THE CANCER LETTER

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NCI Raises New Questions About Duke Genomics Research, Cuts Assay From Trial

By Paul Goldberg

In a new setback to a controversial group of genomics researchers at Duke University, NCI officials eliminated a biomarker test from an ongoing phase III clinical trial.

The decision by the NCI Cancer Therapy Evaluation Program to remove the Lung Metagene Score assay from the trial conducted by the Cancer and Leukemia Group B challenges a Duke technology that has not previously attracted scrutiny.

The Duke group, headed by Joseph Nevins and Anil Potti, has made so many errors in their publications that the university suspended three clinical trials based on the group's technology. The trials were later restarted.

"We have asked [CALGB] to remove the Lung Metagene Score from the trial, because we were unable to confirm the score's utility," CTEP Director Jeff Abrams said to The Cancer Letter.

NCI's decision May 10 to eliminate the assay from the 1,525-patient

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In the Cancer Centers:

Maryland Wins $12.3 Million To Renovate Research Labs At Greenebaum Cancer Center

UNIVERSITY OF MARYLAND SCHOOL OF MEDICINE has received $12.3 million in NIH grants to renovate research laboratories of the University of Maryland Marlene and Stewart Greenebaum Cancer Center and to build core facilities that will provide key support services to cancer researchers. The funds are part of $1 billion made available through the American Recovery and Reinvestment Act for construction or renovation of research facilities.

The NIH's National Center for Research Resources awarded a $5 million C06 construction grant to renovate laboratories on the eighth floor of the School of Medicine's Bressler Research Building at 655 W. Baltimore St. Another $7.3 million G20 Core Renovation, Repair and Improvement grant will be used to consolidate existing core laboratories and build new facilities on the sixth and seventh floors of the Bressler Building. These new core laboratories will provide "shared services" to cancer researchers and other scientists at the University of Maryland School of Medicine and other professional schools at the University of Maryland, Baltimore. Many of these support services benefit the cancer center, which is part of the School

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Experts Question Validity Of Duke's IRB Investigation

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trial of adjuvant chemotherapy in non-small-cell lung cancer was based on a biostatistical review, Abrams said. The review was prompted in part by problems in other aspects of work by the Duke group, he acknowledged.

"When the issues came up with the review by Duke of their studies, we decided to review the LMS score in the trial we sponsored," Abrams said.

LMS is a prognostic model that was being tested for its ability to identify non-small-cell lung cancer patients who may be at high risk of recurrence.

The assay is different from the previously questioned work by Duke scientists. While earlier assays were used to predict sensitivity to chemotherapy, the function of LMS was to gauge the risk of disease recurrence.

The data were acquired differently as well. The Duke group's chemosensitivity tests were based largely on analysis of the 60 cell lines NCI uses as an initial screen for cancer drug candidates. The chemosensitivity test seeks to determine whether RNA expression could be correlated with response to chemotherapy. The LMS test is based on analysis of tumor tissues. Also, the Duke scientists use different statistical modeling methods to produce these tests.

NCI's decision to eliminate LMS from an ongoing trial is all the more remarkable, because the assay was not used to select patients for therapy in the randomized trial, which means that there was no plausible risk to patients.

While all tumors in the trial were analyzed with LMS, neither patients nor their treating physicians were given the scores. Correlation with the patients' outcomes was to be done retrospectively.

According to a government-run database, the trial started accruing last March. In an earlier version, the study was known as "A Randomized Phase III Trial to Evaluate the Potential Utility of a Genomic Prognostic Model to Identify Stage I NSCLC Patients as Candidates for Adjuvant Chemotherapy." Now, it's called "Chemotherapy or Observation in Treating Patients With Stage I Non-Small Cell Lung Cancer."

A summary of the trial is posted at http://clinicaltrials.gov/ct2/results?term=CALGB+30506.

Duke Suspended Earlier Trials Amid Allegations

The Duke researchers emerged as pioneers of personalized medicine four years ago, when Nature Medicine published their paper claiming that microarray analysis of patient tumors could be used to predict response to chemotherapy.

The finding seemed promising enough to trigger both enthusiasm and scrutiny.

At M.D. Anderson Cancer Center, biostatisticians Keith Baggerly and Kevin Coombes attempted to verify this work when oncologists asked whether microarray analysis could be used in the clinic. The two were unable to reproduce the results, and instead found a series of errors, including mislabeling and an embarrassing "off-by-one" error, where gene probe identifiers were mismatched with the names of genes.

The closer they looked, the more errors they found.

The M.D. Anderson statisticians estimate that they devoted about 1,500 hours to checking the work of the Duke group. These efforts—dubbed "forensic bioinformatics"—culminated in a paper in the November 2009, issue of the Annals of Applied Statistics.

"Unfortunately, poor documentation can shift from an inconvenience to an active danger when it obscures not just methods but errors," the paper stated. "Patients in clinical trials are currently being allocated to treatment arms on the basis of these results."

This was, indeed, the case. Duke was conducting three randomized phase II single-institution trials that used the technology to assign patients to treatment (NCT00545948, NCT00509366, and NCT00636441). Baggerly and Coombes argued that these trials "may be putting patients at risk." The paper is posted at http://

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The allegations prompted Duke to suspend the three trials, one of which (NCT00636441) was co-sponsored by the Department of Defense (The Cancer Letter, Oct 2, Oct. 9, Oct. 23, 2009). Also, university officials launched an internal review of the scientific underpinnings of the trials.

Duke's Institutional Review Board consulted three directors of cancer centers and a separate panel of biostatisticians. Ultimately, both groups were said to conclude that the trials could be restarted.

This was announced in a statement signed by two Duke deans, who declared that "an examination of the underlying scientific methodology that had been published by the Duke investigators, and used in these trials, was confirmed by reviewers' own independent analysis using the respective datasets and prescribed methods of analysis," which led the reviewers to conclude that "the approaches used by the Duke clinical predictors are viable and likely to succeed."

The statement was signed by Michael Cuffe, vice dean, medical affairs, at Duke University School of Medicine, and Sally Kornbluth, vice dean for research (The Cancer Letter, Jan. 29).

However, some very important information remained shielded from public view at the time Duke made its announcement. First, the text of the report prepared by outside scientists was not released. "While the reviewers approved of our sharing the report with the NCI, we consider it a confidential document," Cuffe said to The Cancer Letter at the time.

Also, none of the outside experts consulted by Duke were publicly identified.

The Cancer Letter Obtains "Confidential" Report

Duke officials apparently did not realize that sharing the report with NCI was inconsistent with their intent to keep it confidential.

Once the report made its way into the institute's hard drives and file cabinets, it became subject to provisions of the Freedom of Information Act, and was obtained by The Cancer Letter.

The report and a related document are posted at http://cancerletter.com/special-reports.

The documents were redacted to eliminate the names of individuals involved in Duke's investigation and to protect trade secrets and patentable data.

Experts asked by The Cancer Letter to review these documents noted that Duke deans Cuffe and Kornbluth were inaccurate in their description of the document's substance and conclusions when they announced completion of the investigation and resumption of the clinical trials earlier this year.

"Having read the committee's report, we must disagree with Duke's representation of the committee's findings," Baggerly and Coombes said in an email after reviewing the documents released under FOIA.

"The committee did a post-hoc analysis to establish the plausibility of the conclusions for a single drug and concluded (via extrapolation) that the approach looked like it *could* work. However, many of the problems involved mislabeling of data. The committee mentions that the detailed responses provided by the Duke investigators appeared to address those concerns, but the Duke investigators have provided mislabeled data in their *corrections* before. There is little discussion of what, if anything, the committee did to verify the provenance of the data."

Also, Baggerly and Coombes disagreed with Cuffe's and Kornbluth's earlier comments that "an examination of the underlying scientific methodology that had been published by the Duke investigators, and used in these trials, was confirmed by the reviewers' own independent analysis."

In the document that was intended not to see the light of day, "the committee explicitly notes (twice!), that the underlying scientific methodology has not yet been published," Baggerly and Coombes said.

"Duke's statement implies other members of the scientific community should be able to replicate the reported results with the data available," Baggerly and Coombes said. "Having tried, we can confidently state that this is not yet true."

Duke spokesman Doug Stokke said the two deans stand by their characterization of the results of the review.

The university has resumed its three phase II trials, officials said.

Report Does Not Quell Concerns

The Cancer Letter asked three biostatisticians not previously involved in the controversy to review the report and respond to a set of questions.

Frank Harrell, chairman of the Department of Biostatistics at Vanderbilt University School of Medicine, said he would not have voted for resumption of clinical trials based on the Duke technology:

"If the information available to me as a committee member were to not greatly exceed what we now have publicly available, my vote would have easily been 'no,'" Harrell said. "It would have been necessary

to reproduce the researchers' results and to perform a stringent cross-validation with a large number of repetitions of the algorithms in order to have sufficient confidence in the results. When serious errors have been documented, including mislabeling samples, and the predictions still 'work,' either an element of luck is involved or the original analyses were not very sensitive to the values in the data.

"That is not to rule out the predictive instrument actually working for patients in the trial. But we would be more comforted had sound reproducible research practices been used throughout. The fact that erroneous data remained on the web site while the outside reviewers were examining the research, and the apparent delay of posting correct information until a new publication is peer-reviewed cast further doubt.

"Speaking quite generally, molecular marker researchers need to decide whether their research is important enough to do rigorously, or whether publication speed is all-important."

The report indicates that some crucial information was not shared with the committee by Duke, said Giovanni Parmigiani, chairman of the Department of Biostatistics and Computational Biology at Dana-Farber Cancer Institute.

"The reviewers were not able to access phenotype information for the 73 reference samples used by the Duke group," Parmigiani said. "This is a severe limitation, as the actual algorithm used to assign patients includes a 'calibration' step on these patients, and this step should be considered part of training. We must therefore infer that the precise algorithm was not available to them. Reviewers thus assessed the algorithm-making machine, but not the algorithm itself. Metaphorically, the reviewers were charged to assess the purveyor of PET scanners, but not the actual PET scanner that is being used in the trial. Why not?"

Gary Rosner, director of oncology biostatistics at Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins, said that the extent of redacting makes it difficult to assess the report.

"It is not clear to me from the report whether the reviewers had access to all of the data and code or just to some of the data," Rosner said. "If we are to feel assuaged by the review, we have to accept the word of unknown reviewers who state that what the Duke researchers actually did was OK when these same reviewers acknowledged that the figures and tables presented in the papers were mislabeled and incorrect and declared that the algorithms were incompletely described."

However, the bar for reproducibility is clear. "'Reproducibility' should mean that one is able to apply the same technique to the same data and get the same results," Rosner said. "The method would be generalizable if one would be able to apply it to a different data set and get good predictions. I think that if someone other than the initial research team is NOT able to obtain the same results as the initial research team when applying the same code to the same data, then it is not reproducible."

Anonymity of reviewers is a problem, too, biostatisticians say.

"Had I been required to do that, I would have immediately resigned from the committee," Vanderbilt's Harrell said. "Lack of transparency should cause any reasonable outside reviewer to be dubious of research claims."

Even membership on Data and Safety Monitoring Boards is not usually kept confidential, Harrell said. "I was once on a DSMB for a cancer clinical trial, and the sponsor (a biotech company) asked all committee members to keep their membership on the committee confidential," he said. "None of the committee members agreed to this requirement, forcing the sponsor to back down."

Rosner agrees. "If the point of the review that Duke requested was to clear the air within the scientific community, then I do not understand why the identities of the outside reviewers are not available," he said. "The Duke investigators met with the reviewers, and I would imagine members of the Duke IRB know who conducted the review.

"Therefore, the identities are being kept from the rest of us, the scientific community, and not from those who carried out the research in question," Rosner said. "Keeping the review panel anonymous seems contrary to the transparency one would have expected in the review process, especially considering that the controversy stems from lack of enough detail to reproduce analyses. If, instead, Duke convened the panel of experts to carry out what was to be a purely internal review, then they certainly have the right to withhold the reviewers' identities. I think, however, that the decision to mask the identities of the reviewers is unfortunate, since it raises yet more questions in an already contentious situation."

Not all documents cited in the report were sent to NCI, institute officials said. Two datasets, described in the report as "supplementary document #2" and "supplement #3" were not shared with the institute.

Also, a cover letter from Duke IRB chairman

John Harrelson states that reviewers were provided with "detailed responses by Drs. Nevins and Potti to the issues raised in the Baggerly paper as well as the detailed description of the methodologies used in the genomic analyses."

These documents didn't make it to Bethesda.

"It appears that those attachments were presumably documents and conversations provided to the reviewers, along with access to all of the primary data, as well as the Annals of Applied Statistics publication," Duke spokesman Stokke said in an email. "If so, these documents were not part of the review that was conducted and provided to the IRB, rather these were among the materials that were provided to the reviewers."

The controversy over Duke's results also appears to extend to underlying biology, as data from another laboratory indicates that the NCI cell line panel cannot be used as a reliable predictor of response in patients.

A group of scientists led by Michael Gottesman, chief of the NCI Laboratory of Cell Biology, recently reanalyzed 400 drug response-relevant genes in the NCI-60 cell line panel and compared their results with fresh clinical samples, finding that gene expression profiles of the cell line panel bear no relation to the gene expression profiles of real tumor samples.

Scientists familiar with this work say that if the cell line panel doesn't reflect real tumors, it's implausible that a predictive signature derived from this panel would work in patients.

Gottesman's results have been presented at several recent meetings, but are yet to be published.

Baggerly and Coombes Critique the Duke Report

The full text of comments by Harrell, Rosner and Parmigiani is posted at http://cancerletter.com/special-reports. *A detailed critique of the Duke documents by Baggerly and Coombes appears below:*

We are happy to see the committee's report, even in redacted form. The report does clarify the charges to the committee, what the committee had access to, and, to an extent, what the committee did to reach the conclusion (cited earlier by Duke) that the "clinical predictors are viable and likely to succeed."

However, the report does not resolve questions about reproducibility and data provenance. Indeed, it does not show even basic aspects of the data used, or discuss serious new problems that arose (and that were reported to Duke) during the course of the investigation. Consequently, the report itself cannot be persuasive that the predictors developed and used in the trials are reliable.

According to the report, the committee members "were given two charges by Dr. Harrelson and the Duke IRB. The first was 'Have the methodology errors originally communicated by the M.D. Anderson Cancer Center researchers, Baggerly and Coombes, been adequately addressed by the Duke investigators?' and the second 'Do the methods as initially developed and as applied in the context of these trials remain valid?'" According to the cover letter Duke sent the NCI, committee members "were provided with a detailed response by Drs. Nevins and Potti to the issues raised in the Baggerly paper as well as a detailed description of the methodologies used in the genomic analyses." Based on the report itself, these included details of both code and supplementary data.

However, these detailed responses, data, and code have not been made available. First, much of the data were redacted from the committee's report obtained by FOIA. But the committee notes that the committee itself did not have enough data to replicate the findings (p.1), "In our review of the methods... we were unable to identify a place where the statistical methods were described in sufficient detail to independently replicate the findings of the papers. Only by examining the R code from Barry were we able to uncover the true methods used." In short, the written descriptions given to the committee appear to have been inadequate, so that the committee had to examine the raw source code in order to figure out what was done. *So not only are the findings irreproducible by others in the scientific community, but the committee itself did not have sufficient information to reproduce them*.

The committee *expected* this additional information would be made available, as they note that "The one area that they [the Duke investigators] have not been fully responsive and *really need to do so* is in clearly explaining and laying our (sic) the specific statistical steps used in developing the predictors and the prospective sample assignments" (emphasis ours). The committee also noted (p.1) that "We further think that to quell further concerns, it may be appropriate to write an expanded version of the response that fully describes necessary details, including tables, figures, and responses to comments. Such a response could be posted on in (sic) appropriate web site such as the Duke controlled web site. The site could also include potentially include (sic) data, methods, and software for the papers that contain identified issues." The committee mentions, in its report, "supplementary document #2" and "supplement #3" (p. 2), but those documents were not sent to the NCI.

Until these data are posted, we do not believe the Duke group has followed the committee's recommendations to "clearly explain" their approach.

In addition to posting data, clarifying the provenance of the specific data used to construct the predictors now being applied in the RCTs is also necessary. Because the Duke group has previously mislabeled data for docetaxel, doxorubicin, and cisplatin among others, confirming the origin of the data that were actually used is vital. The committee's answers to their first charge repeatedly cite data from the detailed responses, but there is no detailed description of what the data used in making the predictors actually were, nor is there any description of how the committee assessed where the data came from, and that they were labeled correctly.

We now move from the first to the second charge. In addressing this charge, the committee again notes problems with reproducibility (p. 4), but comments that "however, by studying the R code from Barry, we were able to develop a parallel approach." The committee used this "parallel approach" to generate "valid" predictors for Adriamycin response, and "believe the approach can generate valid predictors in general."

The extent of redaction here makes it difficult for us to assess what was done. For now, we will simply note two reservations. First, extrapolation from one drug to others with potentially different mechanisms of action seems a stretch. This is particularly the case since the MDA133 patients were treated with a combination regimen (TFAC) as opposed to the single agent under study. Second, the committee notes at the end of the section that, "The preceding analysis supports the viability of the approach, and in reviewing the R code and results from Barry we have found nothing that indicates that the predictions in the trial would be completely one-sided or reversed as suggested by Baggerly and Coombes." We read this as saying that the predictions they obtain appear better than chance. But was this obtained with cell line sensitivity labeled as the drug sensitivity information would suggest? This is not clear to us, and we noted in our paper that "sensitive/resistant orientations of the Salter et al. (2008) heatmaps are correct for … A[driamycin] … Heatmap orientations in Potti et al. (2006) are reversed for … A … However, sample predictions shown in both … Potti et al. (2006) and … Salter et al. (2008) suggest results better than even … [Potti et al. (2006) *p*-values: … A = 0.024 … Salter et al. (2008) *p*-values: … A = 0.01 …]." In other words, predictions better than chance have been reported using both correct and incorrect orientations of cell line labels, and we can't tell which were used here. The general approach of using cell line data to derive signatures of response has always *sounded* plausible, but the devil is indeed in the details—precisely how does this work, and on precisely what data?

With respect to the data used in the report, even the most basic details have been redacted. Based on correspondence with the NCI FOIA office, the NCI chose to redact just the names of the authors, to protect confidentiality. The Duke legal office evidently redacted descriptions of raw data as well. It is not clear to us what FOIA principle (like confidentiality or proprietary information) could be used to justify the redaction of the most basic scientific data that would be reported in a journal (or deposited at the website of a journal).

In our Jan. 29 note to The Cancer Letter, we commented on the need for the scientific community to have access to raw data: "While we expect that the conclusions of the panel [committee] are valid given the data presented to them, we are asked to trust that these data were correct, without seeing those data." In that same note, we explained why we were unwilling to extend that trust, noting that new data involving drugs being used in trials (cisplatin and pemetrexed) was posted to the web with all of the clinical validation samples mislabeled, *even while the investigation was ongoing*.

We reported these new problems to Duke on Nov 9, 2009. All of the Duke data sites descending from http://data.genome.duke.edu/ were removed from the web in late November 2009. When these pages reappeared in early April 2010, the web site for the cisplatin paper (http://data.genome.duke.edu/JCO.php) no longer contained gene lists or numerical data, but did contain the comment "please note that the published gene lists have errors, please contact authors for clarification." Similarly, the web site for the adriamycin paper (http://data.genome.duke.edu/NatureMedicine.php) no longer contains any supplementary files, just the comment "We apologize for any inconvenience caused. Please contact us for clarification." No "correct" data have been posted.

Given that additional problems arose even during the course of the investigation, we fear similar errors in data supplied to the committee might invalidate many of their conclusions. *The report makes no mention of these new problems*, even though we know the Duke IRB knew about them; we received email acknowledgement of our report on which the head of the IRB was cc'ed. Did the IRB inform the committee about them?

In summary, the committee's conclusions that "we believe the predictors are scientifically valid" are

based on the accuracy of data nobody else has seen or checked including, from what we can tell, even the committee. The same types of mistakes continued to be made during the course of the investigation, despite the report's reassurance (p.3, under 5a) that "It appears that checks are in place to prevent a similar reoccurrence of these types of events."

Given the numerous errors we have documented, we remain unpersuaded, absent seeing the actual data, that there is sufficient justification to restart clinical trials. We find this situation frustrating, since, as we have noted before, we would love to use such a method (and improve patient care) at our own institution *if the method works*. Based on the report, it appears that the Duke group has already assembled some data, code and responses. The committee has suggested that these be posted, telling the Duke investigators that they "really need" to be more responsive in this regard. To the extent that these responses clarify approaches already published, or correct active errors in the literature, we cannot sympathize with the Duke investigators' decision to defer posting until a new paper can be prepared and published in the "peer-reviewed literature," particularly when clinical trials - based on the results in question - were restarted without such deferment. As we stated in our note of Jan. 29, "*If they are ready to restart clinical trials, they should be ready to supply the data*."

We would be interested to learn whether the NCI, which received copies of the report, believes sufficient justification has been provided for going forward with these or any similar trials based on this approach.

NIH News:

NIH To Honor Kirschstein With Scientific Symposium

NIH has scheduled a "day of celebration and science" on May 17 to honor the life and accomplishments of Ruth Kirschstein, the former NIH deputy director and senior advisor who died last Oct. 6.

The celebration will begin at 9 a.m. at the Natcher Conference Center and conclude with a poster session and reception from 5:30 p.m. to 7:30 p.m. Presentations will be webcast on http://videocast.nih.gov/summary.asp?live=8700.

Over more than five decades at NIH, Kirschstein made stellar contributions to biomedical research, including her early work on the development of a safety test for the polio vaccine and her later efforts to organize the NIH response to the AIDS epidemic. Kirschstein was the first woman to direct an institute on campus, and she twice served as acting NIH director.

Several recipients of the Ruth L. Kirschstein National Research Award will talk about their research and reflect on the inspirations of their work. The speakers will include Laurie Boyer of Massachusetts Institute of Technology, Howard Chang of Stanford University, Francis Lee of Weill Cornell Medical College, Alfredo Quiñones-Hinojosa of Johns Hopkins University, Gonzalo Torres of the University of Pittsburgh, Dorothy Sipkins of University of Chicago, Anna Penn of Stanford University, Sara Cherry of University of Pennsylvania, and Julie Pfeiffer of University of Texas Southwestern Medical Center.

"Ruth Kirschstein was a pioneer," said NCI Director John Niederhuber. "She was also an extraordinary leader and a dedicated scientist. Above all, I believe she was the embodiment of one of the principles I hold most dear—that it is an unparalleled honor to devote one's career to the service of others."

In the Cancer Centers:

MSKCC Names Martin Tallman Chief Of Leukemia Service

(Continued from page 1)

of Medicine and the University of Maryland Medical Center.

"These NCRR grants will enable us to build new, modern laboratory facilities for our researchers that hopefully will pave the way for major breakthroughs in cancer research," said **Kevin Cullen**, director of the University of Maryland Marlene and Stewart Greenebaum Cancer Center and professor of medicine and director of the Program in Oncology at the University of Maryland School of Medicine.

The newly renovated space will be used by individual molecular and structural biology researchers and will also house core labs for confocal microscopy, proteomics, flow cytometry, tissue-culturing and tissue-related services such as histology and immunohistochemistry as well as the Genomics Core Facility, which provides cutting-edge genomic support for researchers.

MEMORIAL SLOAN-KETTERING CANCER CENTER said **Martin Tallman** has been appointed chief of the Leukemia Service in the Department of Medicine and professor of Medicine at the Weill Cornell Medical College.

Tallman was professor of medicine at the Northwestern University Feinberg School of Medicine

and associate chief of the Division of Hematology/Oncology at Northwestern University. He is an expert in the management and development of new treatments for patients with both acute and chronic leukemia. He has been at the forefront of several key clinical trials that have led to new standards of care. Tallman chairs the Leukemia Committee of the Eastern Cooperative Oncology Group.

YALE CANCER CENTER said **Howard Hochster** was appointed professor of medicine in medical oncology, medical director of gastrointestinal oncology, and associate director of clinical research. Hochster joins Yale from New York University School of Medicine and the NYU Cancer Institute, where he was a professor of medicine and director of the Gastrointestinal Cancer Program. He also served as director of the NYUCI Clinical Trials Office for six years, and was principal investigator for the Eastern Cooperative Oncology Group at NYU for the last 16 years.

SWEDISH CANCER INSTITUTE (Seattle) and Elekta finalized a strategic partnership that includes the institute's acquisition of multiple cancer management solutions, including radiation-therapy treatment systems, treatment planning workstations, electronic medical record systems, clinical service, and a radiosurgery system. Elekta will also provide expertise in process transformation, technology enablement, and strategic marketing.

SOUTHWEST ONCOLOGY GROUP and The Hope Foundation announced the 2010 Charles A. Coltman Jr. Fellowship awardees: **Joanne Jeter** and Daniel Persky, both of the University of Arizona. The program funds outstanding young investigators from SWOG member institutions and helps fellows develop expertise in clinical trials methodology, protocol activation, and management. Two fellows are selected annually by an independent panel and are awarded $100,000 intended primarily for salary support for two years.

Jeter is an assistant professor of clinical medicine at the Arizona Cancer Center and has been involved in the SWOG Melanoma and Prevention Committees. Persky, an assistant professor of clinical medicine at the AZCC, conducts research to increase survival rates for patients with diffuse large B-cell lymphoma.

ROSWELL PARK CANCER INSTITUTE named **Annie Deck-Miller** as senior media relations manager in the Office of Public Affairs, Department of Marketing. Deck-Miller will develop and execute a comprehensive media relations program at RPCI. Deck-Miller was the managing editor and general manager of the Buffalo Law Journal for five years and, prior to that, was a reporter covering the science, legal, education, marketing and arts beats for Business First of Buffalo.

Organizations:

Gynecologic Societies Select First Breast Cancer Fellow

SOCIETY OF GYNECOLOGIC ONCOLOGISTS and the American College of Obstetricians and Gynecologists have named **Marcia Humphrey Schmidt** as the initial recipient of their jointly developed Breast Cancer Fellowship for gynecologic oncologists.

After completing her fellowship in gynecologic oncology at the University of South Florida in June, Humphrey Schmidt will become the first to participate in the one-year fellowship training program dedicated to the care and treatment of breast cancer and related disease.

Humphrey Schmidt will complete her fellowship at the Breast Health Center at Women and Infants Hospital in Providence, Rhode Island, affiliated with the Brown University Alpert Medical School. Her fellowship will be supported through a $75,000 grant from the American College of Obstetricians and Gynecologists.

LYMPHOMA RESEARCH FOUNDATION announced the election of **Steven Bernstein** and **Pedro Jares** to the Executive Committee of LRF's Mantle Cell Lymphoma Consortium.

Bernstein is a professor and co-director of the Lymphoma Program at the James P. Wilmot Cancer Center. Jares is a molecular biologist at the Pathology Department, Hospital Clinic of Barcelona, and scientific coordinator of the Genomics Unit of the IDIBAPS (Institut de Investigacions Biomèdiques August Pi i Sunyer), University of Barcelona.

CORRECTIONS: Due to overzealous spell-checking in a word processing program not normally used by The Cancer Letter editors, names were misspelled in the April 23 issue, in an article on awards presented during the American Association for Cancer Research annual meeting. **Elaine Fuchs** received the AACR-Women in Cancer Research Charlotte Friend Memorial Lectureship. The first annual Landon Foundation-AACR INNOVATOR Award for Research in Personalized Cancer Medicine was presented to **W. Kimryn Rathmell**, of University of North Carolina at Chapel Hill. **Michael VanSaun**, of Vanderbilt University Medical Center, received the Pancreatic Cancer Action Network-AACR Career Development Award.