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OCG PERSPECTIVE

Introducing the OCG Communications Fellow and First e-Newsletter of 2012

Hello! My name is Shannon Behrman, and I am the Health Communications Fellow at the Office of Cancer Genomics (OCG). Before I started here in July, I was finishing up my graduate work in the laboratory of Dr. Peter Walter at the University of California, San Francisco (UCSF) – a wonderful place for biomedical research.

YEAR-END REVIEW

2011: A Year of Progress and Change for the Office of Cancer Genomics

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TARGET PROGRAM HIGHLIGHTS

TARGETing High-Risk Acute Lymphoblastic Leukemia

Stephen Hunger, M.D. is Professor of Pediatrics, Ergen Family Chair in Pediatric Cancer, and Chief of the Section of Pediatric Hematology/Oncology/BMT at the University of Colorado School of Medicine and Children's Hospital Colorado. Dr.

PRECISION ONCOLOGY

Building a Knowledge Network of Disease for Precision Medicine: Taking a Few Lessons from Cancer

Unmistakably, we are entering a new and exciting epoch of cancer and biomedical research. Since the signing of the National Cancer Act 40 years ago, tremendous scientific breakthroughs have forged a huge paradigm shift in our understanding of cancer.

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Introducing the OCG Communications Fellow and First e-Newsletter of 2012

Shannon Behrman, Ph.D.

Hello! My name is Shannon Behrman, and I am the Health Communications Fellow at the Office of Cancer Genomics (OCG). Before I started here in July, I was finishing up my graduate work in the laboratory of Dr. Peter Walter at the University of California, San Francisco (UCSF) – a wonderful place for biomedical research. Although grateful for my enriching scientific education, I graduated with a strong desire to explore my other science-related interests, namely science writing and communications. And, so, I jumped at the chance to participate in the National Cancer Institute's Health Communications Internship Program in the summer of 2011. Paired with the Office of Cancer Genomics, I ironically knew very little about genomics and even less about cancer. My experience with cancer was mostly personal: my thesis advisor was diagnosed with throat cancer the second-to-last year of my tenure in the lab. Throughout the course of his radiation and chemotherapy treatments, my peers and I watched him painfully waste away into a shadow of a person. Fortunately for him, the treatments proved successful in the end, but it certainly left us all wondering, "With so many advancements in scientific research, is that the best we can do for cancer care?" This same question is what drives OCG in all of its cancer genomics research efforts, and I was thrilled to take on the challenge of being their Web ambassador. I just needed to learn more about cancer genomics before I could write well-informed materials for OCG.

Now armed with a bit more knowledge on the subject, I am pleased to introduce the first 2012 issue of the OCG e-Newsletter:

Ringing in the New Year is always a time for reflection. With several individual projects stirring in the Office and a new Center for Cancer Genomics recently inaugurated, 2011 was a prodigious year for OCG. Inspired by the year's progress, OCG staff got together to collaboratively review the meaningful highlights in, *2011: A Year of Progress and Change for the Office of Cancer Genomics* [2]. This article also takes a snapshot of OCG as it starts the New Year and forecasts what to expect as we flip through the 2012 calendar.

One success story from 2011 springs from the TARGET initiative and is further described in the subsequent article, *TARGETing High-Risk Acute Lymphoblastic Leukemia* [3]. Dr. Steve Hunger, Professor of Pediatrics at the University of Colorado School of Medicine, surveys the substantial progress this TARGET group has made in uncovering the genetic abnormalities of a high-risk subgroup of childhood acute lymphoblastic leukemia (ALL). Dr. Hunger also discusses subsequent efforts taken in translating the resulting discoveries into the clinic.

Outside the purview of OCG, the American Association of Cancer Research (AACR)

declared in their *Cancer Progress Report 2011* that the field of cancer research is standing on the precipice of change with "enormous optimism and new hope" for improved cancer care. The AACR Report lauds precision medicine (a form of medicine that uses an individual patient's molecular information to tailor a treatment plan) as holding great potential for enhancing the survival and quality of life of cancer patients. A committee of the National Academies recently devised and published a proposal to forge a new era of precision medicine. The Academies' report comprehensively lays out a framework for using a centralized, community-driven approach to develop new disease classifications that would be used ubiquitously in the clinic. If you're interested in learning more about their proposal, including its justifications and implications, then read *Building a Knowledge Network of Disease for Precision Medicine: Taking a Few Lessons from Cancer* [4].

And, finally, OCG strives to inform the cancer research community and the general public of important findings, activities, and resources generated from or related to its many cancer genomics projects. Adhering to this mission, OCG is participating in the upcoming AACR Annual Meeting 2012 – a conference covering every facet of cancer research. At this meeting, TARGET will be featured in a special NCI-hosted session. Read more details about the AACR meeting and the TARGET session in this announcement [5].

Thank you for reading! I hope you enjoy this issue of the OCG e-Newsletter.

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YEAR-END REVIEW

2011: A Year of Progress and Change for the Office of Cancer Genomics

Shannon Behrman, Ph.D.; Jean C. Zenklusen, Ph.D.; Robin Broughton, Ph.D.; Jaime Guidry Auvil, Ph.D.; Daniela Gerhard, Ph.D.

As we close the curtain on 2011, the Office of Cancer Genomics (OCG) is inspired to reflect on the year's milestones. 2011 was a year of great progress and change for OCG. The three OCG initiatives, Cancer Genome Characterization Initiative (CGCI), Therapeutically Applicable Research to Generate Effective Treatments (TARGET), and Cancer Target Discovery and Development (CTD²), nurtured a variety of cancer genomics-related projects that will continue into 2012. Although each project is in a different phase in its lifecycle, they all have made several noteworthy accomplishments. In this article, we review the year's happenings for OCG and its projects. We also project our aspirations for the new year.

Here are quick links to these sections of the article:

The Office of Cancer Genomics (OCG)
Cancer Genome Characterization Initiative (CGCI)
Therapeutically Applicable Research to Generate Effective Treatments (TARGET)
Cancer Target Discovery and Development (CTD²)

The Office of Cancer Genomics (OCG)

In January, Dr. Harold Varmus, NCI director, underscored his commitment to cancer genomics research by announcing the formation of the Center for Cancer Genomics. This new center integrates much of the cancer genomics efforts at NCI, including the Office of Cancer Genomics (OCG) and The Cancer Genome Atlas (TCGA)Opens in a New Tab [6]. Almost one year since the announcement, the Center for Cancer Genomics is in full operation with Dr. Barbara Wold at the helm as the Interim Director. OCG is looking forward to a new year of growth and opportunity under Dr. Wold's vision and direction.

Cancer Genome Characterization Initiative (CGCI)

Non-Hodgkin Lymphoma

Pushing the boundaries of advanced methodologies in cancer genomics research, CGCI initiated a project several years ago to resolve the genetic events driving the two most abundant forms of non-Hodgkin lymphoma (NHL)Opens in a New Tab [7], follicular lymphoma (FL), and diffuse large B-cell lymphoma (DLBCL). Despite progress from other research groups in unearthing genomic abnormalities of FL and DLBCL, the precise molecular mechanisms contributing to these two NHLs were largely unclear.

Last year, however, a group of CGCI investigators discovered a potential role for impaired histone modification in the development of NHL. Meddling with histone modification could lead to the deregulated expression of a large number of genes, including many genes previously implicated in cancer development. Curiously, they found recurrent mutations for one amino acid (Tyr641) in the histone modifying gene, *EZH2*, in a subset of NHL tumors. This single amino acid (Tyr641) mutation showed altered activity in *in vitro* assays.

A larger-scale sequencing effort published in 2011 confirmed the importance of histone modification in NHL pathogenesis. The CGCI investigators confirmed that two other histone modifying genes, *MLL2* and *MEF2B*, are frequently mutated in NHL tumors. They also revealed a list of several genes not previously implicated in NHL tumor biology.

2012 will be a promising year for this project as investigators continue to perform pre-clinical functional studies in mice. They are testing the efficacy in targeting the histone modifying genes, predominately EZH2, as a new form of therapy for NHL patients. And, as Ryan Morin explained in the previous issue [8] of the OCG e-Newsletter, "We have a much larger list of genes predicted to be under selection in NHL that we are currently following up on."

HIV+ Tumor Molecular Characterization Project (HTMCP)

To gain insight into the potentially unique molecular features of tumors in patients infected with human immunodeficiency virus (HIV), the NCI's Office of Cancer Genomics (OCG) and the Office of HIV and AIDS Malignancy (OHAM)Opens in a New Tab [9] jointly created the HIV+ tumor molecular characterization project (HTMCP) [10]. The HIV-infected population, despite the widespread use of life-sustaining

antiretroviral drugsOpens in a New Tab [11], has a higher risk of incurring some types of cancer as compared to the general population. The mechanisms underlying this disparity are largely unknown. HTMCP hopes to address this gap in understanding by utilizing state-of-the-art genomic technologies to pinpoint genetic changes and/or uncover hidden viral agents specific to these tumors. The tumor types included in this project are cervical cancer, diffuse large B-cell lymphoma (DLBCL), and lung cancer.

With assistance from the AIDS Malignancies ConsortiumOpens in a New Tab [12] and experts for each disease type, OCG developed detailed procedures for the acquisition, handling, shipping, and processing of samples this year. Using these refined procedures, HTMCP investigators are now collecting DLBCL and lung samples from North American institutions and have even started genomic and transcriptomic sequencing of 3 of the DLBCL cases. Next year, investigators will start collecting samples of all three tumor types from three African institutions.

As samples continue to accumulate from an increasing number of sources in 2012, the exciting phase of genomic sequencing and analysis will soon begin. HTMCP expects to have the majority of the projected 100 cases per tumor type in the analytical pipeline by the end of 2012.

Burkitt Lymphoma Genome Sequencing Project (BLGSP)

Launched by NCI in 2010, the Burkitt Lymphoma Genome Sequencing Project (BLGSP) [13] is funded by the Foundation for Burkitt Lymphoma Research and coordinated by the Foundation for the National Institutes of HealthOpens in a New Tab [14]. Burkitt Lymphoma (BL)Opens in a New Tab [15] is a cancer that commonly affects people of equatorial Africa and children. Current chemotherapy regimens are effective in approximately 40-90% of BL patients, depending on age, stage of the disease, treatment regimen, and site of the treatment facility. Hence, new treatments are needed to improve their efficacy as well as reduce their toxicity. The goal of BLGSP is to develop a genomic databank for BL to inform a deeper understanding of its molecular pathogenesis and facilitate improvements to its detection and treatment. Projected to take up to five years to complete, BLGSP will compile a list of genetic changes present in BL tumors in order to identify potential biological markers and/or drug targets. The study will include adult and pediatric patients with different types of BL: sporadic, endemic, and HIV-positive sporadic BL. BLGSP will also track clinical data on each BL tumor so associations between clinical parameters and genetic abnormalities can be discovered.

BLGSP is now set to begin accruing tissues in early 2012 and hopes to complete tissue accrual December 2013. By collaborating with a large-scale pediatric epidemiology study of BL in East Africa, BLGSP anticipates it will soon meet its tissue accrual goals for patients with the endemic form of the disease. Thus, efforts in the new year will focus on obtaining tissues from patients with sporadic and HIV-associated BL.

Although still in the early stages of tissue acquisition, BLGSP holds much promise as the gateway towards an improved molecular understanding of one disease disparately afflicting African populations and children.

Therapeutically Applicable Research to Generate Effective Treatments (TARGET)

Recognizing a plateau in the improvement of outcomes for children suffering from cancer, NCI launched a pilot in 2006 entitled Therapeutically Applicable Research to Generate Effective Treatments (TARGET). Six years later, TARGETOpens in a New Tab [16] is a large-scale NCI-supported program that uses cancer genomics methods to investigate five different pediatric cancers: acute lymphoblastic leukemia (ALL)Opens in a New Tab [17], acute myeloid leukemia (AML)Opens in a New Tab [18], neuroblastoma (NBL)Opens in a New Tab [19], osteosarcoma (OS)Opens in a New Tab [20], and Wilms tumor (WT)Opens in a New Tab [21]. The goal of TARGET is to use advanced genomic technologies to inform the development of more effective, less toxic drugs for childhood cancers.

This year, all five TARGET disease teams have made significant progress in identifying and characterizing genetic changes in pediatric tumors. The TARGET acute lymphoblastic leukemia (ALL) team published the largest pediatric cancer genome sequencing effort reported to date, outlining 4 key cancer signaling pathways (including the Janus kinase signaling pathway) as potentially contributing to ALL pathogenesis. They also found that frequency of mutations within these four major pathways varies greatly across genetic subtypes, thereby revealing promising new therapeutic targets in certain subsets of childhood ALL. The other teams will soon complete their analyses with promising new discoveries about the other pediatric cancers in the coming year.

TARGET looks forward to an exciting new year of data generation, analysis, and collaboration that will ultimately lead to better outcomes for children with debilitating diseases. All sequencing and molecular characterization data from each TARGET project will be made available to the research community in a user-friendly format on the TARGET website. You can learn more about TARGET's latest research, how to access new data online and more at a special NCI-hosted two-hour session at the upcoming American Association for Cancer Research Annual Meeting, which takes place March 31-April 4, 2012. Read the announcement [5] in this issue of the newsletter for more details.

Cancer Target Discovery and Development (CTD²)

The Cancer Target Discovery and Development (CTD²)Opens in a New Tab [22] initiative takes a uniquely integrative and comprehensive approach to cancer genomics research. Wading through the flood of complex genomics data generated by the research community, the goal of CTD² is to identify key genetic features of tumors and experimentally validate them through biological, chemical, and computational methods. Unique genetic features of tumors may provide targets for more effective therapeutics or markers for a patient's outcome or the disease itself.

The five Centers comprising the CTD² pilot phase —also known as the 'CTD² network'—have achieved an impressive level of project integration and success, especially considering the short time frame the research has taken place. After having just completed its second and final year of operation, the current CTD² network has produced a number of exemplary publications. Adding to its list of accomplishments, the network's highly efficacious data sharing format has caught the attention of other NIH-sponsored projects (such as the Library of Integrated

Network-based Cellular Signatures, LINCSOpens in a New Tab [23]), which are now considering its adoption.

Due to the success of the CTD² pilot phase, the NCI's Senior Program Leadership proposed the development of the pilot into a new NCI-supported program. The Board of Scientific Advisers approved this proposal less than one year ago, in the spring of 2011. Rapidly following this approval, NCI issued the request for applications for the new CTD² program. The applications have been reviewed by a special emphasis panel assembled by the NCI's Division of Extramural Affairs and will award new network Center grants in the spring of 2012.

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TARGET PROGRAM HIGHLIGHTS

TARGETing High-Risk Acute Lymphoblastic Leukemia

Stephen Hunger, M.D.

Stephen Hunger, M.D. is Professor of Pediatrics, Ergen Family Chair in Pediatric Cancer, and Chief of the Section of Pediatric Hematology/Oncology/BMT at the University of Colorado School of Medicine and Children's Hospital Colorado. Dr. Hunger is an internationally recognized expert in the molecular genetics and treatment of childhood acute lymphoblastic leukemia (ALL). He currently serves as Chair of the Children's Oncology Group (COG) ALL Disease Committee where he oversees the design and conduct of large-scale translational and clinical research studies on pediatric ALL. He also leads the Therapeutically Applicable Research to Generate Effective Treatments (TARGET)Opens in a New Tab [16] high-risk ALL project, which is a partnership between the Children's Oncology Group (COG)Opens in a New Tab [24], the Office of Cancer Genomics [25], the Cancer Therapy Evaluation ProgramOpens in a New Tab [26], and research groups from the University of New Mexico (UNM) and St. Jude Children's Research Hospital (SJCRH). Through highly collaborative team science, the TARGET project has unearthed new insights into the genetic abnormalities of high-risk ALL and identified novel prognostic markers and therapeutic targets. Below, Dr. Hunger highlights the progress of the TARGET project and subsequent efforts taken in translating the discoveries into the clinic.

Acute lymphoblastic leukemia (ALL)Opens in a New Tab [27] is the most common cancer in children worldwide. The outcome for childhood ALL has increased dramatically over the past 40 years, such that the 5-year survival rate now exceeds 90% (1). Despite improvements in survival, there remains a significant population of childhood ALL patients with a high risk of relapse. Accurately identifying patients at high risk for relapse at the time of diagnosis and treating them with novel, targeted therapies can enhance their outcomes. This rational approach to cancer treatment has proven successful in treating one subtype of ALL with an extremely poor prognosis, Philadelphia chromosome-positive (Ph^+) ALL (2). Ph^+ ALL is characterized by a chromosome translocationOpens in a New Tab [28] that causes constitutive activation of a tyrosine kinase (BCR-ABL), which contributes to the development of

leukemia. By adding the tyrosine kinase inhibitor imatinib (Gleevec) to an intensive chemotherapy regimen, the Children's Oncology Group (COG) showed they could dramatically improve the outcome of children with Ph^+ ALL (3). These results suggest that therapies targeting specific genetic alterations, such as BCR-ABL, could be an effective form of treatment for other subtypes of pediatric high-risk ALL.

Using Ph^+ ALL as a paradigm, the Therapeutically Applicable Research to Generate Effective Treatments (TARGET) high-risk ALL project set out to identify key genetic alterations of high-risk ALL with the ultimate goal of discovering new diagnostic markers and/or therapeutic targets. In the pilot phase of TARGET, investigators analyzed both leukemia and germline specimensOpens in a New Tab [29] from children with high-risk ALL (excluding those with the Ph^+ ALL subtype) using high-throughput genomic methods including gene expression profiles, analysis of DNA copy number abnormalities, and targeted gene sequencing (4). This integrated approach led to a number of observations with important biological and therapeutic implications for high-risk ALL (5-10, 13).

Briefly, TARGET high-risk ALL investigators discovered frequent alterations in four gene pathways, which included three genes or gene families not previously known to be involved in ALL (*IKZF1*, *JAK*, and *CRLF2*):

- The sequencing of 120 genes from a large number of cases revealed that somatic mutationsOpens in a New Tab [30] most commonly occurred in these key pathways: B-cell development, TP53/Rb signaling, Ras signaling, and JAK signaling (5). Selectively targeting any of these four pathways holds much promise in preventing relapse in high-risk ALL patients.
- Deletions and/or mutations of *IKZF1* occur in about one-third of high-risk ALL cases and are associated with a poor outcome (6), making it a potentially useful prognostic marker. *IKZF1* encodes the lymphoid transcription factor IKAROS, which is involved in B-cell development.
- Mutations in the *JAK* family genes, particularly *JAK2*, occur in about 10% of high-risk ALL cases (7,9,10). Janus kinase (JAK) is a family of tyrosine kinases that relays cytokine-mediated signals in the JAK signaling pathway. In cell lines expressing a *JAK2* mutant, the JAK inhibitor ruxolitinib suppressed the beginning stages of leukemia. As a result, COG developed a phase I clinical trial of ruxolitinib in children with plans to develop clinical trials of ruxolitinib plus chemotherapy in children with ALL.
- Mutations in tyrosine kinases other than JAK are rare, but possibly important, in the development of individual cases of high-risk ALL (11,12).
- Also part of the JAK signaling pathway, the cytokine receptor-like factor 2 *CRLF2* has increased expression in a subset of high-risk ALL cases. The overexpression of *CRLF2* is due to cryptic genomic rearrangements with other genes (8,10). In about half of the cases, the *CRLF2* rearrangements are accompanied by JAK mutations (and frequently contain *IKZF1* alterations). Adding the JAK inhibitor ruxolitinib to cell lines co-expressing the CRLF2 rearrangement and JAK mutations blocks its transformation (8). Studies are ongoing to determine the efficacy in using JAK inhibitors to treat *CRLF2*-overexpressed ALL as well as the frequency and prognostic significance of these various molecular alterations.

Additionally, TARGET investigators were able to identify ALL patients with a higher

risk of relapse following traditional chemotherapy regimens through gene expression profiling (9,13,14). As a result, molecular tests incorporating gene expression profiles are being developed for clinical application. Stratifying childhood ALL patients based on their prognosis helps to identify patients for whom novel therapies might be useful.

In summary, the comprehensive genomic approach of the TARGET project has successfully produced novel insights into the molecular underpinnings of high-risk ALL. These insights are currently being translated in pre-clinical and clinical studies (5-10,13), but there is still much to learn. The TARGET project, now in its second phase, is analyzing whole genomes and/or exomes of ALL cases relapsed within 3 years of initial diagnosis using next generation sequencing. To shed light on the evolution of the genomic landscape in pediatric ALL, the TARGET group is analyzing "trios" that include samples of ALL taken at initial diagnosis and relapse, as well as germline samples. The long-term goal of the ALL TARGET project is to improve the quality of life and survival of children suffering from ALL.

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PRECISION ONCOLOGY

Building a Knowledge Network of Disease for Precision Medicine: Taking a Few Lessons from Cancer

Shannon Behrman, Ph.D.

Unmistakably, we are entering a new and exciting epoch of cancer and biomedical research. Since the signing of the National Cancer Act 40 years ago, tremendous scientific breakthroughs have forged a huge paradigm shift in our understanding of cancer. Traditionally, cancer was viewed as a singular disease defined by the organ or tissue of origin, such as brain or kidney cancer. This view of cancer has now widened. Molecular evidence demonstrates that cancer is a collection of hundreds of diseases, not just one, each defined by unique, intrinsic molecular changes. Intrinsic molecular changes can drive tumor growth and resistance through a myriad of ways that researchers are quickly bringing to light. From a researcher's standpoint, these changes are the "achilles heels" of cancer cells and can be specifically targeted with drugs for more effective, less toxic therapies.

Trastuzumab (Herceptin), one example of a targeted therapy, combats one subtype of breast cancer that is more aggressive and less responsive to hormone treatment. By blocking the protein human epidermal growth factor 2 (HER2) on the surface of cancer cells, trastuzumab selectively kills these cells. But, it is only effective in 20% of breast cancer cases that actually overexpress (express too much) HER2. A simple genetic test informs breast cancer patients whether they overexpress HER2 and would, thus, benefit from taking trastuzumab.

Taking Lessons from Breast Cancer

As we learn more about the molecular makeup of patients and their tumors from large-scale genomic efforts such as the Office of Cancer Genomics' TARGETOpens in a New Tab [16] and CGCIOpens in a New Tab [31] initiatives, we can use this information to guide therapeutic strategies that lead to better outcomes, much as we are doing with breast cancer. This tailored approach to medicine, called precision medicine, will transform the way we think about patients and treatment—not just for the different types of cancer, but for many other diseases as well.

Towards Precision Medicine

In order to usher in a new era of precision medicine in this country, we must first refine our molecular understanding of human diseases. Thanks to advances in the

Human Genome Project and the "$1,000 Genome" project, we have made great progress in decoding many different diseases including cancers. However, a number of daunting challenges remain, such as the cost-prohibitive and time-consuming process of drug design and development as well as the difficulty of molecular data analysis in keeping pace with accelerating sequencing technologies. Recognizing an opportunity for change in a defining moment in biomedical research, a committee of the National Academies generated a framework for developing "a new taxonomy of human disease based on molecular biology." The committee comprehensively spells out their insightful recommendations, while addressing the many anticipated challenges, in the recently released report *Toward Precision Medicine: Building a Knowledge Network for Biomedical Research and a New Taxonomy of Disease*.

As the report explains, there is an institutionally ingrained lag in the timely adoption of useful and life-saving discoveries in the clinic. Susan Desmond-Hellmann, the chancellor of UCSF and co-chair of the committee, said, "Biomedical research information can take years to trickle to doctors and patients, while wasteful health care expenditures are carried out for treatments that are only effective in specific subgroups. Meanwhile, researchers don't have access to comprehensive and timely information from the clinic. Opportunities are being missed to understand, diagnose and treat diseases more precisely, and to better inform health care decisions." Dr. Desmond-Hellman certainly takes lessons from cancer research. Before her election to UCSF, she first served as the vice president and then as president of development and product operations at Genentech, which is a company that helped develop many anti-cancer targeted therapies including Herceptin.

Introducing the Information Commons and the Knowledge Network

To improve the granularity of disease taxonomy for better informed health care, the committee proposes the exchange of information between all of the stakeholders in medicine—the biomedical researchers, epidemiologists, clinicians, patients, biotech and pharmaceutical companies, and health care providers—through the sharing of patient data in a repository named the Information Commons. The Information Commons would be a secured, dynamic repository of data covering a large number and array of patients. Patient information would include molecular "-ome" data such as the genome, metabolome, and microbiome (the genomic information of the unique spectrum of bacterial flora inside a human body); medical histories such as physical and social environments; and health outcomes. The data repository would take advantage of the recent advances in information technology, biological information, and the shift in public attitudes on data-sharing.

The Information Commons would be a treasure trove of raw data for health-related population studies. Stakeholders could interrogate and integrate the many different layers of data to address any number of questions like, 'Is genotype X associated with the resistance to drug Y?' or 'Does living in one specific geographic region increase one's risk of cancer?' Insights gleaned from these interrogations would be deposited into a centralized, constantly evolving network called the Knowledge Network. This Knowledge Network will be easily searchable and widely accessible to a range of users, including clinicians and researchers. Doctors could use the Network to learn of the consequences of various clinical decisions. And, researchers could use the Network to build upon previous insights and fill in the gaps of our understanding

of a variety of diseases. To ensure accuracy and credibility of the Knowledge Network, the report underscores the development of a systematic process of validation.

What would emerge from the Knowledge Network would be a deeper understanding of disease mechanisms and predispositions as well as greater improvements in disease detection, diagnosis, and treatment. This integration of data would be used to define new taxonomies of disease that will allow doctors and patients to customize treatment plans that will more likely benefit the patient.

How Do We Get There?

There are a considerable number of institutional, cultural, and regulatory barriers to overcome in order to make the Information Commons and Knowledge Network successful enterprises. For instance, making patient information accessible to the stakeholders while still protecting the rights of patients will be a very thin tightrope to walk. To address these challenges, the committee recommends conducting observational pilot studies that would fill the Information Commons with data, while simultaneously imparting a more efficient process for the ethical sharing of patient information.

For these pilot studies to work, the report suggests providing incentives (at least in the beginning phases of the pilots) to promote widespread data sharing and interdisciplinary collaboration from all stakeholders, including those from the private sector. The lessons learned from these pilot studies would inform the development and implementation of a new discovery model of disease.

If successfully implemented, the National Academies' framework of developing new taxonomies of disease would greatly impact health care. Soon patients won't have to gamble their health on a "one-size-fits-all" approach to their treatment. For cancer patients, especially, the promise of precision medicine gives much hope in turning this affliction that was once largely considered life-threatening into something much more manageable.

You can download PDF files of both the summary and full report from the National Academies Press websiteOpens in a New Tab [32] for free. You may also purchase the paperback version of the full report.

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