NATIONAL ADVISORY COUNCIL FOR HUMAN GENOME RESEARCH
SUMMARY OF MEETING[1]
May 17, 2010

The Open Session of the National Advisory Council for Human Genome Research was convened for its fifty-ninth meeting at 8:30 A.M. on May 17, 2010 at 5635 Fishers Lane Conference Center in Rockville, MD. Eric Green, Director of the National Human Genome Research Institute, called the meeting to order.

The meeting was open to the public from 8:30 A.M. until 5:30 P.M. on May 17, 2010. In accordance with the provisions of Public law 92-463, the meeting was closed to the public from 5:30 P.M. on May 17, 2010 until adjournment for the review, discussion, and evaluation of grant applications.

Council members present:

Michael Boehnke
Mark Chee
Rex Chisholm
Richard Cooper
Jorge Contreras Jr.
Claire Fraser-Liggett
Richard Gibbs
Geoffrey Ginsburg
Richard Myers
Pearl O'Rourke
Pilar Ossorio
David Valle
Richard Weinshilboum

[1] For the record, it is noted that to avoid a conflict of interest, Council members absent themselves from the meeting when the Council discusses applications from their respective institutions or in which a conflict of interest may occur. Members are asked to sign a statement to this effect. This does not apply to "en bloc".

Staff from the National Human Genome Research Institute:

Ajay, DER
Assya Abdallah, DER
Sanja Basaric, OD
Tsegahiwot Belachew, DER
Vivien Bonazzi, DER
Vence Bonham, OD
Ebony Bookman, OD
Joy Boyer, DER
Lisa Brooks, DER
Comfort Browne, DER
Joseph Campbell, DER
Debbie Chen, DER
Cheryl Chick, DER
Monika Christman, DER
Priscilla Crockett, DER
Christine Cutillo, DER
Camilla Day, DER
Corina Din-Lovinescu, DER
Elise Feingold, DER
Adam Felsenfeld, DER
Barbara Fuller, OD
William Gahl, OD
Jonathan Gitlin, OD
Mary Glynn, OD
Peter Good, DER
Bettie Graham, DER
Eric Green, DIR
Alan Guttmacher, OD
Mark Guyer, DER
Lin Gyi, DER
Linda Hall, DER
Sarah Harding, OD
Lucia Hindorff, OD
Heather Junkins, OD
Rebecca Kolberg, OD
Rongling Li, OD
Carson Loomis, DER
Rebecca Lowdon, DER
Teri Manolio, OD
Jean McEwen, DER
Keith McKenney, DER
Enrique Michelotti, DER
Janis Mullaney, OD
Anita Nagwani, OD
Ken Nakamura, DER
Brad Ozenberger, DER
Jacqueline Palchik, DER
Jane Peterson, DER
Dylan Perry, DER
Rudy Pozzatti, DER
Lita Proctor, DER
Laura Rodriguez, OD
Jeff Schloss, DER
Geoff Spencer, OD
Jeff Struewing, DER
Larry Thompson, OD
Elizabeth Thomson, DER
Susan Vasquez, DER
Lu Wang, DER
Christopher Wellington, DER
Kris Wetterstrand, DER
Judith Wexler, DER
Rosann Wise, OD
Simona Volpi, DER
Julia Zhang, DER

Others present for all or a portion of the meeting:
Joann Boughman, American Society of Human Genetics
R. Rodney Howell, American College Medical Genetics
Sharon Terry, Genetic Alliance
Rhonda Schonberg, National Society of Genetic Counselors

INTRODUCTION OF NEW MEMBERS AND STAFF, LIASONS AND GUESTS

Mark Guyer noted that the following members have retired from NHGRI Council: David Page, Paul Sternberg, and Eric Boerwinkle.

Dr. Guyer introduced liaisons Joann Boughman, Rodney Howell, and Rhonda Schonberg.

Dr. Guyer introduced new NGHRI staff: Simona Volpi (Program Director), Lita Proctor (Program Director), and Judith Wexler (Program Analyst).

FUTURE MEETING DATES

The following dates were proposed for future meetings: September 13-14, 2010, February 7-8, 2011, May 16-17, 2011, and Sept. 12-13, 2011.

DIRECTOR'S REPORT

Supplementary material from the Director's Report is available at www.genome.gov/DirectorsReport.

I. GENERAL NHGRI UPDATES

New Appointments. Eric Green was appointed Director of NHGRI in December of 2009. At about the same time, Alan Guttmacher, former Acting Director of NHGRI, accepted a position as the Acting Director of NICHD. Mark Guyer is currently the Acting Deputy Director of NHGRI. Ellen Rolfes has been appointed as the NHGRI Deputy Executive Officer and Ann Fitzpatrick as the new NHGRI Budget Officer. NHGRI is currently seeking candidates to fill the positions of Scientific Director and Deputy Director.

Planning Process. NHGRI is in the process of developing a new strategic plan for genomic research. It is expected that the final plan will be published by December 2010. Details regarding the planning process are available at: www.genome.gov/Planning. As part of the planning process, NHGRI solicited white papers and web-based feedback from the community regarding the future of genomics in early April 2009. Many workshops were held throughout 2009 and 2010, including one on the future of Large-Scale Sequencing in March 2009 and workshops on Cloud Computing and Genomic Informatics and Analysis in March 2010 and April 2010, respectively.

A draft plan is currently in development for presentation at the 'Finale' Meeting, to be held on July 6-8 at the Airlie Center in Warrenton, VA. Video access will be available for those who cannot attend in person.

II. GENERAL NIH UPDATES

As outlined in previous Director's reports, NIH is looking to pursue the five major themes that were identified recently by the new Director, NIH: 1) High-Throughput Technology, 2) Translational Medicine, 3) Benefiting from Health Care Reform, 4) More focus on Global Health, and 5) Reinvigorating and Empowering the Biomedical Research Community. In this context, NIH is developing two new approaches to therapeutics developments.

The first is the **Cures Acceleration Network (CAN)** program, which is the part of the Health Care Reform Act that assigns to NIH the task of advancing the development of new treatments and cures by reducing barriers between laboratory discovery and clinical trials. It provides flexible funding and has an authorized budget for FY2010 of $500M.

Another NIH initiative is the **Therapeutics for Rare and Neglected Diseases (TRND)** program, the goal of which is to develop candidate drugs for rare and neglected diseases not addressed by the private sector. It is funded at $25M for FY2010. Currently there are three ongoing projects, schistosomiasis, Niemann-Pick disease Type C, and Hereditary Inclusion Body Myopathy. NIH will be soliciting proposals for this program in FY 2011.

NIH is currently recruiting for the positions of NIH Deputy Director and NCI Director (Update: Harold Varmus was appointed as the new NCI Director).

III. GENOMICS UPDATES

New Memberships. New members elected to the Institute of Medicine include NHGRI grantees Zac Kohane and Russ Altman. New members were elected to the National Academy of Sciences include NHGRI grantees Trudy Mackay and Kevin Struhl.

Awards. NHGRI grantees Jim Kent and David Haussler received the 2009 Curt Stern Award from the American Society of Human Genetics; this award is given for outstanding achievements in the field of human genetics. Bill Gelbart was given the George W. Beadle Award for creating FlyBase, the central repository for *Drosophila* genome data. Francis Collins and Craig Venter were awarded the 2009 Presidential Medal of Science. Dr. Collins, along with David Botstein and Eric Lander, was also awarded the10th Annual Albany Medical Center Prize. Maynard Olsen was given the 2010 American Society for Microbiology Promega Biotechnology Research Award. Elaine Mardis received the Scripps Genomic Medicine Award, given to researchers who have an "extraordinary impact on genomic medicine". Teri Manolio, the Director of Office of Population Genomics at NHGRI, was given the Presidential Rank Award which honors high-performing senior career employees for "sustained extraordinary accomplishment".

Several new high-throughput sequencing platforms were introduced at the Advances in Genome Biology and Technology Meeting (AGBT) held on February 24-27, 2010.

IV. EXTRAMURAL ACTIVITIES

Sequencing.

- New partnerships and collaborations were announced including Broad/Mexico, WashU/ St. Jude, and Illumina/BGI.
- The genome sequence of a songbird (zebra finch) was completed and published in *Nature*. More than 800 genes were found to play a role in the male zebra finch's ability to learn songs from his father.
- The Genome 10K project was launched, with the purpose of organizing communities to provide DNA samples from 10,000 species, representing all extant vertebrate groups.
- South Africans, twins with multiple sclerosis, actress Glenn Close, and Neanderthals were among those whose complete genomes were recently sequenced.
- A quick analysis by NHGRI showed that considerably more ARRA funds were spent by other institutes on medical sequencing than by NHGRI, indicating that the sequence-based approach to understanding the genetic basis of disease is becoming increasingly widespread.

ENCODE/modENCODE.

- The mid-course review for the ENCODE (Encyclopedia of DNA Elements) and modENCODE programs was held in April 2010.
- The consortia recently published two *Science* papers.
- The modENCODE consortium is preparing a fly/worm integrated analysis for publication.
- The ENCODE consortium is preparing an 'ENCODE 101' paper to describe how to get access to and use ENCODE data.

KOMP. The KOMP (Knockout Mouse Project) is on target for its goal of producing 8500 null mutants by 2011.

Other.

- Quarterly NCBI/NHGRI meetings will be held to address the bioinformatics needs of NHGRI projects.
- The Basic Behavioral and Social Science Opportunity Network (OppNet), is an ARRA-funded program that will solicit proposals for several areas of behavioral research including: Social Gradients, Stress, Health Behavior, and Capacity Building. $10M of ARRA funds were allocated to this program and will be used for competitive supplements and K18 awards.

V. NIH COMMON FUND PROJECTS

Current Programs.

- The total number of probes discovered by the **Molecular Libraries Program** has doubled in the past year and now stands at 153**.** A midcourse review of the program is scheduled for August 2010.

- **The Genotype-Tissue Expression (GTEx)**, a 2.5 year pilot program, will fund its laboratory and tissues collection sites in June 2010. If the pilot is successful in demonstrating feasibility and value, the project will scale to 1000 donors in Years 3-5.
- **The Human Microbiome Project (HMP)** consortium is preparing four manuscripts for publication. A review of the HMP Demonstration Projects will be held on June 2-3, 2010.

New Programs. NHGRI was asked to take the lead on several new Common Fund programs, including LINCS (Library of Integrated Network –based Cellular Signatures), Protein Capture Reagents, the Human Heredity and Health in Africa (H3Africa) component of Global Health, and Mouse Genotyping (KOMP 2) programs. More information on these programs is available at www.genome.gov/Pages/About/NACHGR/May2010AgendaDocuments/DirectorsReport-May2010.pdf

VI. NHGRI OFFICE OF THE DIRECTOR

Population Genomics. The GWAS catalog (www.genome.gov/gwastudies) now includes more than 540 publications and 2600 SNP-trait associates.

Community Outreach. DNA Day was held on April 23, 2010. Ambassadors visited 25 schools on the Washington DC metro area to educate students on genomics. The Genomics Career website (www.genome.gov/GenomicsCareers) was launched to showcase interviews and interactive videos of genomic professionals. The NHGRI Talking Glossary (www.genome.gov/glossary) was revamped to include color illustrations, 3D animations, and quizzes.

VII. NHGRI INTRAMURAL RESEARCH PROGRAM

New Appointments. Cynthia Tifft has been appointed as the NHGRI Deputy Clinical Director, and Larry Brody as the Chief of the Genome Technology Branch.

Awards. Intramural investigator Charles Venditti won the American Society of Gene and Cell Therapy (ASGCT) received the Outstanding New Investigator Award. Intramural investigator Fabio Candotti was elected to the ASGCT board.

PRESENTATION: UPDATE ON GENE PATENTING

Council members Jorge Contreras and Pilar Ossorio gave a presentation, which had previously been requested by the Council, on the topic of the current status of gene patenting,.

Requirements for Patentability. For an "invention" to be patentable, US law requires that it has 1) patentable subject matter 2) utility 3) novelty and 4) non-obviousness.

Patent Law & Litigation. Intellectual property right is defined by a claim, and consists of the right to exclude others from using the things captured within the claim without permission. The lowest level of patent litigation in the US is the District Court or the Patent Office and the highest level is the Supreme Court.

Patentable Subject Matter (ACLU vs. Myriad). In the late 1990's, scientists from Myriad isolated the BRCA1 and BRCA2 genes and obtained patents on them. In 1996, Myriad began to offer BRCA1/2 screening tests and the company has been consistent in suing others who have attempted to offer the same services. After much dispute, Myriad is now the only US provider of commercial BRCA1 & 2 screening. It has been alleged that these gene patents have had several adverse effects, including overpriced screening, the inability of customers to receive confirmatory testing from a second laboratory, and interference with ability of researchers to investigate multi-gene diseases. In May 2009, the ACLU (American Civil Liberties Union), representing a group of plaintiffs consisting of associations, researchers, advocacy groups, and patients, sued Myriad and asked the court to invalidate fifteen claims of Myriad's seven BRCA1/2 patents. They argued that genes are a "phenomena of nature" and are therefore un-patentable subject matter as stipulated in previous court cases. Myriad counter-argued that isolated DNA is different from DNA found in nature, and the Patent Office expressly allowed patenting of isolated genetic material. The Court ruled in favor of the ACLU and invalidated Myriad's claims, for the reason that "isolated DNA is not markedly different from native DNA as it exists in nature." Further proceedings are expected.

Utility (Eli Lilly vs. Human Genome Sciences). In 1996, HGS patented a sequence for neutrokine-α, a protein of unknown function. The claim listed several potential uses for the protein. Eli Lilly, which was developing antibodies for neutrokine-α, challenged the patent. This case was brought to a UK appeals court. In the UK, it is required that the patent description disclose a practical way of exploiting the invention and this requirement was not deemed to be satisfied by claiming an interesting research result without specified application. Therefore, the patent was struck down by the UK court system due to the unknown utility of the protein.

SACGHS Report on Gene Patents and Licensing. In February 2010**,** the Secretary's Advisory Committee on Genetics, Health, and Society (SACGHS) reviewed the clinical impact of gene patents and licensing practices on access to genetic testing and made the following recommendations: 1) exemption from infringement of patents should be granted for patient care and research, 2) there should be a requirement for non-exclusive licensing of diagnostic genetic technologies, and 3) steps should be taken to ensure that clinically useful genetic tests are equitably available and accessible to patients.

PRESENTATION: NEW MODELS FOR LARGE PROSPECTIVE COHORT STUDIES

Teri Manolio discussed lessons learned from US prospective cohort studies and the development of a plan to go forward. The UK has produced the BioBank, which is recruiting about 1000 participants per day over a three-year period. It was funded at $90M.

Centralized vs. Distributed Models. Larger studies require different, not scaled, approaches than smaller studies. The cost per participant is the driving force for efficiency. A distributed model allows investigators to apply for awards and send data in to a centralized location. A centralized model opens nodes as long as they are productive, however there will be a loss of intellectual input from academic centers.

Embed in Infrastructure for Recruitment and Follow-Up. Invitations should be sent from legitimate and relevant societies and associations. Availability of EMR data is important as it minimizes the need for individual follow-ups.

Accept Low Recruitment Yield. Participation rate is inversely proportional to the location of the participating centers; therefore centers need to be placed strategically across the US.

Discussion. Council believes that this is a great opportunity for NHGRI to set the bar for consent, return of results, and other issues.

CONCEPT CLEARANCE: eMERGE

Jeff Struewing present a concept clearance proposal or Phase 2 of the eMERGE program.

Background. eMERGE Phase I is a 4-year program that began in late 2007 with the goal of defining phenotypes from EMR data, conducting GWA studies using those phenotypes, reducing risk to patient privacy from sharing of EMR data, and developing community consultation procedures for conducting such research. Five biorepositories were set up to conduct GWA studies of six site-specific phenotypes in roughly 18,000 subjects, along with a network-wide study of the phenotype of resistant hypertension in additional 1,800 subjects. These 20,000 subjects will be electronically phenotyped and analyzed for hypothyroidism. Six additional phenotypes are being assessed using ARRA funds.

eMERGE is unique in defining phenotypes from EMR data through data extraction and other informatics tools. Enhanced data cleaning has shown potential actionable chromosomal anomalies. Although mining EMR data expands the potential for conducting genomic research, it also expands risks to patient's privacy. eMERGE is addressing these problems by examining the potential for linkage between standardized clinical information and the patient's identifying information in their EMRs. Investigators have developed methods to extract the potentially linkable data and modify them to minimize risk threats to confidentiality of patient medical information. A Consent and Community Consultation group was also created within the program to address this and other concerns about genomic research linked to EMRs. There are some limitations to eMERGE phase I program, including a low proportion of minority patients and lack of pediatric or other specialty settings.

Proposal. In Phase 2, the goals of the initial phase will be expanded:

- 5-8 biorespositories will be supported to expand the phenotype library and ensure wide validity of the data,
- the number and diversity of participants and sites will be increased,
- GWA results will be incorporated in participants' EMRs to explore their value in clinical decision making.

Other aspects of the proposed Phase 2 project are:

- A separate RFA will be issued to support the Coordinating Center.
- Within the first year of Phase 2, investigators will initiate the use of genotyping data in clinical care.
- Selection of Phase 2 sites will be based on: performance in Phase 1, population diversity, availability of high-quality GWA genotyping data, consent for sharing individual level data through dbGaP, and other criteria.

- The sites and the Coordinating Center will be funded by U01s (Cooperative Agreements).
- NHGRI will commit around $30M over four years to support eMERGE Phase 2. Roughly $5M of the funds will support repeat genotyping as needed.

Discussion. It was mentioned that more emphasis needs to be paid attention to the reproducibility of phenotyping.

This concept was approved by Council.

CONCEPT CLEARANCE – LARGE-SCALE SEQUENCING PROGRAM

Adam Felsenfeld presented a concept clearance proposal for renewal of the Large-Scale Sequencing Program.

Background. The Large-Scale Sequencing Program currently funds three Genome Sequencing Centers, which have increased their capacity in the past two years from 0.15 TB to 150 TB per year. It is now possible 1) to sequence thousands of genomes, including hundreds of whole genomes and exomes; 2) determine the sequence basis of Mendelian diseases; 3) understand the genetics of complex diseases through sequencing of candidate regions; 4) obtain low-cost whole genome sequences of many organisms; and 5) perform well-powered metagenomic studies. In addition to the Genome Sequencing Centers, NHGRI used ARRA funds to establish medical sequencing "Discovery Centers," each of which focusies on a specific disease.

Proposal. Staff presented a Concept Clearance document to the Council that proposed that the Large-Scale Sequencing Program renewal consist of four separate initiatives:

1. Large-scale Genome Sequence and Analysis Centers.
    - Funding mechanism: 4 years, Cooperative Agreements.
    - This component will continue the current genomic sequencing centers aspect of the sequencing program, with emphasis on big, compelling projects. There will be a mechanism for community- initiated projects.
2. A Center for Mendelian Disorders.
    - Funding mechanism: 4 years, Cooperative Agreement(s).
    - One or two centers will take on the sequencing of Mendelian diseases. It/they will be responsible for coordinating sample acquisition, maintaining exome sequencing and analysis capability, and generating and maintaining a resource for investigators researching Mendelian diseases.
3. Clinical Sequencing Exploration Projects
    - Funding mechanism: 3 years, Cooperative Agreements.
    - This component seeks to bridge the gap between genomic information and clinical application. NHGRI will solicit approximately 5 projects in which a clinical researcher will obtain substantial genomic information from patients and devise how to best use this data for clinical purposes. Since this activity will raise several ethical and legal issues, these awards will have a substantial ELSI component.
4. Robust analysis tools
    - Funding mechanism: 4 years, RO1 and SBIR grants.

- This initiative will solicit projects to convert research grade informatics tools from the funded centers and elsewhere and make them robust and available for community use.

Budget. Currently the sequencing program is funded at around $110M/year. For the renewal, each component would be allocated a certain amount of the total budget: $90M for initiative 1, $10M for initiative 2, and $5M each for initiatives 3 and 4.

This concept was approved by Council.

CONCEPT CLEARANCE: NHGRI REPOSITORY FOR HUMAN GENENTIC RESEARCH

Bettie Graham presented a concept clearance proposal for the continuing the contract that supports the NHGRI Repository for Human Genetic Research.

Background. A RFP was announced on October of 2005 to establish a NHGRI Sample Repository for Human Genetic Research. The contract was awarded on August 2006 and will expire on July 2011. The Repository now includes samples from the HapMap, 1000 Genomes, and HMP projects. The DNA and cell lines from the HapMap samples have been valuable resources for many research programs. Mechanisms are in place to ensure all research proposed is consistent with informed consent. Furthermore, the Repository promotes extensive communication with the donor communities through Community Advisory Groups and provides quarterly reports on sample use.

Proposal. The Repository continues to fill a need, as indicated by the considerable demand for the samples by the research community. NHGRI, therefore, proposes to reissue the RFP. Since the contract will expire at the end of July 2011, the RFP needs to be published by August 2010. However, unlike the first competition, which was done as a sole-source solicitation, this will be a free and open competition. The Statement of Work is the same as the previous one (more information can be found at www.genome.gov/Pages/About/NACHGR/May2010AgendaDocuments/ConceptClearance-NHGRISampleRepositoryForHumanGeneticResearch.pdf). The Repository will be supported as a cost-reimbursement contract. The cost of the contract will be partially offset by sale of samples to qualified scientists in both the public and private sectors. Discounts will be given to scientists from developing countries. This will be a 5-year contract.

Discussion. It was mentioned that the cost to the NHGRI for maintaining the Repository is usually between $120 -175K per month and that it generates around $30K-60K per month in revenue, although it is difficult to accurately predict the cost. It was suggested that funding two repositories instead of one may be more cost-effective.

This concept was approved by Council.

MEETING REPORTS: Cloud Computing Workshop and NHGRI Informatics and Analysis Planning Meeting

Vivien Bonazzi presented summaries of the Cloud Computing Workshop and the NHGRI Informatics and Analysis Planning Meeting.

Computational Challenges. The amount of sequence data being produced is outpacing the ability to handle them computationally. Specifically, robust infrastructure including storage, capacity, hardware and software, and data security is needed. Software tools, including new and improved analysis tools, and tools that can scale to new architectures, as well as better methods for processing raw data, and new mechanisms for data visualization and representation, are also needed.

Cloud Computing Workshop. Cloud Computing is defined as a shared pool of computing resources that can be rapidly deployed with minimal managerial effort or service provider interaction. Current commercial cloud providers include services from Amazon, Microsoft (Azure) and Google.

Optimally, data generators would send data into a "Cloud" where the data could be used by both power users and casual users. At the Cloud Computing Workshop, held on March 2010, several topics were discussed, among them different cloud environments, genome data repository needs (NCBI, Sanger, EBI, etc), technical challenges (bandwidth, security, etc), and potential pilot projects. Conclusions and outcomes from the meeting included:

- Cloud computing is not optimized for genomics data or tools.
- Complex genomics analysis pipelines are currently very difficult to configure.
- Cloud computing CPU and storage costs are declining.
- Security is a key concern for all cloud providers.
- Cloud computing is most viable for small to mid-size groups that have little or no IT infrastructure.
- Microsoft, Amazon and Google are interested in a Microsoft/Google/NSF- like program with NHGRI/NIH. NIH CIT is also interested in participating in the program.

NHGRI Informatics and Analysis Planning Meeting. Conclusions and recommendations from the meeting, which was held on April 2010, included:

- Infrastructure needs to be improved in order to support data management and analysis.
- New and improved methods for data integration are needed.
- Informatics needs should be addressed early and often in new genomic research projects.
- Robust Informatics analysis solutions should also be provided to smaller groups.
- There is a need for improved tools to analyze reference genomes.
- New and improved tools for data visualization are needed.
- All data should be deposited in open access databases.
- No publication embargoes or other restrictions should be placed on data access.

Discussion. Council agreed that informatics needs should be discussed early in the project planning process, along with ethics issues. NCBI should participate in the initial planning stages of a project.

PROJECT UPDATE : 1000 GENOMES PROJECT

Lisa Brooks give an update on the 1000 Genomes Project.

The goal of the 1000 Genomes project is to identify 95% of the SNPs that have frequencies of at least 1% in the human populations studied, with deeper coverage in exons. Structural variants will not be

found as comprehensively since they require more sequence coverage and are harder to detect. There are currently three pilot projects – low coverage, deep coverage, and gene-region capture. The pilot projects have produced a lot of sequencing data, and eight million novel SNPs have been discovered (dbSNP entries increased by 70% as a result).

Plans are now underway for the full-scale project. The intent is to sequence 2500 samples at 4X coverage across the genome. In addition, deep exome sequencing will also be done for all the samples. Data will be produced in several phases. Data from about 1000 samples will be available by July 2010. Data from an additional 1500 samples will become available throughout 2010 -2011, although if some samples take longer to obtain then those data would not become available until 2012. For genotyping, up to 10 million SNPs will be analyzed with 4 new Illumina arrays. Structural variants will also be examined in certain sets of samples.

Currently, the 1000 Genomes Consortium is working on 1) publishing a paper on the pilot project, 2) developing a more streamlined data processing pipeline and a more robust tracking system, 3) genotyping the samples, and 4) developing tools for the average researcher to access and use the data. A new advisory group was created for the program.

Discussion. It was mentioned that the Data Coordination Center has had difficulties in obtaining and releasing the data in a timely manner. Clarity on the sample timeline is still a major issue.

PROJECT UPDATE - TCGA/CANCER GENOME SEQUENCING

Brad Ozenberger gave an update on TCGA/Cancer Genome Sequencing.

The goal of TCGA is to have complete genomic characterization data for 50 cancer types within 5 years. Characterization of the first 3000 samples, much of which is being supported with ARRA funds, requires an accrual of 160 samples per month and is intended to be completed by September 2011 (19 months from now). By July 2010, TCGA expects to achieve its first milestone with the complete characterization of 600 samples, and accrual of 1500 samples.

There are 5 tumor projects currently underway in TCGA: glioblastoma (GBM; whole genomes and whole exomes), ovarian cancer (exome data and beyond will be included in a soon-to-be published manuscript), acute myelogenous leukemia (AML), and colon and rectal cancers.

In April 2010, the TCGA Steering Committee held its bi-annual meeting in Bethesda, MD. Some outcomes of from the meeting include reconsideration of the tumor qualification criteria (with respect to tumor size and tumor purity for inclusion, and for matched “normal” controls), reorganization of the tumor projects (develop a working group for each tumor type), and reorganization of project governance.

Discussion. It was mentioned that the stringent sample qualification criteria was justifiable for the TCGA pilot project, but is unrealistic for the full scale project.

COUNCIL – INITIATED DISCUSSION

Topics for next Council meeting should include:

- Next iteration of the strategic plan for the future of genomics.
- A presentation on the training portfolio.
- Discussion or presentation of 3rd generation sequencing.
- Continuation of discussion on informatics issues.

ANNOUNCEMENTS AND ITEMS OF INTEREST

Dr. Guyer directed Council to the Council folders containing items of interest, reports from liaisons, and workshop summaries.

CONFLICT OF INTEREST

Dr. Guyer read the Conflict of Interest policy to Council and asked them to sign the forms provided.

REVIEW OF APPLICATIONS

In closed session, the Council reviewed 162 applications, requesting $44,045,055. The applications included 84 research projects, 15 ELSI grants, 31 RFAs, 1 research center grant, 2 conference grants, 1 career transition award, 16 SBIR Phase 1 grants, 2 SBIR Phase 2 grants, 1 STTR Phase 1 grant, 1 STTR Phase 2 grant, 4 individual training grants, 1 continuing education training award, and 3 education project grants. A total of 104 applications totaling $34,886,492 were recommended.

I hereby certify that, to the best of my knowledge, the foregoing minutes are accurate and complete.

_____ _____

Date

Mark Guyer, Ph.D.
Executive Secretary
National Advisory Council for Human Genome Research

_____ _____

Date

Eric Green, M.D, Ph.D.
Chairman
National Advisory Council for Human Genome Research