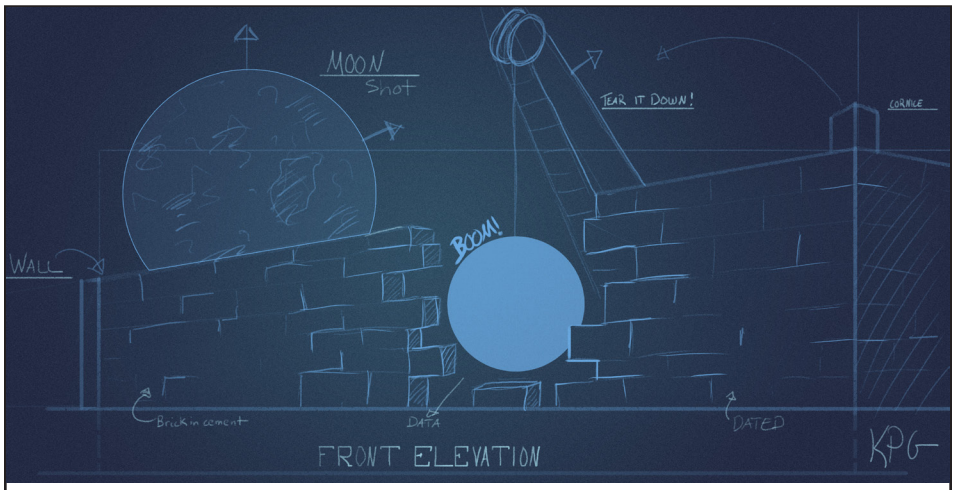
THE CANCER LETTER

June 24, 2016 • www.cancerletter.com • Vol. 42 No. 25



Stanford, Intermountain and Providence Use Syapse Platform to Integrate Their Data

By Matthew Bin Han Ong

Three health systems—Stanford Cancer Institute, Intermountain Healthcare and Providence Health and Services—have agreed to eliminate the electronic barriers between their medical records, tumor registries and genomics databases.

The three entities said they have started to use a common IT platform to achieve interoperability and guide clinical decision-making.

(Continued to page 2)

Conversation with The Cancer Letter

Hirsch: I Dropped Out to Start Syapse

Jonathan Hirsch was studying neuroscience at Stanford University when he wandered into two oncology classes and saw an opportunity to change the way health systems handle genomic data.

"I started getting really immersed in molecular oncology, and the challenges in implementing molecularly guided treatment started coming together with the challenges in utilizing complex data," Hirsch said to The Cancer Letter.

(Continued to page 6)

In Brief

NCI Surgery Branch Resumes Enrollment In Suspended Immunotherapy Trials

THE NCI SURGERY BRANCH resumed enrollment of patients in clinical protocols evaluating immunotherapy as a treatment for patients with metastatic cancer.

(Continued to page 15)

Three Health Systems Use Syapse to Integrate Databases

(Continued from page 1)

That platform is Syapse, a startup that is emerging as an important player in the ongoing conversation on bioinformatics and data sharing in oncology, led by Vice President Joe Biden and the National Cancer Moonshot Initiative.

On June 6, Biden announced the NCI Genomic Data Commons as part of the moonshot. The publicly accessible $20-million database consolidates NCI's diverse datasets and contains raw genomic data and analyses of tumors, as well as clinical data on enrollment and treatment (The Cancer Letter, June 6).

Biden is expected to discuss other data-sharing initiatives at the National Cancer Moonshot Summit June 29 at Howard University in Washington, D.C.

Syapse, an informatics software program that integrates oncology data from electronic health records with genomic data, is making inroads into the U.S. health sector.

On June 2, Syapse launched the Oncology Precision Network, or OPeN, which enables interoperability between 79 hospitals and 800 clinics across 11 states. Stanford Cancer Institute, Intermountain Healthcare and Providence Health and Services jointly announced the network, which currently has 200,000 active patients and accrues about 50,000 new cancer cases each year.

Through OPeN, Syapse enables physicians in the network to search for specific gene mutations, synthesize treatment plans and compare patient outcomes from the merged multi-institutional database—and find matching clinical trials.

Experts in oncology bioinformatics say that Syapse is a pioneer because its software is licensed and can be adapted to individual health systems and institutions to achieve interoperability.

By contrast, most research consortia and data vendors generate revenue through collaborations with industry or by selling patient data.

"You'd be amazed how few are really doing this," said James Ford, associate professor of medicine and genetics in the division of oncology at Stanford University. "A few years ago, there was almost none. So really the answer is, they were quite visionary in seeing that this is a need coming down the road with genomics and things like that.

"I would say they were really the first to set up—in kind of a small startup manner as opposed to a big lumbering company—so they were nimble and able to work with individual partners in terms of building a software system that works," Ford said to The Cancer Letter. "It was pretty obvious upfront that they were capable of doing that and tweaking the software for each system's particular needs.

"How you do that at a big academic center like Stanford is completely different from a large Utah-based network of hospital sites. They can do those things in real time."

Syapse's annual subscription fee starts at a little under $500,000 a year and depends on the number of users and the amount of tech support.

Besides OPeN, leading oncology data consortia that are comparable in terms of patient volume and accrual include:

• **The American Society of Clinical Oncology's CancerLinQ**. Launched in 2010, CancerLinQ is expected to use patient care data from millions of physician and patient records from practices and hospitals to provide feedback and clinical decision support to care providers. When the system is completed, doctors will be able to receive personalized insights based on up-to-date findings (The Cancer Letter, Feb. 20, 2015).

• **The American Association for Cancer Research's Project GENIE,** for Genomics, Evidence, Neoplasia, Information, Exchange. The initiative, a multi-phase data-sharing project designed to improve clinical decision making, includes AACR and seven institutions in genomic sequencing.

• **ORIEN, the Oncology Research Information Exchange Network,** founded by Moffitt Cancer Center and The Ohio State Comprehensive Cancer Center.

Editor & Publisher: Paul Goldberg
Associate Editor: Conor Hale and Matthew Bin Han Ong
Intern: Katie McKinney and Laura Brawley

Editorial, Subscriptions and Customer Service:
202-362-1809 Fax: 202-379-1787
PO Box 9905, Washington DC 20016
General Information: www.cancerletter.com

Subscription $405 per year worldwide. ISSN 0096-3917. Published 46 times a year by The Cancer Letter Inc.

Proud To Be Recognized As One Of The Nation's Best.

We are now an NCI-designated *Comprehensive* Cancer Center.

University of Maryland Greenebaum Comprehensive Cancer Center has achieved the National Cancer Institute's highest designation. While this is an honor, what's more important is the progress we are making in fighting and preventing cancer:

NCI Designated Comprehensive Cancer Center

- Discovery of galeterone, an FDA fast-tracked compound developed to treat hormone-resistant prostate cancer
- Invention of GammaPod™, a radiotherapy system for treating breast cancer in a prone position to better protect the heart
- Immunotherapy trials that train patients' own T cells to attack blood and lung cancers
- Population health-related discoveries with risk and prevention implications for cervical cancer

University of Maryland
Marlene and Stewart Greenebaum Comprehensive Cancer Center

Learn more at **UMGCCC.org**

M E D I C I N E O N A M I S S I O N

ORIEN is a self-governed alliance of NCI-designated cancer centers built around a standard consenting and processing protocol called Total Cancer Care (The Cancer Letter, March 13, 2015).

Speaking at the annual meeting of the American Society of Clinical Oncology in Chicago June 6, Biden challenged these initiatives to interoperate and share data with NCI's Genomic Data Commons (The Cancer Letter, June 10).

Ford: How Data Should Be Organized

With the advent of precision medicine, academic cancer centers have invested millions to build tumor registries and sequence patient genomic data.

These data troves now exist at many institutions, but experts say researchers have difficulty figuring out how the data can be used to guide clinical decisions, especially since individual institutions are electronically isolated and limited to their own patient pool.

Moreover, the absence of data standards and the lack of interoperability—even between hospitals that use the same EMR vendors—pose additional barriers. Physicians are unable to link genomics with conventional EMR systems, including Epic and Cerner, which have yet to provide a comprehensive solution for accommodating the data.

"It's so hard, particularly for academic centers," Ford said. "I mean, big networks like Kaiser or Intermountain Health have many sites that are already networked together and share a common platform.

"But academic centers tend to all be homegrown. Each one has its own system and its own health records and the IT part of this hooking them together—it's easy to say, 'Oh, we should all just network together, and it's easy to do,'—but practically, it's very hard to do, and to do that within the law and patient health information protection.

"One thing that traditional electronic health records are not good at is dealing with large genomic tests. They haven't sorted out how to manage that in the system with these large file sizes and many genomic data points in a patient and how you link that to outcomes of the patient somehow. This in many ways is serving a need that we can't really do from a research point of view, even from a clinical management point of view, in this age of personalized or precision genomics.

"It's just a challenging thing, the whole problem, and that I think is the sweet spot that Syapse is trying to show expertise at."

Syapse aggregates data in a way that gives a treating physician all the tools to guide clinical decision-making, Ford said.

"From a physician's point of view, it's been incredibly useful to me, because it's a central place where I can see all the pieces of information about a patient that I want," Ford said. "It has both the genomic test sequencing data and the tumor, the actionable variance that were found, the potential treatment options that those would suggest, the report and the comments from our molecular pathologist about that tumor, and then ultimately, if the patient had a targeted agent, how they responded.

"So, all those things in one place, which is how it should be, and it's impossible based just on electronic health records.

"It's helpful to other physicians because they can go in and look those things up, they can go see particular patients eligible for clinical trials, things like that. It's just very useful to have many different kinds of information in one place that previously has been difficult to do in one place."

Syapse's mission is consistent with the goals of the moonshot, Ford said.

"Syapse connects multiple health care sites—academic, community, large systems—that have different health records and patient types, and networks all of them together for the benefit of learning more about precision medicine and individual cases that are often rare in any one place," Ford said. "Putting many places together will gather more power on that information."

Nadauld: It's Been Working

Syapse is designed to work in both academic and community practice settings, said Jonathan Hirsch, founder and president of Syapse.

"Traditionally, it has been very difficult to coordinate the sharing of knowledge of best practices between the academic center and their community affiliates," Hirsch said to The Cancer Letter. "One of the things our software does for an academic center is help them disseminate those best practices out from their experts to the community affiliates, and then receive back information about the care journey of those patients, compliance with those best practices, and outcomes.

"When it's time to have the patient maybe referred to the academic center or to have the patient matched to a clinical trial at the academic center, our software can help automate that process rather than what occurs today, which is essentially the phone calls back and forth between different organizations and emails and

disorganized mess."

As a member of OPeN, Stanford can use Syapse to access de-identified patient information in large enterprise data warehouses, or EDWs, at Intermountain and Providence, which the health systems use for internal data reporting and analysis.

Although the EDWs at the two systems consolidate tumor registries, laboratory test results, and other health information, the warehouses don't necessarily enable physicians to match patients with clinical trials or utilize genomics data in clinical decision-making.

Intermountain Healthcare chose Syapse because the platform aggregates and compiles genomic data as well as clinical outcomes data, said Lincoln Nadauld, director of precision oncology at Intermountain, a non-profit based in Salt Lake City that operates 22 hospitals and more than 185 physician clinics.

"Intermountain has an enterprise data warehouse already in place for many of those elements. What we didn't have was a way to organize all of those standard data elements that we've been collecting for years, along with genomic data and clinical trials matching and targeted oncology treatments," Nadauld said to The Cancer Letter. "The big thing for us is Syapse understood what we were trying to accomplish—and they spoke the language—Syapse understands that goal and vision and could help us achieve it.

"We have an EMR and that's good for standard labs and vital signs and drugs, and stuff like that—we use Cerner—but it does not handle genomics data. That's big and kind of difficult, and genomics data, for clinical purposes, is new enough that none of these EMRs have really been set up for that.

"When we adopted the Syapse solution to handle the genomics data and clinical trials matching, etc., we then had to start building this link between Syapse and our electronic data warehouse. It's been working.

"For the first time, in a significant way, multiple health organizations can tear down the silos and begin sharing data, because that's how we can improve patient outcomes."

Brown: Never Too Soon for Genomics

For the Swedish Cancer Institute, Syapse is an unprecedented and efficient solution for the institute's clinical trial operations, said Thomas Brown, executive director of SCI.

"For us at Swedish Cancer Institute, our ultimate goal was really focused on clinical trials matching," Brown said to The Cancer Letter. "Syapse, a cloud-based system that can handle semi-structured data, has an emerging amount of experience effectively bulking on to the electronic medical record and specifically to Epic."

According to Brown, Syapse specifically enables SCI to:

• Identify relevant on or off-label therapies that relate to the genetic alterations, mutations,

• Prioritize clinical trials for which specific mutations are relevant—these two purposes require identified data—and

• De-identify data for data-mining research.

SCI is a part of Providence, a non-profit that operates 34 hospitals and 600 physician clinics. SCI is one of the first sites to use Syapse, Providence is in the process of implementing Syapse throughout its network.

Before signing on in 2015, Brown said the institute looked at other platforms offered by companies such as Oracle and Flatiron, and ultimately decided to go with Syapse.

"We're a non-university research practice with a focus on early-phase clinical trials," Brown said. "What we're really after was an IT platform that could help us collect, organize, and analyze the molecular phenotypic information, in this case, the genomic information, in the context of the clinical data that's within Epic or EMR."

Syapse is key to SCI's personalized medicine program, Brown said.

"We have an enterprise data warehouse that is the common data to the different instances of Epic in Providence, and the scrubbed data from those different instances that's used to interact with Syapse," Brown said. "In addition, we have tie-ins to our formal tumor registry—that has very nicely scrubbed data—and also we're tying in our clinical trial management system. That integrated IT platform is really one of the key aspects to our personalized medicine initiative.

"We also have a registration protocol, in other words, all of the patients for whom the panel is ordered, based on clinical, medical necessity, and then patients are asked to consider participation on an IRB-approved registration protocol. The purpose of the protocol is to observe how clinicians use this information. So every time a treatment decision is made, we want to make note of whether the molecular phenotypic data are factored in or not.

"At least, every year, we revisit the patient's updated clinical status in the context of their molecular phenotypic information, in the context of any mutational data that derive from their tumor. Over time, we anticipate adding horizontal, serial genomic reassessments using liquid biopsy technology, or just repeating the molecular profiling of patients' tumors on a subsequent biopsy

over time.

"We've entered over 750 patients to this registration protocol, and it allows us, in a very disciplined way, to evaluate the impact of genomic profiling in the day-to-day clinical setting.

"We also have a molecular tumor board that meets every two weeks and, of course, the other piece has been the implementation of our IT platform. Lastly, we've just opened a state-of-the-art early-phase clinical trials unit that specifically focused on molecularly targeted therapies that derive from our personalized medicine initiative."

Critics may contend that it's too early to "routinely" rely on genomics data for patient treatment, but the science needs to be tested, Brown said.

"One can take the stance that things are too uncertain at this point, and one needs to wait before routinely using this technology—again, as a research practice, we felt it important to be involved, but to do so in a disciplined way in the context of this IRB-approved registration protocol," Brown said. "We also have a molecular tumor board that meets every two weeks and, of course, the other piece has been the implementation of our IT platform.

"Lastly, we've just opened a state-of-the-art early-phase clinical trials unit that specifically focused on molecularly targeted therapies that derive from our personalized medicine initiative."

Brown said he hopes the uptake of Syapse through OPeN will help expedite access to data and clinical trials for patients and providers.

"The point is we wanted to come together to share de-identified data, both for clinical purposes and to be available for data-mining research," Brown said. "OPeN itself is not a clinical trials cooperative group, but we feel that OPeN will facilitate clinical trials by giving patients and providers access to molecular data that will help allow access to relevant clinical trials."

Conversation with The Cancer Letter

Hirsch: I Dropped Out to Start Syapse Information Company

(Continued from page 1)

"During one of my Stanford classes, I said, 'I think that there is a company to be built here,' and I dropped out of grad school and started Syapse."

Eight years later, Syapse, an informatics software program that integrates oncology data from electronic health records with genomic data, is being used in 79 hospitals and 800 clinics across 11 states.

"Our focus as a company is on care transformation, so we want to be at the point of care with the oncologists when they're making that treatment decision for the patient," Hirsch said. "We want to be there when they're considering ordering a molecular test, selecting a targeted therapy, considering a clinical trial.

"We charge the health systems a software-as-service fee, specifically an annual subscription fee for our software platform and a per-user fee," "We do not sell data, so our revenue comes from health systems paying for the value of our software.

"As far as our support for and work with Vice President [Joe Biden's] Cancer Moonshot, I'm afraid you'll have to stay tuned for June 29 to learn more."

Hirsch spoke with Matthew Ong, a reporter with The Cancer Letter.

Matthew Ong: *What is Syapse, and what unmet need or problem does it solve in oncology bioinformatics*?

Jonathan Hirsch: These days, everyone is talking about precision medicine, but few have implemented it at scale due to the tremendous operational challenges in making these complex programs work. Syapse enables health systems to clinically implement oncology precision medicine through a software solution that pulls together all of the data, decision support, workflow, and quality improvement pieces that are truly needed for real-world clinical operations.

Specifically, oncology groups have a huge problem pulling together the relevant patient clinical, molecular, and treatment data to understand the full care journey of the patient. They have a problem understanding what the best practices are for treating a patient using precision medicine. They have a problem operationalizing complex precision medicine clinical workflows, such as molecular tumor boards, and finally they have an issue both measuring outcomes and rapidly learning from those outcomes at scale to improve best practices.

Each of those problems is massive, and in many ways are fundamental problems within the medical system today. Syapse is the software system that solves those challenges for those health systems, with an eye towards making precision medicine a reality for the largest number of cancer patients possible.

MO: *How did Syapse come about? When did you start thinking about big data problems in health information technology and oncology?*

JH: We started up in the earliest form back in 2008. At the time, I was in graduate school at Stanford studying neuroscience, and I had previously done a lot of work in molecular mechanisms of neurological diseases, specifically diagnostic and treatment paradigms based on those molecular mechanisms.

I didn't have a big plan at the time to start a precision medicine company, but I had worked in academic medical centers, I'd worked in clinical research, I'd worked in biopharma, so I had personally seen that physicians and other members of the healthcare ecosystem lacked proper software tools to make proper use of complex data and information. Taking one look at the new EMRs being put into medical centers at the time more than confirmed this!

The issues of molecularly guided care were on my mind when I, frankly, wandered into two oncology courses focusing on molecular diagnostics and the molecular basis of oncology treatment. I started getting really immersed in molecular oncology, and the challenges in implementing molecularly guided treatment started coming together with the challenges in utilizing complex data. I thought, "How are oncologists and care teams, particularly outside of the academic centers, going to move into this era of molecularly-driven treatments if they don't have the necessary tools, software, services, etc., to deal with this complex data, help guide treatment decisions, and learn from real-world outcomes at scale?"

During one of my Stanford classes, I said, "I think that there is a company to be built here," and I dropped out of grad school and started Syapse. This was in the depths of the recession of 2008, so for the first three years of the company it was basically just me full time, with two co-founders working part-time, and a bunch of grad students we hired on as interns building initial prototypes and testing it out in the market.

We got going as a "real" company a few years later, around the end of 2010 or early 2011. That's when we hired a small team, moved out of the dining room and garage, and into a real office. We had our first production software and early adopters in mid-2011 through mid-2012. The first two health systems we started working with were Stanford and Intermountain back in late-2012 and 2013.

MO: *How exactly does Syapse solve these precision medicine challenges in its design?*

JH: Our software focuses on four key areas: data integration, decision support, clinical workflow, and quality improvement. The first component that we have is we build out is our data integration platform that is very good at going into the various different electronic systems within the medical center, such as the electronic medical record, imaging systems, pathology systems, etc., and extracting all of the relevant cancer information about those patients, pulling it into a centralized database, and structuring and normalizing that data so you have the full patient record.

This is an extraordinarily complex process that many claim to do, but few do successfully. We are able to be successful in solving this data integration problem because of the semantic computing platform we have built, which normalizes messy data into best-practice oncology knowledge models that we have spent years building, and the packaged data integration pipes we have built to hook into the databases of EMRs and other standard clinical system.

Additionally, we bring together the clinical data with molecular (genetic, genomic, etc.) test results from in-house and send-out molecular labs. We have developed an interoperability framework for molecular testing, called the Syapse Lab Certification Program, which enforces a best practice data schema for the exchange of structured molecular test results.

The second area of focus is clinical decision support functionality. Having integrated the full, longitudinal patient data, our software can fire decision support rules at different points in the patient's care journey, suggesting molecular tests to order, matching the patients to drugs and clinical trials, and more. Unlike others, we do not pursue a "black box" approach to our CDS functionality, meaning Syapse is not developing algorithms and new clinical protocols behind the scenes and forcing doctors to use them.

Instead, we allow each health system to fully control the clinical best practices that are embedded in our software and used for CDS. Whether those are the best practices developed by the institution themselves, standards in the public domain or developed by groups such as ASCO, created by a third party vendor, or even shared by one Syapse-partner health system with another.

The third focus area is the clinical workflow and

care coordination software framework. It is critical to streamline complex processes such as molecular test ordering, molecular tumor boards, specialty drug procurement, and clinical trials eligibility assessment so that all of the key clinical stakeholders can focus on patient care rather than fill out forms and manage logistics.

An example of this workflow optimization is using the data we've integrated on the patient to automatically fill out a clinical trial eligibility assessment form. We focus a lot of providing workflow tools for care coordination, such as a dashboard that a nurse navigator can use to monitor the status of patients in a precision medicine clinical program, and solve workflow bottlenecks such as drug procurement. Additionally, our workflow software integrates with the EMR, so that a physician has a seamless experience moving from their current clinical software environment to ours.

The fourth area of focus is our quality improvement and learning health system framework. Our software tracks patient outcomes, both through direct documentation in our software and well as through data we integrate from imaging, drug administration, and other system. What we do that is a bit special is we can link the outcomes directly to the full care journey and the decisions made in our software, such as changing a patient from chemo to a genomically targeted agent as a result of a molecular test.

Our software enables this outcomes tracking at scale within a health system, so the end result is that each health system is building a massive real-world evidence database in our software, linking clinical history, molecular and genomic data, treatment decisions and implementation, and outcomes. Our software then contains tools to enable physicians at point of care, expert review groups such as molecular tumor boards, and health system administrators to all use this information to advance quality initiatives.

For example, an oncologist at point-of-care can say, "I'm seeing a patient with a rare signature of tumor type and molecular aberrations, what do I do for this patient sitting in front of me?" Our software can help that physician contextualize that rare patient case into a larger population and use the real-world population information to determine the appropriate treatment course. We call that feature "Similar Patients." And, we can enable the physician and the administrators at the health system to understand the broader population dynamics and trends, and derive practices from their real world data that then get codified in our CDS functionality.

Enabling precision medicine as a real-world clinical program in a community setting is quite complex, and really does require a focus on these four pillars of data integration, decision support, clinical workflow, and quality improvement.

MO*: Who is currently using Syapse and what is your business model?*

JH: We work with large health systems and physician networks. Those might be large integrated delivery systems such as Intermountain Healthcare, community health systems such as Providence Health & Services, or academic medical centers such as Stanford Cancer Institute. Those are some examples of organizations we work with.

Our business model is that we charge the health systems a software-as-service fee, specifically an annual subscription fee for our software platform and a per-user fee. We do not sell data, so our revenue comes from health systems paying for the value of our software.

We tightly align ourselves with the health systems—the health systems are both our customers as well as our long-term strategic partners. We're really trying to enable the health systems to improve the quality of care that they're delivering, and use precision medicine as the lynchpin for a broader transformation into a value-based care framework.

MO*: You're saying that this is a solution that's available to both academic centers as well as community health systems?*

JH: Absolutely. I think the power of the solution increases when you have a broader network that you need to serve. For an academic center, for example, you may have a physician who's an expert in non-small cell lung carcinoma, and that's all they see and all they treat, but that academic center may have a network of community affiliates who aren't experts.

Traditionally, it has been very difficult to coordinate the sharing of knowledge of best practices between the academic center and their community affiliates. One of the things our software does for an academic center is help them disseminate those best practices out from their experts to the community affiliates, and then receive back information about the care journey of those patients, compliance with those best practices, and outcomes.

When it's time to have the patient maybe referred to the academic center or to have the patient matched to a clinical trial at the academic center, our software

can help automate that process rather than what occurs today, which is essentially the phone calls back and forth between different organizations and emails and disorganized mess.

To give you a concrete example, an academic center may run a molecular tumor board that provides treatment guidance for patients seen by their community affiliates. Our software supports the MTB referral workflow, the data aggregation and case presentation, recording and disseminating the treatment guidance back to the community affiliate, and tracking adherence to the guidance and outcomes.

MO: *How are you different from other data software? What is it that you offer that is unprecedented compared to what else is out there?*

JH: There are a few things that are really unique about us. The first is the focus on clinical care transformation. There are many others playing in the precision medicine and oncology data space who are focused on the research side, which is certainly a worth place to focus.

But our focus as a company is on care transformation, so we want to be at the point of care with the oncologists when they're making that treatment decision for the patient. We want to be there when they're considering ordering a molecular test, selecting a targeted therapy, considering a clinical trial.

We've built our company and product around this mission. That means our product needs to be comprehensive, to satisfy the needs of our clinical users and health system customers. For example, providing molecular data in isolation isn't helpful; you have to provide the molecular data in the context of the clinical information. Providing decision support in isolation isn't helpful if you don't connect the drug recommendation to the subsequent clinical action to help start a procurement process for that drug. And doing all that without tracking outcomes isn't useful either, because you don't know what's working and what's not working, and you can't rapidly bake that knowledge into updated best practices.

Our focus on point of care decision-making and clinical transformation, and the comprehensiveness of product we've built to support that, is the primary thing that makes us unique as a company.

The second thing is the fact that we are aligned directly with the health systems and the physician groups, rather then aligned with the pharmaceutical companies, for example. We're not selling data. We're not monetizing data. We're really aligned with the health systems and patients in their pursuit of better care and better treatment decisions.

The third thing is our demonstrated success in implementing precision medicine across different environments: academic medical centers and community practices; in multiple health systems across the country—West Coast, Pacific Northwest, Midwest, East Coast; and in the context of a variety of different IT ecosystems and challenges such as different EMRs, no EMRs, lots of documentation, lack of documentation, in-house versus send-out molecular labs, and more.

MO: *So Syapse can be customized to meet specific needs of each health care system?*

JH: We have a set of best practices—not medical best practices—but workflow best practices and data best practices. We come to a health system with that robust set of operational best practices based on all of the successful precision medicine implementations we've done with health systems. Each new health system benefits greatly from that shared set of operational best practices.

But at the same time we do recognize that each health system has unique aspects to them, and in particular, that all health systems desire to be in control of the clinical best practices that they and their care teams are using. We can configure our software to use the medical best practices of any individual health system that we work with, or we can help them share best practices with each other.

MO: *What is the Oncology Precision Network and how many members and patients does the consortium currently have?*

JH: The Oncology Precision Network (OPeN) is an effort to rapidly improve patient care by making it easy for health systems to share de-identified cancer patient data and the knowledge gained from this real-world evidence. Syapse has partnered with some of our key customers to launch this initiative: Intermountain Healthcare, Providence Health & Services, and Stanford Cancer Institute are the founding members of OPeN.

OPeN unlocks that data from the siloes of the different health systems so we can as an industry more rapidly advance our state of knowledge and understanding in cancer precision medicine and make more rapid progress in figuring out what the right treatments are for particular patients. The network gets together these health systems and helps them share this information in a regulatory-compliant fashion that respects patient privacy. Data being shared includes demographics, clinical history, tumor genomics, and

treatments. OPeN members agree not to monetize the aggregated data asset, but rather to use it for clinical care purposes. In those aspects, OPeN is unique among the major cancer data sharing initiatives out there.

Amongst the three founding health systems, Intermountain, Providence, and Stanford, OPeN covers, 11 states, 79 hospitals, and when we're at full implementation we'll be at about 50,000 new cancer cases per year and 200,000 active patients under management. It's a big network, but it's just a starting point where we are at right now.

OPeN has deliberately chosen a controlled launch strategy. The three founding health systems and Syapse have been working very closely together to build and successfully launch the network. That has resulted in a rapid launch of the software framework with a large number of patients and integrated data already in the system. It is very exciting to see it live!

OPeN will start onboarding additional health systems later this year, and our goal is full geographic coverage of the U.S.

MO*: Do participating health systems use a standard protocol for consenting and registering patients in a HIPAA, PHI-compliant way? What's the process?*

JH: There will not be a standard research protocol that has to be followed. The patients whose data are in OPeN represent real-world cancer patients, not a rigidly formalized research study.

There is plenty of room for different members of OPeN to have different approaches. For example, Swedish Cancer Institute at Providence has a Personalized Medicine Research Program that has a specific protocol and study calendar, but the other institutions have their own approaches and protocols. The point of the network is to capture as much real-world experience as possible and to rapidly learn from this data.

Of course, there has to be consideration for HIPAA, HITECH, and the other regulations. The three founding health systems and Syapse have come together to create a standard data use and data sharing agreement that all OPeN members will sign on to, and that agreement goes into the details of what information can and cannot be shared, the HIPAA and HITECH protections, and much more. Constructing the OPeN contract may have been as challenging as implementing the data aggregation, normalization, and sharing software!

MO*: Is the consortium novel or are there efforts that are similar?*

JH: The consortium is novel from the standpoint that we are capturing and tracking the real-world experience of cancer patients across many different health systems and EMRs, including not just clinical data but also genomics and treatments. OPeN is doing so without prescribing that a specific research protocol be used.

We are taking data from each of the organizations participating in OPeN and we are normalizing and mapping all of the data so that the end result is a standardized dataset but not from a standardized research protocol. The reason why that's really important is we want to actually see the variance in workflow and the variance in treatment decisions across the different organizations—across the academic centers, the non-academic research environments, and the community environment—represented in the system and the very different geographies and patient populations in the system.

The point of the network is to learn, and to do so quickly. It's to learn what works better than not, what situation is better than others, are there treatments that work well in academia and clinical trial settings that don't work well in community practice for certain reasons. OPeN is really intended to, first of all, support point of care decision-making and second, to learn from the real-world treatment experience rather than run another clinical trial.

That's what differentiates OPeN versus all the other efforts that are out there.

MO*: What role do you foresee science playing in Vice President Biden's Moonshot? We all know he has selected and endorsed NCI's Genomic Data Commons. What does Syapse have to offer in furthering the Moonshot's data-sharing goals?*

JH: As you can tell from the description of Syapse and OPeN, Syapse and OPeN are very much spiritually aligned with what the Vice President is trying to do with the Cancer Moonshot. We are very much in favor of unlocking data from siloes, and enabling the use of real-world cancer patient experiences and data in informing clinical decision-making for today's patients

As far as our support for and work with the Vice President's Cancer Moonshot, I'm afraid you'll have to stay tuned for June 29 to learn more.

MO*: What's up next for Syapse? What are your projections for Syapse in oncology 5 or 10 years from now?*

JH: Certainly, one of our major goals is to democratize access to precision cancer care to as great an extent as possible. What you'll see Syapse doing

over the next 5 years is growing our relationships with large community health systems, whether those are integrated networks or large hospital and physician groups, and driving the expansion and utilization of precision cancer care throughout the community.

We're trying to move precision cancer care up earlier and earlier in the care journey of the patient and figure out when it makes sense for an earlier stage patient to receive a precision medicine-guided approach to cancer care.

The next thing that you'll see Syapse doing is increasingly merging the precision medicine approach with a value-based or at-risk payment paradigm. We are big believers in the fact that precision medicine is not only clinically effective, but also a cost effective mechanism for treating cancer patients when you set up the proper financial relationships and all parties involved are at risk.

You're going to see Syapse doing more and more work to enable health systems to go at-risk for larger portions for their cancer population, and to establish relationships with payers—whether it's an owned payer or a third-party payer—to make that happen.

Joint BSA-NCAB Meeting

Moonshot's Strength: Avoiding a Specific Endpoint for Success

By Conor Hale

How will the success of the moonshot be measured? NCI Acting Director Doug Lowy touched on the subject during the joint meeting of the institute's Board of Scientific Advisors and the National Cancer Advisory Board June 21.

The moonshots of the 1960s were essentially engineering problems that had tangible goals. Cancer is an evolutionary problem, and the stated goal of the moonshot in cancer research, led by Vice President Joe Biden, is perhaps deliberately vague: to achieve a decade's worth of progress in just five years.

"Has there been any discussion of an endpoint that you can point to—like planting the flag on the moon, or sequencing the three-billionth base pair of the genome project?" asked BSA member Lincoln Stein, director of the Informatics and BioComputing Platform at the Ontario Institute for Cancer Research, during the meeting. "Something that looks like an achievable endpoint?"

"Not a single achievable endpoint, no," responded Lowy.

"I think, perhaps in part because we've been trying to advance the important notion that there are enormous gaps still in our understanding of cancer, our knowledge about it, and our ability to deal with it," Lowy said. "If there were a single target point, it might imply that, well, once we do that, then we're done."

"I had even heard the vice president talk about the difference between the original moonshot and this moonshot," added NCAB Chair Tyler Jacks, director of the Koch Institute for Integrative Cancer Research at MIT. "That was one defined, achievable endpoint—and he talks about the fact that cancer is at least 200 diseases, and it is complex. So I think in his mind as well there's not a single planting of the flag."

"So he gets it," said Stein.

The question came up over how to best illustrate advancements made with moonshot funding to members of Congress, who will have to continue to vote for it in the future.

"I've heard Dr. Lowy talk to Senate members, House members, staffers—and the things that I see really resonating with them are ideas explaining circulating tumor cells, blood tests, biomarkers, early detection; things that are tangible to them," said M.K. Holohan Quattrocchi, director of NCI's Office of Government and Congressional Relations. "Other things take a little more understanding and work and seem more abstract and amorphous, but that's one area that really gets traction."

"When Dr. Lowy talks about implementing things that we know work now—implementing them on a wider scale—other people can do the kind of presentations that show what kind of cost savings, and what kind of decreased incidence and mortality that those interventions would bring. Those are very meaningful," she said.

"So there are sort of different groups. There are people much more concerned about health disparities within their communities. There are people who are much more concerned about specific diseases where there is very little ability for early detection and intervention. So I think it's sort of finding the examples that are very concrete."

In his opening remarks to the joint meeting, Lowy listed the ways NCI is using recent appropriations for several projects, including $70 million for the Precision Medicine Initiative.

He specified administrative supplements providing funds to improve preclinical models for evaluating targeted therapeutics; to support collaborative efforts to enhance preclinical drug

development and preclinical trials utilizing patient-derived xenograph models; and to support biomarker development and correlative studies associated with clinical trials of immunotherapy.

"I just want to make it clear that not everything that's important is going to be supported by the moonshot, and that NCI will continue to support a great deal of other meritorious research, as well as new initiatives," said Lowy.

A transcript of Lowy's remarks, as well as updates from Jim Doroshow, director of the NCI Division of Cancer Treatment and Diagnosis, and Warren Kibbe, director of the NCI Center for Biomedical Informatics and Information Technology, appears below. Doroshow discussed an expansion of the NCI MATCH trial, increasing the number of patients screened from 3,000 to 5,000, while Kibbe detailed the recent launch of the Genomic Data Commons.

The transcript follows:

LOWY: I would like to welcome everyone and tell you that this is a busy day, an active day. Many of us and many of you have been really extraordinarily engaged in the vice president's initiative, and we're going to be devoting a certain amount of time to that, but I also want to point out that we are going to be discussing the president's Precision Medicine Initiative in oncology, as well as some other aspects.

I first want to discuss PMI in several ways, because this year we received the $70 million appropriation for it, and I wanted to tell you some aspects of how we are making use of those funds. Jim is going to be talking about the MATCH trial, which is pivotal to that, and Warren is going to be discussing the Genome Data Commons. I am going to really just try to tell you about some of the activities.

As many of you will remember, it's a presidential initiative to improve cancer treatments through genomics, and there are preclinical models to advance predictive oncology to get the right drug to the right patient at the right time, in addition to developing the databases. So as I mentioned, Jim will discuss MATCH; and Warren, the databases. But let me tell you about some of the funding announcements that have come out just in the last two months or so.

One is to improve preclinical models for evaluating targeted therapeutics and immunotherapy, and there's an administrative supplement for the cancer center grants for canine immunotherapy in collaboration with the centers and the veterinary schools, of which there are more than 20 that are involved in this network. Also, there are administrative supplements to support collaborative efforts to enhance preclinical drug development and preclinical trials utilizing patient-derived xenograph models.

In addition, administrative supplements to support biomarker development and correlative studies associated with clinical trials of immunotherapy. Let me just give you an example of one of those trials, and this is the Merkel cell carcinoma trials which were recently published in the New England Journal of Medicine, supported by the immunotherapy group—Paul Nghiem is the first author.

In those Merkel cell carcinoma trials, there were patients who were virus-positive—they contained the polyomavirus—as well as patients who were virus-negative, whose tumors did not. And both groups of patients had long-term responses to a PD1 checkpoint inhibitor. What was particularly interesting about those responses were, first, that there really isn't—with conventional therapy—long-term responders, whereas more than half of the patients treated with the inhibitor gave a response. And second, there are enormous differences in the number of mutations that are present in the patients who responded.

The patients who are virus-negative are very analogous to patients who have melanoma, and they have, on average, about 1,100 mutations per tumor genome. By contrast, the patients who are virus-positive have fewer than 15 mutations per tumor genome, but both groups responded.

So one obvious hypothesis is that one or more of the tumor virus-encoded epitopes is actually immunogenic in this particular setting—and I'm not trying to say if somebody from this group submits an application that that's the kind of application that would be supported. But I just think that these hypothesis generating—by being able then to go forward and look at mechanisms, is something that we're particularly interested in and excited about.

There also are studies on how the microenvironment in pancreatic adenocarcinoma will affect immunotherapy. And, you know, we have been giving emphasis to pancreatic carcinoma as an important recalcitrant cancer. And then there are other administrative supplements to improve optimization for T cell therapies and for GMP manufacturing processes for the production of autologous T cell therapy products.

Finally, administrative supplements to U10 cooperative agreements and SPOREs to study mechanisms of cancer sensitivity and resistance to

therapy, utilizing samples and information from clinical human trials, and to create a repository of molecularly analyzed samples of resistant disease—and expand the use of tumor-profiling methods, such as circulating tumor cells and fragments of tumor DNA in the blood, to understand and monitor disease progression.

I would like to turn now to talk about the vice president's initiative, or the moonshot…I just wanted to give you really a little bit of context. This was initially announced at the State of the Union, where President Obama said I'm putting Joe in charge of mission control. It's really an opportunity for focused research to accelerate progress and to take advantage of current advances in the understanding of cancer and recent technological innovation, and to apply the knowledge and innovation to focus on specific projects that can have a substantial impact on understanding or improving the outcome for patients.

But I just want to make it clear that not everything that's important is going to be supported by the moonshot, and that NCI will continue to support a great deal of other meritorious research, as well as new initiatives.

In addition to the vice president's initiative being heavily dependent on new understanding and new innovative technology, there is also the other end of the spectrum where he wants to try to increase the implementation and dissemination of standard of care of what we already know works and one of the working groups on the Blue Ribbon Panel is devoted to implementation and implementation research.

I now am going to turn the microphone over to Jim, who is going to talk with you about two different important areas: one is the MATCH trial, and the other is our proposal to develop a formulary that is, if you will, qualitatively based on what has happened with the MATCH trial, but really expanding it, so we can think in very serious ways about combination chemotherapy or immunotherapy and targeted treatment from drugs from multiple companies.

DOROSHOW: Thanks, Doug. Let me just say that the impetus for doing this really came in two ways:

Number one, from discussions with many of you and many others, especially cancer center directors and others, who have made clear how difficult it has been over the years to get access for investigator-initiated trials using investigational agents—and in particular the negotiations required to get two drugs from two different companies. It may take a year or better, it may never happen. And that has been a major roadblock to the initiation of precision medicine initiatives at many cancer centers, which is easy to understand because of these kinds of administrative difficulties.

So that, together with what we learned about putting together the drugs for the MATCH trial, which we spent the better part of two years negotiating with twenty-plus companies to get 24 compounds, that I'll talk about in a minute, that are now part of that trial. I have an office, I apologize if I said this to you before, next to our tech transfer lawyer in our office suite, and he's a very aggressive person, and I know he's on the phone with a company when I can hear him through the wall.

And it really is a major achievement to have negotiated one trial with basically a whole series of clinical trials agreements that relate to that single trial that produced, if you will, a formulary of drugs that produce to this umbrella approach to precision medicine. So I never thought that was possible until he actually accomplished that, and his name is Jason Cristofaro, and I want to call him out because he spent a great deal of time doing this.

About a year ago when it was clear that MATCH was going to open and this approach actually had legs, we started thinking about how we could do something not exactly the same, but actually some way to produce a formulary that addressed the needs of the community, to create a system in which NCI could be an honest broker to get compounds from companies to cancer center investigators or other investigators who need agents, in particular for combination trials. So we've been talking and trying to put together a program that would actually be initiated with investigator-initiated INDs, INDs that the NCI would not hold, but NCI would act as a broker to get and distribute drugs from a common list of compounds.

And there are, as you might guess, many, many details about how that would work. But two weeks ago we had a meeting with 20 companies at ASCO that went very well. And, in fact, we have sent out to them, if you will, a pledge as well as a form and basically an initial, kind of novel CRADA, that would allow us to work with them and to work with other companies. And we're hoping actually to get responses before the moonshot summit at the end of the month. I don't know if that will happen, but we've certainly had positive reviews from several companies, and I'm hopeful that, by the end of the year, we'll at least have our initial batch of drugs and initial group of companies that have agreed to this process so we can make them available to all of you.

So let me just then segue to the MATCH trial very

briefly. Many of you know that it reopened on the 31st of May, and it reopened in a variety of different ways. I think it's improved. We now have 24 arms in this phase II umbrella trial, and there will be combinations.

We put in, using the PMI money, additional resources at both the processing center and the sequencing center, so that they can do their work more expeditiously and keep up with the kind of demand that we observed in the last few months of last year—where we basically had this interest in this enormous amount of accrual.

We have also provided resources to increase the number of patients screened from 3,000 to 5,000, which based on the initial 800 patients who have been studied, should give us a match rate based on what the statisticians tell us of about 20 percent. And given that approximately 1,000 patients will actually get treated on one of these phase II trials, we've also put in the resources to do a full—in addition to the MATCH screening panel—to do a full molecular characterization of the tumors of all of the patients who actually get treated.

So we really take maximum advantage of this trial, and we're very grateful for the money that came in as part of the Precision Medicine Imitative, because that really allowed us to do all of those things.

LOWY: Thanks. Now Warren is going to tell us about the Genomic Data Commons…

KIBBE: It's great to be here, and I would like to talk very briefly about the Genomic Data Commons.

So for those of you who haven't heard a lot about it, the Genomic Data Commons has really been the project that Lou Staudt, here at NCI, and his colleagues have been pushing very hard to make sure it happens. Folks at the University of Chicago have been instrumental in it; Bob Grossman is the PI for the Genomic Data Commons and we have great partners at the Ontario Institute for Cancer Research and also at Leidos Biomedical, making all this happen.

So what's been really exciting, and the reason I'm showing slides, is that Vice President Biden came and spoke at ASCO, and also visited the University of Chicago. So I've got a few slides of that event. As you can see, the vice president on the left exhorting to all of us that we make sure we make our data available, and that's Bob Grossman right behind him Lou Staudt to his left, or to your right. There was a tremendous amount of publicity, and it was all beautiful…

And you can see that it wasn't just a couple of pictures. He really walked around and got to know the whole crew that was involved in making the Genomic Data Commons possible, and he was genuinely really, really enthusiastic. And that was wonderful to see.

He also then went, immediately afterward, to ASCO where he gave, I believe, a 35-minute talk, and he mentioned the Genomic Data Commons for eight of those minutes. So there's again tremendous interest and tremendous support by the vice president for this. So I think that's been just wonderful.

Again, part of the reason the Genomic Data Commons is such a focus for us, is it's really an opportunity for us to support FAIR—so making data findable, accessible, interoperable and reusable. Those are terms that Force 11 has been really responsible for defining, and also the GDC as part of the NIH Commons, and thinking about then how we participate with lots of other kinds of research that's happening all across NIH. And there are lots of pieces to this.

I don't want to belabor it, but the Genomic Data Commons is real, it's available, and we're looking forward to people putting their data in it.

When it went live, it went live with about 4.1 petabytes of data, and roughly 1.5 petabytes of harmonized data—actually that number came out to be closer to 2 petabytes of harmonized data. And what's really exciting is not just TCGA, but it's also TARGET and the cancer genome characterization initiative data. So that's all available now through the Genomic Data Commons.

I'm just going to show you a pretty picture because I can't resist pretty pictures—that is when you go to the data portal, what you'll see. And if you go to upload data, you actually get a similar kind of graphical view relative to how many specimens and samples you're going to upload where you currently are. So it's a nice dashboard, helping people with their submission process. And we'll see how all of your folks at your organizations like to use it, and please feel free to tell me when things don't work. I know who to talk to.

I want to mention the GDC itself is really part of a foundation. It's not the only piece. In particular, the cloud pilots are really important as we think about how do we make these data more accessible—and in particular how do we give people credit for all the data that they've submitted.

The algorithms that they've developed and attach next to data—and then all the users that come in and want to see and analyze data—how do we make sure that there's appropriate credit to everyone for the work that they're doing? And we think that the GDC, plus the cloud pilots, give us the first view into that new

kind of data ecosystem.

But I want to highlight that it's not just the GDC and the cloud pilots. On the left, that's how will we're thinking about the well-characterized research data that's being generated in all of our organizations. It's just as important to realize that there are lots of cohort studies, clinical trials, and observational studies that are generating data that may not include genomic information today, but there's an opportunity to really engage patients and make patients part of this process.

The other side, on the right-hand side, is really learning from every single patient. And that's an incredibly important part of this, and we're not sure exactly how to make that happen yet, but we recognize that the GDC alone isn't the whole picture.

Funding Opportunity

SU2C, Merck Taking Proposals For New Uses for Keytruda

Stand Up To Cancer announced a request for proposals under SU2C Catalyst, a program supporting clinical trials and translational research.

Funded in collaboration with Merck, the grants will support investigation of new uses of the company's anti-PD-1 therapy, Keytruda (pembrolizumab), alone or in combination with other agents from Merck or other companies.

Proposals for the Merck project grants must be submitted to the American Association for Cancer Research, SU2C's scientific partner, by July 20. The RFP and complete details are available at Proposal Central. AACR will administer the program.

Merck support for SU2C Catalyst is expected to enable as many as four projects with funding in the range of $1 million to $3 million each.

Keytruda is indicated in the U.S. for the treatment of patients with unresectable or metastatic melanoma; and for non-small cell lung cancer tumors expressing PD-L1, with disease progression on or after platinum-containing chemotherapy.

The project must include pembrolizumab alone or in combination with other compounds, biologics, diagnostics, or devices intended as therapeutic interventions, and/or methods for biomarker identification for any cancer. The project is not limited to Merck products, however. If a product is proposed for use that is marketed or is under development by another company, SU2C plans to facilitate the necessary collaborative agreements.

In Brief

NCI Surgery Branch Resumes Enrollments in Immunotherapy

(Continued from page 1)

The trials were suspended two months ago as part of the NIH-wide problem with production of compounds, and were restarted June 17 after renovations to the immunotherapy cell production facility operated by the branch (The Cancer Letter, April 22).

The cell lab is run by **Steven Rosenberg**, chief of the NCI Surgery Branch and one of the pioneers of immunotherapy.

The branch has restarted its accrual of patients with metastatic cutaneous melanoma, uveal melanoma, lung cancer, or common epithelial cancers, including patients with metastatic gastrointestinal cancers, who have progressed through standard treatment for potential enrollment on one of the cell transfer immunotherapy protocols. Additional information is available at the NCI Surgery Branch Immunotherapy Referral Center at 301-451-1929, or IRC@nih.gov.

RAJESH GARG was named president and CEO of **Cancer Treatment Centers of America**. He also is a member of the company's national board of directors.

At McKinsey & Company, Garg worked with many health care companies developing strategic growth, operations, and business development programs and initiatives. Garg earned an M.D. from Stanford Medical School, a J.D. from Yale Law School, and a B.A. in genetics and sociology from the University of Pennsylvania. Prior to joining McKinsey & Company in 1992, he practiced medicine and law in California.

THE PROSTATE CANCER FOUNDATION named **24 Young Investigator Award winners.**

Members of the Class of 2016 were selected from a pool of 128 applicants from 77 institutions across 15 countries.

Successful proposals included the use of genomics to predict prognosis and personalize treatments, as well as immunological approaches. The projects predominantly concentrated on treatment-resistant prostate cancers, the foundation said, while others addressed the relationship of lifestyle factors and aggressive disease.

The awards make three-year investments in early career scientists, and awardees are mentored by leaders in prostate cancer research. Each award is matched dollar-for-dollar by the investigator's institution. To date, the foundation has provided funding to 202 young investigators, representing a total investment of $42.3 million in 10 countries.

The 2016 winners are:

• Rohit Bose, Memorial Sloan Kettering Cancer Center

• Ginevra Botta, Harvard University, Dana-Farber Cancer Institute

• Albert Chang, University of California, San Francisco

• Alastair Davies, University of British Columbia

• Renee de Leeuw, Thomas Jefferson University

• Eleonora Dondossola, MD Anderson Cancer Center

• Christopher Kloss, University of Pennsylvania

• Christos Kyriakopoulos, University of Wisconsin

• David Labbé, Harvard University, Dana-Farber Cancer Institute

• Reem Malek, Johns Hopkins University

• Mark Markowski, Johns Hopkins University

• Joaquin Mateo, U.K. Institute of Cancer Research

• Sean McBride, Memorial Sloan Kettering

• David Miyamoto, Harvard University, Massachusetts General Hospital

• Hao Nguyen, University of California, San Francisco

• Russell Pachynski, Washington University

• Loredana Puca, Weill Cornell Medical College

• Steven Rowe, Johns Hopkins University

• Simpa Salami, University of Michigan

• Bryan Smith, UCLA

• Jean Tien, University of Michigan

• Quoc-Dien Trinh, Harvard University, Brigham and Women's Hospital

• Hung-Ji Tsai, Johns Hopkins University

• Jelani Zarif, Johns Hopkins University

Details of the winner's proposals are available on the foundation's website.

SHUANZENG "SAM" WEI and **PHILIP PANCARI** joined **Fox Chase Cancer Center.**

Wei joined the department of pathology at Fox Chase Cancer Center as an assistant professor, where he will specialize in surgical pathology and cytopathology.

Pancari joined the department of hematology/oncology at Fox Chase Cancer Center, providing additional physician support for the Fox Chase Cancer Center–Temple University Hospital Bone Marrow Transplant Program.

Wei is a licensed, board-certified pathologist who earned his medical degree from North China University of Science and Technology in Tangshan, China, where he then worked as an instructor in the department of pathology. He earned his PhD degree in pathology in 2004 from Peking Union Medical College in Beijing, where he also completed one-year surgical pathology residency training.

He later finished postdoctoral research fellowships in the department of biological chemistry at the University of California, Irvine, and in the department of urology at Johns Hopkins University School of Medicine. Then he completed a combined anatomic pathology and clinical pathology residency, a surgical pathology mini-fellowship, and most recently, a fellowship in cytopathology in June—all at the Hospital of the University of Pennsylvania.

Pancari is a licensed, board-certified physician. He earned his undergraduate degree in chemistry at the Richard Stockton College of New Jersey. After earning his medical degree at Boston University School of Medicine, Pancari worked as an internal medicine intern, and later as a resident at Thomas Jefferson University Hospital in Philadelphia. In 2013, he became a hematology/oncology fellow at Temple University and Fox Chase Cancer Center.

TYLER JACKS, SUSAN HOCKFIELD and **PHILLIP SHARP**, all of MIT, published a report on merging approaches from multiple scientific disciplines to produce breakthroughs in medical research.

The report, "Convergence: The Future of Health," was presented at the National Academies of Sciences, Engineering, and Medicine.

Jacks is the David H. Koch Professor of Biology and director of MIT's Koch Institute for Integrative Cancer Research; Hockfield is president emerita of MIT; and Sharp is an Institute Professor at MIT and a Nobel laureate.

The report recommends advancing convergence research, but emphasizes the shortage of federal funding for convergence fields as an important obstacle.

"Convergence science has advanced across many fronts, from nanotechnology to regenerative tissue," said Sharp. "Although the promise has been recognized, the funding allocated for convergence research in biomedical science is small and needs to

be expanded. In fact, there is no federal agency with the responsibility to fund convergence in biomedical research."

"About a third of all MIT engineers are involved in some aspect of convergence," said Sharp. "These faculty are having an enormous impact on biomedical science and this will only grow in the future. Other universities are beginning to evolve along similar paths."

The report outlines convergence-based approaches in three major disease areas: brain disorders, infectious diseases and immunology, and cancer. It also presents case studies of four emerging technology categories: advanced imaging in the body, nanotechnology for drug and therapy delivery, regenerative engineering, and big data and health information technology.

The report also points to several new federal initiatives that are harnessing the convergence research model to solve some of society's most pressing health challenges.

For example, the BRAIN Initiative, launched by the Obama administration in 2013, seeks to improve understanding of how individual cells and neural circuits interact, in order to develop new ways to treat and prevent brain disorders. And the National Cancer Moonshot Initiative, launched earlier this year to accelerate research to develop cancer vaccines and early detection methods and genomic tumor analysis, will also operate largely using convergence tools and approaches, the report says.

Funding for the report was provided by the Raymond and Beverly Sackler Foundation, The Kavli Foundation, and the Burroughs Wellcome Fund.

THE PANCREATIC CANCER ACTION NETWORK, along with advocates and survivors, gathered on Capitol Hill this week to urge Congress to fund federal cancer research.

"To ensure Congress continues to make cancer research funding a priority, we need even more committed individuals to join our efforts," said Julie Fleshman, president and CEO of the Pancreatic Cancer Action Network. "More funding has the potential to save lives, provide hope to those affected and ignite the cancer research community. Cancer research funding is an area that unites us all."

The group also invited supporters to call their members of Congress to ask for increases in cancer research funding, appealing for an appropriation of $34.5 billion for the NIH, including $5.9 billion for NCI, and to fully fund the National Cancer Moonshot Initiative.

THE LEUKEMIA & LYMPHOMA SOCIETY and the **American Society of Hematology** will collaborate to promote new treatments for acute myeloid leukemia, which the organizations say has not seen a change in the standard of care for more than 40 years. They plan to educate both patients and healthcare practitioners of the importance and availability of AML clinical trials.

"LLS exists to find cures and to ensure access to treatments for all blood cancer patients, and both LLS and ASH are dedicated to advancing the understanding, diagnosis and treatment of blood cancers, so our missions are truly aligned," said Louis DeGennaro, LLS's president and CEO.