members received NIH Merit Awards and Service Certificates.

**Group Merit Awards**

The Children and Family Studies Group, including Martha Linet, M.D., Chief of the Radiation Epidemiology Branch, received a Group Merit Award for scientific leadership and persistent effort to conduct high quality epidemiologic research, provide training to build cancer research capacity, and to foster collaboration with Chinese scientists.

The IFNL4 Discovery Group, including Thomas R. O’Brien, M.D., M.P.H., Ludmila Prokunina-Olsson, Ph.D., and Wei Tang, Ph.D., was recognized for the discovery of a new human interferon gene and its common genetic variant that affects clearance of hepatitis C infection.

The Chernobyl Study Team, which included Andre Bouville, Ph.D., Alina Brenner, M.D., Ph.D., Elizabeth Khaykin Cahoon, Ph.D., Vladimir Drozdovitch, Ph.D., Maureen Hatch, Ph.D., Mark Little, D.Phil., Jay Lubin, Ph.D., Kiyohiko Mabuchi, M.D., Dr.P.H., Evgenia Ostroudova, M.D., Ph.D., and Abigail Ukwuani, M.P.A., received a Group Merit Award for path-breaking studies of thyroid cancer in persons exposed at young ages to fallout and of leukemia in radiation-exposed clean-up workers following the Chernobyl accident.

The NCI Federal Cohort Consortium Secretariat Members Group, including Patricia Hartge, Sc.D., Robert Hoover, M.D., Sc.D., Director of the Epidemiology and Biostatistics Program, and Geoffrey Tobias, was recognized for outstanding and sustained scientific and managerial leadership of the NCI Cohort Consortium.

In addition, many DCEG staff received NCI Appreciation Awards in recognition of outstanding services to NCI as move coordinators for the 2013 relocation to the NCI Shady Grove facility. DCEG move coordinators included Bridget Bell, Renée Bremer, M.S., Sandra Brown, Gabriela Cadena, David Check, Christine Crawford, Prisca Fall-Keita, M.A., Jecholia Gallagher, Armen Ghazarian, M.P.H., Sadie Holmes-Lillie, Ka Lai Lou, Ingrid Navard, Jenna Nober, Mila Oasan, Barbara Rogers, Tawanda Roy, Alyssa Voss, M.P.H., and Tricia Wilkerson.

**DCEG Length of Service Certificates**

Several Length of Service certificates were awarded to DCEG staff:

Forty years of service: Catherine McClave, M.S., Chief of the Office of Communications and Special Initiatives

Thirty years of service: Roni Falk, M.S., and Kristin Kiser, M.H.A., M.S.

Twenty years of service: Michelle Lathrop

Ten years of service: Rachael Stolzenberg-Solomon, Ph.D., M.P.H., R.D.
Gladys Glenn, Physician-Researcher, Retires

In January, Gladys M. Glenn, M.D., Ph.D., retired from NCI after 30 years of government service. Dr. Glenn received her M.D. in 1976 and a Ph.D. in molecular biology in 1979 from the University of Pennsylvania Schools of Medicine and Graduate School, respectively, in Philadelphia. She completed her internship and internal medicine residency in 1982, becoming board certified in internal medicine. After oncology fellowship training at the Johns Hopkins Oncology Center in Baltimore, Maryland, Dr. Glenn joined NCI’s Laboratory of Immunobiology in 1984. While there, she began molecular biology investigations with her colleagues that led to identification of the von Hippel-Lindau (VHL) disease gene, the first of several hereditary kidney cancer susceptibility genes identified later by this group of multidisciplinary associates.

Dr. Glenn became credentialed at the NIH Clinical Center, and over the next decades she combined research work with clinical responsibilities, all focused on hereditary kidney cancer. During her subsequent service in the NCI Cancer Diagnosis Branch, Dr. Glenn received the Public Health Service Special Achievement Award for her work in clinical investigative screening.

In 1996, Dr. Glenn joined DCEG’s Genetic Epidemiology Branch, where she continued as physician and clinical genetic investigator in the screening clinic. In early 2010, Dr. Glenn joined the Clinical Genetics Branch (CGB). As a staff clinician, she participated in and contributed to CGB's ongoing studies of familial testicular cancer and inherited bone marrow failure syndromes, and the new study of DICER1-related familial pleuropulmonary blastoma.

Stephen Chanock, M.D., Division Director, commented, “Dr. Glenn’s combination of formal training in internal medicine, medical oncology, and molecular biology positioned her to be one of the early major players in the clinical genetics revolution. We are deeply indebted to her for her service, both to the NIH/NCI scientific enterprise and her dedication to the countless men and women afflicted by hereditary kidney cancer. Their lives have benefited beyond measure from her life’s work.”

DCEG Post-Docs Receive Sallie Rosen Kaplan Fellowship

Four DCEG fellows were selected to receive the 2014 Sallie Rosen Kaplan (SRK) Postdoctoral Fellowship for Women Scientists in Cancer Research: Anna Coghill, Ph.D., M.P.H., Immunoepidemiology and Infections Branch; Ashley Felix, Ph.D., Hormonal and Reproductive Epidemiology Branch, Kristin Guertin, Ph.D., M.P.H., Nutrition Epidemiology Branch; and Rena Jones, Ph.D., M.S., Occupational and Environmental Epidemiology Branch.

The goal of the SRK program is to better equip NCI female postdoctoral fellows to remain in a biomedical research career. Fellows will receive additional mentoring and will take part in seminars and workshops designed to strengthen leadership skills.
The DCEG Fellows Awards for Research Excellence (D-FARE) program provides funding for travel to scientific meetings or conferences to fellows who have made exceptional contributions to research projects. These contributions may include formulating research ideas, developing study designs, conducting fieldwork and analysis, or interpreting results. Each of the recognized fellows also must have played a major role in drafting a manuscript. Special consideration is given to projects in which fellows demonstrate growth beyond the discipline of their previous training.

The D-FARE program was established because scientific meetings are integral to the fellowship experience. The awards enable a greater number of fellows to participate in meetings, where they present their work, hear about new scientific developments, and establish vital connections with other scientists.

This year, seven D-FARE winners were chosen by members of an ad hoc DCEG committee. Winners received a $1,500 travel award to present their research at a scientific meeting.

The 2014 D-FARE recipients and the titles of their abstracts are:

**Hannah Arem, M.H.S., Ph.D.**
“Leisure time physical activity and mortality: Is more better?”

**Clara Bodelon, Ph.D., M.S.**
“Transvaginal ultrasound (TVU) scans and detection of ovarian cancer in the Prostate, Lung, Colorectal and Ovarian (PLCO) trial”

**Ashley S. Felix, Ph.D., M.P.H.**
“Inverse associations between tubal ligation and endometrial cancer stage in the Gynecologic Oncology Group 210 Trial”

**Jinping Jia, Ph.D.**
“Functional characterization of the pancreatic cancer *TERT-CLPTM1L* risk locus on chr5p15.33”

**Hilary Robbins, M.S.P.H.**
“Excess burden of cancer among HIV-infected persons in the United States”

**Meredith Shiels, Ph.D.**
“Cigarette smoking and systemic immune and inflammation markers”

**Britton Trabert, Ph.D., M.S., M.S.P.H.**
“Serologic markers of *Chlamydia trachomatis* infection and ovarian cancer risk”
**Scientific Highlights**

**Bladder Cancer**

**Genetic Susceptibility**

A new genome-wide association study and meta-analysis of approximately 7,000 bladder cancer cases and 12,000 controls of European descent identified two new loci that achieved genome-wide statistical significance (rs10936599 on 3q26.2 and rs907611 on 11p15.5) as well as two additional loci that approached genome-wide statistical significance (rs6104690 on 20p12.2 and rs4510656 on 6p22.3). (Figueroa JD, Ye Y, Siddiq A, et al. *Genome-wide association study identifies multiple loci associated with bladder cancer risk.* *Hum Mol Genet* 2014;23:1387–1398)

**Urine Concentration and Genetic Susceptibility**

The authors found an association between a representative genetic variant (rs10775480) of *SLC14A1*, a gene linked to bladder cancer in genome-wide association studies, and urine concentration, as measured by urinary specific gravity, among 275 population-based controls enrolled in the New England Bladder Cancer Study, suggesting a possible mechanism for the increased bladder cancer susceptibility associated with rs10775480. (Koutros S, Baris D, Fischer A, et al. *Differential urinary specific gravity as a molecular phenotype of the bladder cancer genetic association in the urea transporter gene, SLC14A1.* *Int J Cancer* 2013;133:3008–3013)

**Breast Cancer**

**Gene-environment Interactions**

This large international collaborative study provided the first strong evidence that breast cancer risks associated with several single nucleotide polymorphisms were modified by established risk factors (age at menarche, parity, breastfeeding, body mass index, height, oral contraceptive use, menopausal hormone therapy use, alcohol consumption, cigarette smoking, and physical activity). (Nickels S, Truong T, Hein R, et al. *Evidence of gene-environment interactions between common breast cancer susceptibility loci and established environmental risk factors.* *PLoS Genet* 2013;9(3):e1003284)

**Genetic Modifiers of BRCA2**

Through the Consortium of Investigators of Modifiers of *BRCA1/2*, the investigators identified stronger associations with breast cancer risk among *BRCA2* mutation carriers for genetic variants in *FGFR2*, *MAP3K1*, *CDKN2A/B*, and *PTHLH* than previously reported and identified a novel susceptibility allele at 6p24 (rs9348512) that was inversely associated with risk. The locus lies within a region containing *TFAP2A*, which encodes a transcriptional activation protein that interacts with several tumor suppressor genes. (Gaudet MM, Kuchenbaecker KB, Vijai J, et al. *Identification of a BRCA2-specific modifier locus at 6p24 related to breast cancer risk.* *PLoS Genet* 2013;9(3):e1003173)

**GWAS in BRCA1 Mutation Carriers**

A multi-stage genome-wide association study (GWAS) of 11,705 *BRCA1* carriers (of whom 5,920 were diagnosed with breast cancer and 1,839 were diagnosed with ovarian cancer), with a further replication in an additional sample of 2,646 *BRCA1* carriers, identified a novel breast cancer risk modifier locus at 1q32 for *BRCA1* carriers (rs2290854) and two novel ovarian cancer risk modifier loci at 17q21.31 (rs17631303) and 4q32.3 (rs4691139).
Inflammatory Breast Cancer Etiology


New Genetic Variants Identified Through Gene-environment Interactions


**Cervical Cancer**

HPV 16 Variants in Taiwan

A study of the associations between variants of human papillomavirus (HPV) 16 and risk of cervical neoplasia among women in Taiwan showed that the Asian variant was the most prevalent variant (81.8%) of HPV 16 in Taiwan and also was associated with a 10-fold increased prevalence of histologically confirmed cervical intraepithelial neoplasia grade 3 or worse, compared to the HPV 16 European variant. (Chang YJ, Chen HC, Pan MH, et al. Intratypic variants of human papillomavirus type 16 and risk of cervical neoplasia in Taiwan. *J Med Virol* 2013;85:1567–1576)

**Colorectal Cancer**

Innate Immunity Gene Polymorphisms

In a case-control study within the Prostate, Lung, Colorectal and Ovarian Cancer Screening Trial, a single nucleotide polymorphism at rs2838732 (*ITGB2*) was associated with colorectal neoplasia, with a stronger association for colorectal cancer than for adenoma, and among never and former smokers but not among current smokers. (Chang CM, Chia VM, Gunter MJ, et al. Innate immunity gene polymorphisms and the risk of colorectal neoplasia. *Carcinogenesis* 2013;34:2512–2520)

Opium Use

Long-term smoking and ingestion of opium, even in low doses, was associated with increased risk of death from both malignant and nonmalignant digestive diseases among the participants of the Golestan Cohort Study, a prospective cohort study in northeastern Iran. (Malekzadeh MM, Khademi H, Pourshams A, et al. Opium use and risk of mortality from digestive diseases: A prospective cohort study. *Am J Gastroenterol* 2013;108:1757–1765)
**Esophageal Cancer**

**GWAS of Esophageal Adenocarcinoma and Barrett Esophagus**

A genome-wide association study (GWAS) compared 2,390 cases of esophageal adenocarcinoma and 3,175 cases of Barrett esophagus with 10,120 controls in 2 phases and identified novel associations of loci at 19p13 (rs10419226) in **CRTC1**, 9q22 (rs11789015), and 3p14 (rs2687201). The study also extended the previously reported association of a loci near the putative tumor suppressor gene **FOXF1** at 16q24 with Barrett esophagus to now include esophageal adenocarcinoma. (Levine DM, Ek WE, Zhang R, et al. *A genome-wide association study identifies new susceptibility loci for esophageal adenocarcinoma and Barrett's esophagus*. *Nat Genet* 2013;45:1487–1493)

**Prediagnostic Plasma Vitamin C in a Chinese Population**

A case-cohort study in China showed that higher circulating vitamin C levels were associated with a reduced risk of incident gastric adenocarcinoma, but no association was found with esophageal squamous cell carcinoma. (Lam TK, Freedman ND, Fan JH, et al. *Prediagnostic plasma vitamin C and risk of gastric adenocarcinoma and esophageal squamous cell carcinoma in a Chinese population*. *Am J Clin Nutr* 2013;98:1289–1297)

**Gastric Cancer**

**Genetic Variants in Fas Signaling Pathway Genes**

An examination of 554 single nucleotide polymorphisms in 53 Fas signaling-related genes using a pathway-based approach identified significant associations for gastric cancer overall and gastric cardia adenocarcinoma, but not gastric noncardia adenocarcinoma, among ethnic Chinese. Among examined genes in the Fas signaling pathway, **MAP2K4, FAF1, MAPK8, CASP10, CASP8, CFLAR, MAP2K1, CAP8AP2, PAK2, and IKBKB** were associated with risk of gastric cancer, and **FAF1 and MAPK8** were significantly associated with risk of both gastric cardia adenocarcinoma and gastric noncardia adenocarcinoma. (Hyland PL, Lin SW, Hu N, et al. *Genetic variants in fas signaling pathway genes and risk of gastric cancer*. *Int J Cancer* 2014;134:822–831)

**Prediagnostic Plasma Vitamin C in a Chinese Population**

A case-cohort study in China showed that higher circulating vitamin C levels were associated with a reduced risk of incident gastric adenocarcinoma, but no association was found with esophageal squamous cell carcinoma. (Lam TK, Freedman ND, Fan JH, et al. *Prediagnostic plasma vitamin C and risk of gastric adenocarcinoma and esophageal squamous cell carcinoma in a Chinese population*. *Am J Clin Nutr* 2013;98:1289–1297)

**Smoking and Alcohol in Relation to EBV-positive Gastric Cancer**

In an international collaborative study of 2,648 gastric cancer patients, a stronger association for smoking, but not for alcohol consumption, was observed among patients with Epstein-Barr virus (EBV)-positive tumors than among patients with EBV-negative tumors. (Camargo MC, Koriyama C, Matsuo K, et al. *Case-case comparison of smoking and alcohol risk associations with Epstein-Barr virus-positive gastric cancer*. *Int J Cancer* 2014;134:948–953)
Liver Cancer

Vitamin D, Incident Liver Cancer, and Chronic Liver Disease Mortality


Lung Cancer

Unique EGFR and KRAS Mutation Pattern Associated with Household Coal Burning

In a study of lung cancer among never smokers from a region in China where coal is typically burned indoors, high mutation frequencies in EGFR exon 18 and KRAS and low mutation frequency in EGFR exon 21 were observed that were strikingly divergent from mutation patterns found in other smoking and never smoking populations from Asia. (Hosgood HD 3rd, Pao W, Rothman N, et al. Driver mutations among never smoking female lung cancer tissues in China identify unique EGFR and KRAS mutation pattern associated with household coal burning. Respir Med 2013;107:1755–1762)

Lymphoma

Cigarette Smoking and Hodgkin Lymphoma

Data from 12 case-control studies in the InterLymph Consortium demonstrated an increased risk of Hodgkin lymphoma among ever smokers overall (odds ratio [OR] = 1.1), which reflected associations with mixed cellularity subtype (OR = 1.6) and Epstein-Barr virus–positive tumors (OR = 1.8) among current smokers. (Kamper-Jørgensen M, Rostgaard K, Glaser SL, et al. Cigarette smoking and risk of Hodgkin lymphoma and its subtypes: A pooled analysis from the International Lymphoma Epidemiology Consortium (InterLymph). Ann Oncol 2013;24:2245–2255)

JAK/STAT Signaling Pathway Genes

In a population-based case-control study among Connecticut women, investigators identified three single nucleotide polymorphisms in STAT3 (rs12949918 and rs6503695) and STAT4 (rs932169) associated with non-Hodgkin lymphoma risk, suggesting that genetic variation in JAK/STAT pathway genes may play a role in lymphomagenesis. (Chen Y, Lan Q, Zheng T, et al. Polymorphisms in JAK/STAT signaling pathway genes and risk of non-Hodgkin lymphoma. Leuk Res 2013;37:1120–1124)

Occupational Exposure to Trichloroethylene

One-carbon Metabolizing Pathway Genes and Gene-nutrient Interaction

A population-based case-control study of non-Hodgkin lymphoma (NHL) among Connecticut women observed significantly reduced risks for the CBS Ex9+33C > T (TT vs. CC), the MBD2 −2176C > T (CC vs. TT), and the FTHFD Ex21+31A > G (AG vs. AA) genotypes, with the reduced risk mainly apparent among those who had higher dietary intakes of vitamin B₆, methionine, and folate, suggesting that variation in several one-carbon metabolizing pathway genes may influence the risk of NHL through gene-nutrient interactions involving dietary nutrient intakes. (Li Q, Lan Q, Zhang Y, et al. Role of one-carbon metabolizing pathway genes and gene-nutrient interaction in the risk of non-Hodgkin lymphoma. Cancer Causes Control 2013;24:1875–1884)

Methods

Combining P-values in Genomic Studies

After genetic regions have been identified in genome-wide association studies, investigators often follow up with more targeted investigations of specific regions. These investigations typically are based on single nucleotide polymorphisms (SNPs) with dense coverage of a region. Methods are thus needed to test the hypothesis of any association in given genetic regions, combining p-values obtained from testing individual SNPs. The authors have devised a permutation-based version of a sequential procedure for testing the global null hypothesis of no association in a region that accounts for correlations of tests based on SNPs in the same genetic region. (Chen HS, Pfeiffer RM, Zhang S. A powerful method for combining P-values in genomic studies. Genet Epidemiol 2013;37:814–819)

Metabolomics in Epidemiology

The authors assessed the variability of a large subset of metabolites among 60 women at baseline and year one of the Shanghai Physical Activity Study, and observed patterns were confirmed in the Prostate, Lung, Colorectal and Ovarian Cancer Screening study. The authors offer guidelines for determining the sample sizes needed to conduct metabolomic studies in epidemiology. (Sampson JN, Boca SM, Shu XO, et al. Metabolomics in epidemiology: Sources of variability in metabolite measurements and implications. Cancer Epidemiol Biomarkers Prev 2013;22:631–640)

Strategies for Developing Prediction Models from GWAS

The authors studied various aspects of building risk prediction models based on single nucleotide polymorphisms (SNPs) from genome-wide association studies (GWAS) to improve discriminatory accuracy, as measured by the area under the receiver operating characteristic curve, using realistic estimates of the distributions of genetic effect sizes, allele frequencies, and linkage disequilibrium patterns based on GWAS data for Crohn’s disease and prostate cancer. The most critical aspect of prediction model building was initial SNP selection, with a single-phase procedure and univariate (marginal) estimation performing best. For complex diseases and samples of 10,000 or fewer cases and controls, one should limit the number of SNPs to tens or hundreds. (Wu J, Pfeiffer RM, Gail MH. Strategies for developing prediction models from genome-wide association studies. Genet Epidemiol 2013;37:768–777)

Testing Multiple Biological Mediators Simultaneously

As a replacement for the Bonferroni correction, the authors propose a permutation approach that tests multiple putative mediators and controls the familywise error rate, which significantly improves the power to detect mediators even when all biomarkers are independent. (Boca SM, Sinha R, Cross AJ, et al. Testing multiple biological mediators simultaneously. Bioinformatics 2014;30:214–220)
**Multiple Myeloma**

**Alcohol Consumption**

An analysis of six case-control studies participating in the International Multiple Myeloma Consortium (1,567 cases, 7,296 controls) observed a significantly decreased risk associated with ever drinking alcohol (men: odds ratio [OR] = 0.7; women: OR = 0.8), with a stronger inverse association when comparing current to never drinkers (men: OR = 0.6; women: OR = 0.6), but null among former drinkers. (Andreotti G, Birmann B, De Roos AJ, et al. *A pooled analysis of alcohol consumption and risk of multiple myeloma in the International Multiple Myeloma Consortium*. *Cancer Epidemiol Biomarkers Prev* 2013;22:1620–1627)

**Obesity**

**Sleep Duration, Weight Change, and Obesity**

In a prospective cohort of 83,377 U.S. men and women aged 51–72 years, the authors observed that participants who reported less than 5 hours of sleep per night had an approximately 40% higher risk of developing obesity than those who reported 7–8 hours of sleep. (Xiao Q, Arem H, Moore SC, et al. *A large prospective investigation of sleep duration, weight change, and obesity in the NIH-AARP Diet and Health Study cohort*. *Am J Epidemiol* 2013;178:1600–1610)

**Oropharyngeal Cancer**

**Incidence and Clearance of Oral HPV Infection in Men**

Among men residing in Brazil, Mexico, and the United States who were HIV-negative and participants in the Human Papillomavirus (HPV) Infection in Men cohort study, newly acquired oral oncogenic HPV infections were rare and most were cleared within one year. Acquisition of oral oncogenic HPV was significantly associated with smoking and not being married or cohabiting, but was similar across countries, age groups, and reported sexual behaviors. (Kreimer AR, Pierce Campbell CM, Lin HY, et al. *Incidence and clearance of oral human papillomavirus infection in men: The HIM cohort study*. *Lancet* 2013;382:877–887)

**Ovarian Cancer**

**GWAS in BRCA1 Mutation Carriers**

A multi-stage genome-wide association study (GWAS) of 11,705 BRCA1 carriers (of whom 5,920 were diagnosed with breast cancer and 1,839 were diagnosed with ovarian cancer), with a further replication in an additional sample of 2,646 BRCA1 carriers, identified a novel breast cancer risk modifier locus at 1q32 for BRCA1 carriers (rs2290854) and two novel ovarian cancer risk modifier loci at 17q21.31 (rs17631303) and 4q32.3 (rs4691139). (Couch FJ, Wang X, McGuffog L, et al. *Genome-wide association study in BRCA1 mutation carriers identifies novel loci associated with breast and ovarian cancer risk*. *PLoS Genet* 2013;9:e1003212)

**Ovulation-inducing Drugs**

In a retrospective cohort of 9,825 women evaluated for infertility at five clinical sites in the United States between 1965 and 1988 with follow-up through 2010, there was no association of ovarian cancer risk with ever use of clomiphene citrate (CC) or gonadotropins, and no evidence was found that any of several more detailed subgroups of usage were related to an increased risk with one exception: women who used CC and remained nulligravid did demonstrate much higher risks than those who successfully conceived compared with nonusers. (Trabert B, Lamb...

**Pancreatic Cancer**

**Absolute Risk Model for Pancreatic Cancer**

Using data from the PanScan Consortium, the authors developed an absolute risk model to identify individuals in the general population at elevated risk of pancreatic cancer that considered current smoking, heavy alcohol, obesity, diabetes > 3 years, family history of pancreatic cancer, non-O ABO genotype, rs3790844(chr1q32.1), rs401681(5p15.33), and rs9543325(13q22.1). (Klein AP, Lindström S, Mendelsohn JB, et al. An absolute risk model to identify individuals at elevated risk for pancreatic cancer in the general population. *PLoS One* 2013;8:e72311)

**GWAS of Survival Among Patients with Pancreatic Adenocarcinoma**


**Lifetime Adiposity and Risk of Pancreatic Cancer**

Using data from the NIH-AARP Diet and Health Study cohort, investigators observed that overweight and obesity at any age are associated with increased pancreatic cancer. (Stolzenberg-Solomon RZ, Schairer C, Moore S, et al. Lifetime adiposity and risk of pancreatic cancer in the NIH-AARP Diet and Health Study cohort. *Am J Clin Nutr* 2013;98:1057–1065)

**Prostate Cancer**

**Genetic Susceptibility Loci, Pesticide Exposure, and Prostate Cancer Risk**

An investigation of single nucleotide polymorphisms (SNPs)–environment interactions between 30 confirmed prostate cancer susceptibility loci and 45 pesticides and prostate cancer risk in the Agricultural Health Study observed significantly elevated risk among men who carried two T alleles at rs2710647 in the EH domain binding protein 1 (EHBP1) SNP and had high exposure to malathion and among men who carried two A alleles at rs7679673 in *TET2* and had high aldrin use. (Koutros S, Berndt SI, Hughes Barry K, et al. Genetic susceptibility loci, pesticide exposure and prostate cancer risk. *PLoS One* 2013;8(4):e58195)

**GWAS of Prostate Cancer Among West African Men**


**Serum Sarcosine and Risk of Prostate Cancer**

In an investigation within the Prostate, Lung, Colorectal and Ovarian Cancer Screening Trial, elevated levels of serum sarcosine were associated with an increased prostate cancer risk, suggesting that sarcosine may be an early biomarker for this disease. (Koutros S, Meyer TE, Fox SD, et al. Prospective evaluation of serum sarcosine and...
**Small Intestine**

Risk Factors for Adenocarcinomas and Malignant Carcinoid Tumors

Based on data from the NIH-AARP Diet and Health Study, age was associated with adenocarcinomas of the small intestine, whereas age, male sex, body mass index, and menopausal hormone therapy use were positively associated with malignant carcinoids. (Cross AJ, Hollenbeck AR, Park Y. *A large prospective study of risk factors for adenocarcinomas and malignant carcinoid tumors of the small intestine.* Cancer Causes Control 2013;24:1737–1746)

**Thyroid Cancer**

Iodine-131 Dose-dependent Gene Expression in Post-Chernobyl Thyroid Cancers

An evaluation of gene expression in 63 paired RNA specimens from frozen normal and tumor thyroid tissues with individual iodine-131 (I-131) doses received from Chernobyl fallout during childhood observed significant associations with expression of eight genes (*ABCC3, C1orf9, C6orf62, FGFR1OP2, HEY2, NDOR1, STAT3,* and *UCP3*) in normal tissue and six genes (*ANKRD46, CD47, HNRNPH1, NDOR1, SCEL,* and *SERPINA1*) in tumor tissue. PANTHER/DAVID pathway analyses demonstrated significant over-representation of genes coding for nucleic acid binding in normal and tumor tissues and for *p53, EGF,* and *FGF* signaling pathways in tumor tissue. (Abend M, Pfeiffer RM, Ruf C, et al. *Iodine-131 dose-dependent gene expression: Alterations in both normal and tumour thyroid tissues of post-Chernobyl thyroid cancers.* Br J Cancer 2013;109:2286–2294)

SNPs in Genes Related to Immune Function and Risk of Papillary Thyroid Cancer

A study of genetic markers in immune-related pathways observed increased risk of papillary thyroid cancer associated with single nucleotide polymorphisms (SNPs) (rs6115, rs6112) in the *SERPINA5* gene. (Brenner AV, Neta G, Sturgis EM, et al. *Common single nucleotide polymorphisms in genes related to immune function and risk of papillary thyroid cancer.* PLoS One 2013;8:e57243)

**Major Editorials, Commentaries, and Reviews by DCEG Scientists**


Buonaguro FM, Gueye SN, Wabinga HR, Ngoma TA, Vermorken JB, Mbulaiteye SM. *Clinical oncology in resource-limited settings.* Infect Agent Cancer 2013;8:39

Chanock SJ. *Sifting through the characterization of hematologic malignancies.* Semin Hematol 2013;50:284–285


Hill VK, Gartner JJ, Samuels Y, Goldstein AM. The genetics of melanoma: Recent advances. Annu Rev Genomics Hum Genet 2013;14:257–279


Mbulaiteye SM. Burkitt lymphoma: Beyond discoveries. Infect Agent Cancer 2013;8:35

Mbulaiteye SM, Buonaguro FM. Infections and cancer: Debate about using vaccines as a cancer control tool. Infect Agent Cancer 2013;8:16


Fellows on the Move

DCEG offers research training opportunities to postdoctoral, graduate, master, and postbaccalaureate level fellows with diverse backgrounds and training. Included below is a list of new and departing DCEG fellows.

Abdul R. Banday, Ph.D., joined the Laboratory of Translational Genomics (LTG) as a postdoctoral fellow in February 2014. Dr. Banday received his bachelor’s degree in biochemistry from the University of Kashmir, India, in 2006. He received an M.Sc. (2008) and Ph.D. (2012) in biochemistry from Aligarh Muslim University in India. In LTG, Dr. Banday will work with Ludmila Prokunina-Olsson, Ph.D., on genomic regions that have been associated in GWAS with increased risk of several cancers. Specifically, he will focus on exploring resources relevant for bladder cancer and for IFNL4, a novel human interferon discovered by the lab, in relation to several cancers and infectious diseases.

Claire Bosire, Sc.D., joined the Nutritional Epidemiology Branch (NEB) as a postdoctoral fellow in October 2013. Dr. Bosire received a B.Sc. in nutrition and dietetics from Egerton University in Kenya, an M.S.P.H. in epidemiology from the University of Alabama at Birmingham, and a Sc.D. in nutritional epidemiology from the Harvard School of Public Health. Dr. Bosire is working with NEB investigators Sandy Dawsey, M.D., and Christian Abnet, Ph.D., M.P.H., on projects related to the etiology and early detection of esophageal squamous cell carcinoma.

Lienard Chang joined the Radiation Epidemiology Branch (REB) as a postbaccalaureate fellow. He received his bachelor’s degree in nuclear engineering at Pennsylvania State University in May 2013 and is currently working toward his master’s degree in health physics at Georgetown University. In REB, he is working with Choonsik Lee, Ph.D., on the development of a computer program for determining individual organ dose calculations from radiological accidents or terrorist events.

Leandro Colli, M.D., Ph.D., joined the Laboratory of Translational Genomics (LTG) as a visiting postdoctoral fellow in November 2013. Dr. Colli earned his M.D. from the University of Sao Paulo in Brazil, where he also completed an internal medicine and clinical oncology residency. Under the mentorship of Stephen J. Chanock, M.D., Division Director, Dr. Colli is focusing on post-genome-wide association studies and functional studies on kidney cancer.

Nicole Deziel, Ph.D., left the Occupational and Environmental Epidemiology Branch to accept a position as associate professor at Yale University in New Haven, Connecticut.

Maki Inoue-Choi, Ph.D., joined the Occupational and Environmental Epidemiology Branch (OEEB) as a postdoctoral fellow in October 2013. She has a joint appointment with the National Institute on Minority Health and Health Disparities. Dr. Inoue-Choi received her M.S. in nutritional sciences from the University of Washington in 2006 and Ph.D. in epidemiology from the University of Minnesota in 2012. Working with her primary OEEB mentor, Mary Ward, Ph.D., Dr. Inoue-Choi will evaluate the extent to which chronic exposures to environmental toxicants from drinking water are associated with the risk of cancers, especially in rural and agricultural areas.
Shivani Jain, M.Phil., joined the Infections and Immunoepidemiology Branch (IIB) as a predoctoral fellow. She recently received a master’s in global health and development from the University College, London and a master’s in epidemiology from the University of Cambridge in the United Kingdom. Ms. Jain is enrolled in a doctoral program at the University of Cambridge through the NIH-Oxford-Cambridge Scholars program. In IIB, she is working with Sam Mbulaiteye, M.D., to investigate the association between Plasmodium falciparum malaria and Burkitt lymphoma.

Scott Kelly, M.S., joined the Hormonal and Reproductive Epidemiology Branch (HREB) as a predoctoral fellow in November 2013 as part of the collaborative doctoral training partnership in cancer epidemiology with George Washington University. Mr. Kelly received an M.S. in biostatistics and epidemiology from Georgetown University in 2009. For his doctoral dissertation, Mr. Kelly is examining the role of hormonal and genetic mechanisms in the pathogenesis of prostate cancer, and conducting novel analyses of incidence trends and survival rates, with HREB mentor Michael B. Cook, Ph.D.

Nicholas Khan joined the Clinical Genetics Branch (CGB) as a postbaccalaureate fellow in November 2013. He received his B.A. in public health studies from the Johns Hopkins University and is earning an M.S.P.H in health policy from the Johns Hopkins Bloomberg School of Public Health. Mr. Khan is working under the mentorship of Jennifer T. Loud, C.R.N.P., D.N.P., Assistant Branch Chief for CGB, and Douglas Stewart, M.D., on several projects, including the association of phenotype and DICER1 mutations in a prospective cohort.

Roelof Koster, Ph.D., joined the Laboratory of Translational Genomics (LTG) as a visiting postdoctoral fellow in December 2013. Dr. Koster earned his M.Sc. in medical biology in 2004 from the University of Groningen, the Netherlands, and his Ph.D. in 2010 from the Faculty of Medical Sciences, University Medical Center Groningen and University of Groningen. In the lab of Stephen J. Chanock, M.D., Division Director, Dr. Koster is conducting follow-up studies of important findings from genome-wide association and sequencing studies.

Stephanie Kovalchik, Ph.D., left the Biostatistics Branch to accept a position as an associate statistician with the RAND Corporation in Santa Monica, California.

Sharon Li joined the Genetic Epidemiology Branch (GEB) as a predoctoral fellow in July 2013. She completed her third year as a medical student at Jefferson Medical College in Philadelphia, Pennsylvania and joined the year-long Medical Research Scholars Program at NIH. Under the mentorship of GEB investigator Philip R. Taylor, M.D., Sc.D., Ms. Li is working on pathway analyses using data from genome-wide association studies to evaluate risk of upper gastrointestinal cancers.

Patricia Luhn, Ph.D., M.P.H., left the Hormonal and Reproductive Epidemiology Branch to accept a position as an epidemiologist with Genentech in San Francisco, California.
Matthew Makowski left the Laboratory of Translational Genomics to pursue a Ph.D. through the Marie Curie Initial Training Network in Developmental and Computational Biology, which is a multi-university program sponsored through the European Union. He will be doing his laboratory work at partner institution Radbound University in Nijmegen, Netherlands.

Candace Middlebrooks, Ph.D., joined the Laboratory of Translational Genomics (LTG) as a Cancer Research Training Award postdoctoral fellow in November 2013. She received an M.S. in natural sciences from the State University of New York at Buffalo, and a Ph.D. in genetics and molecular biology from Emory University in Atlanta, Georgia. Under the mentorship of LTG investigator Ludmila Prokunina-Olsson, Ph.D., Dr. Middlebrooks is working on a project that involves genetic and functional analysis of association signals identified through bladder cancer genome-wide association studies.

Estelle Ntowe, M.H.S., joined the Radiation Epidemiology Branch (REB) as a predoctoral fellow in October 2013. Ms. Ntowe received a bachelor’s degree in life sciences from Pennsylvania State University, and a master’s in environmental health science from the Johns Hopkins Bloomberg School of Public Health. In REB, she is working with Amy Berrington de González, D.Phil., on treatment and lifestyle-related risk factors for second cancers in the Kaiser Breast Cancer Survivors Cohort.

Cuiju Wen, M.S., joined the Occupational and Environmental Epidemiology Branch (OEEB) as a predoctoral fellow in October 2013. Ms. Wen received a B.S. in preventive medicine from Sun Yat-Sen University in China in 2002. She received her M.S. in occupational and environmental health from Southern Medical University in China in 2010 and is currently working on her doctoral degree. In OEEB, Ms. Wen is working with Qing Lan, M.D., Ph.D., M.P.H., and Nathaniel Rothman, M.D., M.P.H., M.H.S., on a study of peripheral blood cell biomarkers in a population of workers exposed to benzene in the petroleum industry in Guangdong, China.

Jincao Wu, Ph.D., left the Biostatistics Branch to accept a position as a mathematical statistician at the Division of Biostatistics in the Center for Devices and Radiological Health of the Food and Drug Administration.

Mingfeng Zhang, M.D., Ph.D., joined the Laboratory of Translation Genomics (LTG) as a Cancer Research Training Award postdoctoral fellow in December 2013. Dr. Zhang received her Ph.D. in molecular and genetic epidemiology from Nanjing Medical University in June 2012, and a M.D. in pediatrics from the same university in 2007. She conducts her research in the laboratory of Laufey Amundadottir, Ph.D., where she studies the genetic susceptibility of pancreatic cancer by analyzing the genome-wide association study, RNA-seq, DNA-seq, and methylation data.