eMERGE Network Steering Committee Meeting
October 9-10, 2012
Bethesda, MD

Attendance

Network Members in Attendance

CCHMC/BCH	Armand Antommaria
CCHMC/BCH	Beth Cobb
CCHMC/BCH	John Harley
CCHMC/BCH	Ingrid Holm
CCHMC/BCH	John Lynch
CCHMC/BCH	Bahram Namjou-Khales
CCHMC/BCH	Cassandra Perry
CCHMC/BCH	Cindy Prows
CCHMC/BCH	Wendy Wolf
CHOP	John Connolly
CHOP	Hakon Hakonarson
CHOP	Brendan Keating
CHOP	Frank Mentch
CHOP	Patrick Sleiman
Geisinger	David Carey
Geisinger	Andy Faucett
Geisinger	Samantha Fetterolf
Geisinger	Helena Kuivaniemi
Geisinger	David Ledbetter
Geisinger	Diane Smelser
Geisinger	Gerard Tromp
Geisinger	Janet Williams
Geisinger	Marc Williams
GH/U WA	David Carrell
GH/U WA	David Crosslin
GH/U WA	Malia Fullerton
GH/U WA	Andrea Hartzler
GH/U WA	Carlos Gallego
GH/U WA	Gail Jarvik
Marshfield	Murray Brilliant
Marshfield	Ariel Braubar
Marshfield	Simon Lin
Marshfield	Cathy McCarty
Marshfield –CC	Marylyn Ritchie
Mayo	Sue Bielinski
Mayo	Chris Chute
Mayo	Mariza de Andrade
Mayo	John Heit
Mayo	Hayan Jouni
Mayo	Barbara Koenig
Mayo	Iftikhar Kullo
Mayo	Jennifer McCormick
Mayo	Jyoti Pathak
Mt. Sinai/Columbia	Steve Ellis
Mt. Sinai/Columbia	George Hripcsak
Mt. Sinai/Columbia	Kash Patel
Mt. Sinai/Columbia	Randi Zinberg
Northwestern	Geoff Hayes
Northwestern	Mike Heathcote
Northwestern	Abel Kho
Northwestern	Laura Rasmussen-Torvik
Northwestern	Maureen Smith
Northwestern	Justin Starren
NHGRI	Camilla Day
NHGRI	Rongling Li
NHGRI	Nicole Lockhart
NHGRI	Teri Manolio
NHGRI	Ian Marpuri
NHGRI	Jean McEwen
NHGRI	Bradley Ozenberger
NHGRI	Eugene Passamani
NHGRI	Erin Ramos
NHGRI	Simona Volpi
NHGRI	Anastasia Wise
NIGMS	Rochelle Long
NICHD	Melissa Parisi
NICHD	Tiina Urv
Vanderbilt	Ellen Clayton
Vanderbilt-CC	Josh Denny
Vanderbilt	Jason Karnes
Vanderbilt-CC	Brad Malin
Vanderbilt	Dan Roden
Vanderbilt	Sarah Stallings
CC	Melissa Basford
CC	Jonathan Haines
CC	Lauren Melancon

ESP Members

UAB	Eta Berner
InterMountain	Stan Huff
UNC	Howard McLeod
Univ. of Pittsburgh	Lisa Parker
Cleveland Clinic	Charis Eng (phone)

Network Invitees and Guests

AAAS	Deborah Runkle
Baylor College of Medicine	Steve Scherer
United States Air Force	Ron Miller
United States Air Force	Cecili Sessions
Univ. of Washington	Debbie Nickerson
Veterans Affairs	Mike Gaziano

Tuesday, October 9

Welcome, Opening Remarks, General Updates – Rongling Li

Rongling updated the Steering Committee on new director of the National Center for Advancing Translational Sciences (NCATS) and new NHGRI organizational structure and division directors. The NIH Fiscal Appropriation was also addressed; the current agreement will keep the government running through March 2013 with regular appropriations to be completed with the next Congress. All workgroups and pilot projects were discussed in relation to the overarching eMERGE implementation flow diagram and the remaining eMERGE Phase II timeline. The Network has been fruitful in its efforts to create new tools, compose publications, submit data to dbGaP and recruit participants. Rongling also presented the goals of the meeting which included:

- Pediatric Sites: (1) Refine milestones & timelines, (2) continue to integrate with other sites, (3) Continue to identify logistic issues related to the uniqueness of pediatric sites.
- Workgroups: (1) Interact among workgroups, (2) Identify areas that need improvement.
- Network Collaborations: (1) Share lessons learned, (2) Identify areas for network-wide products
- Collaborate with other networks, consortia, EHR vendors and other institutions.

In addition to the goals for the meeting Rongling outlined what NHGRI hopes the Network will take away from the meeting:

- Obtain input from the ESP members on year 1 progress and future directions
- Refine the milestones/timelines for the eMERGE PGx project and genomic medicine pilot studies
- Identify network challenges and propose possible strategies/approaches to overcome them
- Identify additional needs between the study sites and coordinating center
- Develop plan for dissemination of the network-wide lessons learned and research results to scientific community

Site Update – Marshfield/Essentia – Murray Brilliant, Cathy McCarty, Marylyn Ritchie

The presentation began with general site updates and personnel changes. Marshfield provided a brief background to their consenting process and relevant statistics. Touch-screen kiosks were deployed with focus groups to get participant reactions on this type of consenting process. After reviewing the results from this study the computer based consenting has been adopted for general Biobank enrollment. The site has been working on GWAS analysis specifically for gene-gene interactions associated with cataracts. In addition, the site has been working with PhenX on gene-environment interactions. Marshfield plans to continue with all projects discussed along with beginning additional gene-gene and gene-environment studies. Like all sites, the Marshfield group has been working on the PGx project. Two primary care physician focus group meetings have been held as well as three patient focus group meetings. Marshfield has made progress in many areas regarding the PGx project including: (1) the creation of a working group with pharmacists, clinical geneticists, biomedical informaticists and clinic IS, (2) IRB approval is pending minor working changes, (3) the design of CDS rules & delivery to physicians for simvastatin and warfarin is completed, (4) tools are in development for Cattails, and (5) planning design for receipt of various data in VCF.

Site Update – GHC/UW – Gail Jarvik

Gail presented an update outlining their three specific aims. In terms of extension of GWAS discovery analysis in EMR, the group is currently working as the primary site for three phenotypes and is also serving as the secondary site for an additional 5 phenotypes. Some preliminary data was shown for all three primary phenotypes. They are working towards appropriate and effective integration of genomic information into the EMR for clinical care through participant-observation of GHC genomics improvement project, performing a qualitative needs assessment with stakeholders by interviewing health system leaders and facilitating focus groups with patient, physicians, and designing and testing of functional prototypes for point-of-care. The qualitative needs assessment has been completed for both health system leaders and patients and physicians, all provided varying opinions about the current state of genetic medicine and concerns. The group has many ongoing collaborations with a variety of consortia and research groups. One large collaborative project facilitated by GHC/UW within eMERGE is the Hemochromatosis penetrance project. There are other areas of penetrance that can be uniquely looked at in the eMERGE data and they plan to explore these other possibilities.

CHOP Aims and Timelines – Hakon Hakonarson

Hakon provided a brief overview of CHOP's Center for Applied Genomics along with the site's milestones and timelines. The site's three main goals were outlined: (1) Collect and integrate phenotypes with EPIC and other databases, (2) Validate new GWAS/genetic results representing actionable variants and integrate into EMRs, and (3) Generate informed consent procedures. To date 7,430 study subjects have been submitted to dbGaP. CHOP also identified lipids as their first network phenotype. A lipids phenotype has already been run in the adult population lead by Northwestern. CHOP also outlined the other algorithms they plan to focus on, which include asthma, GERD, ADHD and atopic dermatitis. CHOP is actively collaborating on C. Diff and VTE and is waiting for the remaining algorithms to be released for implementation Network-wide. A re-consent form is in place and several meetings are scheduled with the IRB chair to discuss the path forward. CHOP will also be looking at 4 different projects relating to pharmacogenomics: adverse events, DMET, morphine response, and asthma response. CHOP was also awarded a supplement for the PGx project and will focus their initial efforts on serious adverse events. They plan on looking at TPNT/thiopurines (CYP2D6), Tegretol (HLA-B*1502) and a range of other variants including but not limited to adrenergic agonists.

CCHMC/BCH Aims and Timelines – John Harley & Ingrid Holm

John began by outlining the specific aims for CCHMC/BCH which include informatics, phenotyping, return of results to patients, and physician perceptions towards return of results. CCHMC and BCH are utilizing a variety of informatics tools: i2B2, SHRINE, cTAKES, and BIRT. The site is currently working on early childhood obesity and autism spectrum disorder as their first 2 network phenotypes. Preliminary research on both phenotypes was shared along with some specifics of each phenotype. In addition to the obesity and autism phenotypes that are underway CCHMC/BCH has a large number of phenotypes that are being considered. John briefly touched on the PGx study and their main objectives. Ingrid spoke to aims 3 and 4. The study population and methods were outlined for Aim 3: Use of COMT and CYP2D6 research results to explore parents' responses to and use of their children's research results and better understand the factors that influence their decisions about learning incidental findings. Primary and specialty care providers of children were utilized as the study population for Aim 4: to explore clinician perceptions of pharmacogenetic

research results after EMR integration. The results viewed by these providers were tracked within the EMR. 30 providers were also interviewed at each site to explore their responses to and use of genomic results. Ingrid also spoke about the dynamic relationship between CCHMC and BCH. Due to the distance between sites there are many challenges and opportunities for their collaboration, and both groups are looking forward to capitalizing on each sites' strengths.

Coordinating Center Update – Jonathan Haines & Josh Denny

The main goal of the Coordinating Center is to make things easier for the entire Network. This goal is executed through supporting sites and workgroups; enhancing phenotyping by data management, phenotype development, and discovery; extracting, evaluating and managing network genotypes; and supporting privacy. Main areas in which the CC continues to assist the Network's organization and productivity include:

- Facilitating network functioning through dashboards, process facilitation, and supporting the publication process.
- Supporting Network visibility & external collaboration by assisting external groups in completing the criteria for affiliate membership, facilitating cross Network "networking", creation and upkeep of www.gwas.net, and the creation of the eMERGE I "Merged Set."
- Providing meeting & communication management by supporting 10 active workgroups, subgroups and leadership calls. Also, supporting three in-person meetings each year.

In the past year of eMERGE Phase II the CC has created new tools to further Network organization, collaboration and productivity:

- Gwas.net has been completely revamped to include easier navigation, public and private sides to the website, calendar information, policies and guidelines, and single sign in navigation for the eMERGE website, PheKB and the eMERGE Record Counter.
- Dynamic Dashboards were created to provide real time status while preventing duplication and errors. These are accessible to any workgroup member through a secure googledoc link.
- PheKB.org serves as a platform to share and collaborate on phenotype algorithms.
- eMERGE Record Counter drives hypothesis generation and facilitates feasibility checks by allowing all eMERGE sites to generate patient counts by selecting specific criteria.

Privacy Update – Brad Malin

The Network has worked to get out the message about privacy to a larger audience by providing guidance to HHS on de-identification, providing testimony before a NCVHS subcommittee, and participating in a panel at public health and law conference in addition to multiple publications that have been approved or are pending approval. Brad reviewed privacy methods and when specific methods would be considered and utilized. He discussed variables such as which data was utilized, the promises/expectations of the IRB (or patients), and where the data would be shared. Brad continued to address the subject of free text and the tools available to properly de-identify these sections of text found within the EMR records. Even when utilizing tools to aid with the de-identification of patient information, there still may be residual inferences. To ensure complete de-identification some scrubbing alternatives were suggested: MIST (The MITRE Identification Scrubber Tool), TALLAL (Tag a little, learn a little), and HIDE (Health Information DE-identification). The method of redaction has its limits but it is not the only option, injecting

surrogated information can hide the leaks. By utilizing this Hiding in Plain Sight method of adding a surrogate component to MIST, this can effectively raise de-identification performance from 95% to >99%. Other areas discussed included the data-centric view, shared demographics, and policies vs. risk-utility. Brad summarized this topic by outlining next steps: (1) Text HIPS evaluation on a large scale, (2) demographic de-identification policies, (3) clinical code anonymization, and (4) other protection strategies (e.g. lab values, patient trajectories).

External Collaborations: Return of Results Consortium – Ingrid Holm, CSER – Gail Jarvik, Return of Results/CSER Pediatrics Workgroup – Ellen Clayton

Ingrid began the presentation with a brief description of the RoR Consortium. The goal of this consortium is to study issues around if, when, and how researchers should return research results arising from genomic studies to participants with the goal of developing best practices. Four different RFAs were put forth by NHGRI to facilitate this goal: (1) Development of a Preliminary Evidence Base to Inform Decision-making about Returning Research Results to participants in genomic studies (R01); (2) Ethical, Legal, and Social Implications of Returning Research Results to Genomic Research Participants (R21); (3) Clinical Sequencing Exploratory Research - CSER (U01); (4) Investigator-Initiated grants (R01). The working groups between the CSER, RoR and eMERGE consortiums have a great deal of overlap, and there are many active collaborations in place between eMERGE and these other two groups. Ellen Clayton reported specifically about the Pediatric Working Group Projects. Currently three main areas are being investigated: (1) testing when the proband neither decides nor is the only recipient of results, defining what parents owe to the child and other family members, and elucidating the role of the other health care practitioners; (2) Impact of genomic approaches on preexisting views about appropriate limits of genetic testing in children; (3) what obligations investigators owe to minors after completion or projects. Gail specifically spoke about the NHGRI CSER program by outlining the goals of the overall program and the project structure at each site. Each site within CSER has three integrated project teams focusing on a variety of topics including: ethical and psychosocial implications of bringing broad genomic data into the clinic, clinical setting being studied and what medical outcomes measured, and sequencing and reporting of genome-scale results to clinicians/EMR. Existing CSER projects encompass a wide variety of areas of study.

eMERGE PGx Collaboration – Debbie Nickerson and Laura Rasmussen-Torvik

Debbie began this session by providing some background on the PGRN-Seq platform. The goal of this platform was to develop a cost-effective next generation sequencing system to find rare variants in key pharmacogenetic genes. Two sample test panels have been composed. Panel 1 consists of 32 trios making up the 96 HapMap samples used. Panel 2 is composed of patient samples with extensive genotype data and is being deemed the golden set. Some preliminary data was discussed, the concordance between the HapMap samples and the PGRNseq are 88/95. The group discussed the CYP2D6 and HLA-B genes of interest and how these two genes will require additional analyses. PGRN is working to further investigate these two genes by exploring PCA/SVD methods, analyzing Mendelian inheritance of copy number state in ABI assay data and investigate variant call differences. PGRN is developing a plan of approach to HLA-B.
Laura walked the Network through an overview of current and planned site activities. In addition, the pediatric sites shared general information about their projects and plans since they will also be participating in eMERGE PGx. Three major types of outcomes were discussed: clinical/ADE, process, and participation feedback. Other topics included the PGx data repository and the discussion of portability of EMR implementation.
Group Discussion:

- It was suggested that each site run the 96 HapMap samples as a pilot validation to compare results.
- Mayo shared their IRB's concern with the outcomes section of their proposal. The IRB feared that some outcomes being tracked in direct relation to physicians would make the physicians feel as though they were being graded. Some sites are overcoming these concerns by labeling it as quality of care. Outcomes can also be measured by system firings and the number of times decision supported was executed, this would not be directly related to a physician.
- The group briefly discussed alert fatigue and how alerts have been turned off at some sites.
- Teri suggested that the group speak with PGRN to see what kind of data they would find valuable to receive back from this project as this could guide the group when creating the online platform for data storage. The group does not believe it will order all required reagents for the entire project immediately, a small number will be ordered since this platform is still a work in progress.
- Outcomes, reagent orders, timelines, and the online database for PGx will be discussed on the workgroup call scheduled in 10 days.

eMERGE Phase II Manuscript Discussion – Marc Williams

Marc Williams addressed the group on behalf of the eMERGE Phase II manuscript team. The group intends to submit this paper to *Genetics in Medicine* and has already spoken with the Editor-in-Chief who is enthusiastic about this paper. The outline of the paper was discussed along with some questions the main writing team had for the Network. All proposed figures were approved for use in the paper. All workgroups with the exception of EHRI and CERC have identified their case studies for the Text Boxes that will appear throughout the paper. Submission is anticipated for February 2013. The group set forth action items for the Network: (1) Confirm authors, (2) Each site will describe their eMERGE activities, (3) Experts write assigned sections. These three action items will be due to Omri and Helena by Thursday, December 6th.

<u>Wednesday, October 10</u>

Opening Remarks – Teri Manolio & Rongling Li

Teri and Rongling briefly welcomed the ESP and thanked the ESP members for their attendance and guidance.

Comments from ESP Chair – Howard McLeod

Howard thanked the Network for its good work and expressed his excitement to hear about the new developments that have taken place since the last meeting. Each ESP member briefly introduced themselves: Eta Berner, Lisa Parker and Stan Huff were in attendance. Charis Eng joined via phone.

eMERGE Network Overview: priorities and goals; review of Progress of Prior ESP Recommendations & Best Practices Topics – Jonathan Haines

Jonathan reviewed the previous ESP recommendations and the eMERGE Network's progress in response to these areas. Many recommendations have been addressed since the last meeting in October 2011 and many more are ongoing efforts by the Network. There were no comments from the ESP at this time.

CHOP – Hakon Hakonarson

Hakon presented an overview of the CHOP site to the ESP highlighting the CAG center infrastructure, site-specific timelines and milestones, and CHOP's plans for the PGx project. The Center for Applied Genomics was founded in 2006 and currently has a staff of 75. CAG focuses on over 60 active disease areas and utilizes resources such as a database linked to the EMR with extensive information on each child. There are approximately 1.1 million visits to CHOP per year with 400,000 new registrants/year. CHOP has over 150K samples genotyped. CAG utilizes a tri-fold encryption process in which a random identifier is assigned to the sample, starting from a unique identifier. Three main milestones along with timeline for completion were discussed: (1) collect and integrate phenotypes with EPIC system and other databases, (2) validate new actionable results (GWAS/seq) and integrate into EMRS for clinical use, and (3) generate informed consent procedures. Four PGx areas of focus were identified: adverse events, DMET, morphine response, asthma response – all of these phenotypes have samples already associated with them.

CCHMC/BCH – John Harley & Ingrid Holm

John began by sharing some CCHMC/BCH statistics including number of samples submitted to dbGaP and available Biobank samples. He went on to discuss the Genetic Pharmacology Service Psychiatry Panel that is being utilized at CCHMC. There are both adult and pediatric panels available; this information is linked to inpatient medication ordering and is included in the patient report. John also presented the CCHMC and BCH specific aims to the ESP; these aims include: Informatics, Phenotyping, Return of Patient results and physician attitudes towards return of results. Each of these aims was briefly outlined along with the current site efforts to fulfill each of these aims. Currently, the sites are working on obesity and autism for their phenotypes and have many others that are under consideration. CCHMC/BCH is also actively involved as the secondary site for numerous Network phenotypes. Ingrid briefly described the BCH site and supplemented John's presentation by outlining aims 3 and 4. She also walked the ESP through the challenges and opportunities their site has by partnering with a hospital like CCHMC. One of the most crucial elements to this collaboration is communication.

Network Project: *Clostridium Difficile* Colitis – David Crosslin and Josh Denny

C. Diff is the Network's first Phase II phenotype. *C. Diff.* can be defined as severe diarrhea/intestinal disease cause by a bacterium. It can be transmitted in hospitals and nursing homes. *C. diff* presents naturally in the gut for some individuals. Disease occurs when competing bacteria in the gut are wiped out by antibiotics and can be life-threatening. For this phenotype a gold and silver standard were defined for cases, and controls were defined by absence of diagnosis codes, absence of any *C. diff* testing, and exposure to high-risk antibiotics. Josh walked the group through the algorithm, outlining the gold standard cases, two types of silver standard cases, and the controls. David presented the validation results from the primary and secondary sites along with the descriptive statistics for the Network. Some very preliminary data was presented with more analysis planned.

Phenotyping Workgroup Update – Josh Denny

The Phenotyping workgroup began by addressing previous ESP recommendations which have been addressed in the past year.

- Build a phenotype library – PheKB.org was created and is now being utilized by the Network and beyond
- Integrate new sites – three cross network phenotypes have been completed, including at the Pediatric sites
- Keeping/marking progress – implementation timelines have been created

The workgroup continued by expressing the number of months it took to complete a phenotype in eMERGE Phase I. The time involved varied from only 8 months to 24 months. The group then presented a list of their planned Phase II round 1 phenotypes, outlining PPV, and cases and controls for *C. Diff*, AAA, and VTE. The group anticipates that it will take the Network until the end of 2014 to fully implement all 3 rounds of Phase II phenotypes Network wide. As previously discussed many eMERGE Phase I phenotypes have been adopted by other institutions and consortia, including SHARP-N, Aurora, DILIN, PGPop, PGRN, VA and others. There has been a great deal of discussion around integrating the pediatric sites into the Network, specifically around phenotypes. The Phenotyping group has worked to integrate the pediatrics sites into the existing timelines for the group and identify overlapping phenotypes for all groups. There are many possible overlaps between these groups, and this ongoing conversation will assist in facilitating further integration. The group is also exploring NQF Quality Data Model – I and –III. The group's next steps include: (1) representing of all existing eMERGE phenotype algorithms as QDM documents, (2) exploring possible extensions as needed, (3) expanding the library of phenotypes using common representational format with the intention of leveraging the SHARP infrastructure, (4) implementing a trial of common execution engine across multiple sites.

Genomic Workgroup Update – David Crosslin

David outlined the genomics workgroup and CC's efforts around the imputation process for the eMERGE I dataset. 45,363 samples from Phase I and Phase II have been imputed so far; however, this number does not include pediatric samples or new samples being processed by adult sites. The group is working to fully evaluate IMPUTE2 vs. BEAGLE, the platform currently being utilized by the group. IMPUTE2 promises faster imputation times with the same accuracy as BEAGLE. The group also outlined their next steps in the imputation process. These include complete QC of imputed sets, merging of the eMERGE-II and eMERGE-I data sets and subsequent QC, evaluation of IMPUTE2 for next round of imputation, and full imputation, QC, and merging of the pediatric site data with Network data. To foster cross-Network collaboration and organization, sites are presenting their site specific phenotype work and progress. All sites will have an opportunity to present an update in the coming months. Beyond imputation the workgroup is looking to facilitate projects focusing on genetic risk scores, gene-gene interactions and collaboration with other workgroups.

eMERGE – PGx Workgroup Update – Dan Roden

Dan provided an overview of the eMERGE PGx project. The overall goal of this eMERGE-PGRN collaboration is to initiate a multi-site test of the concept that sequence information can be coupled to electronic medical records for use in healthcare. Both the eMERGE Network and PGRN have different strengths that complement one another. The PGRN-Seq platform, being utilized by eMERGE, consists of 84 very important pharmacogenes. These genes were selected via nomination from the 14 PGRN sites. Some preliminary performance statistics were presented and, all genes are

performing well with the exception of CYP2D6 and HLA, which are currently being worked on to enhance their performance. The target enrollment from all Network sites along with individual site genotyping plans and PGx candidate drug-gene pairs were briefly discussed. Most sites are focusing on four main drugs: clopidogrel, warfarin, simvastatins and abacavir. All sites have plans for EHR Integration at varying levels and are all in different stages of the IRB approval process. Mayo has already received approval for this project from their IRB. Each site also has outlined their plans for how subjects will be selected to participate in this study. Moving forward the workgroup has created an aggressive timeline and within the next 2-4 weeks the group plans to:

- Acquire test sets for local lab validation
- Determine how many reagents will be ordered from Nimblegen
- Finalize process outcome measures
- Finalize the format of the variant database and how phenotypic information will be accessed
- Finalize the marker manuscript plan

EHR Integration Workgroup Update – Joseph Kannry

The EHRI workgroup presented a brief status update for each site concerning their EMR activities. All sites are working on various aspects of the process and are in different stages of completion. A color coded table was presented that visually displayed the site specific progress in the areas of:

- Variants selected
- Internal Approvals
- Architecture/Design
- Development
- Implementation
- Evaluation

Network projects may include a centralized infobutton that would evaluate utility of HL7 Infobutton protocol for delivering information about actionable variants. Another project described was the variant naming project that would evaluate the utility of HL7 and Human Genome Naming Convention (HGNC) names for EHR integration. The group is also working to complete the 'Omic Chasm paper that the group anticipates will be published in a special issue of JAMIA. The final manuscript is due at the end of October.

CERC Workgroup Update – Andy Faucett & Maureen Smith

The CERC workgroup presented a comprehensive update of their current efforts to the ESP. The workgroup has been working on many PGx related activities. Consent elements have been discussed among the group, and a list of needed elements has been circulated, with most sites making their consent forms available on the private side of the eMERGE website. The topic of short consents has also been discussed and adopted by some sites. These 1-2 page consent forms would be accompanied by informational brochures and FAQs. The group continues to share educational materials and focus group feedback. Another area of focus is Physician and Patient Consultation. Most sites are conducting some form of physician and/or patient consultation. Through focus groups and other mechanisms the workgroup has received some key feedback from both the physicians and patients they have worked with. The pediatric sites have been actively contributing to the discussions and are experienced with CERC issues. Even though pediatricians are more receptive to genetic testing, what results will be reported back is still an ongoing discussion topic.

During earlier workgroup discussions the topic of CLIA/CAP regulations was discussed. It has been determined that most questions around CLIA/CAP have been answered; however, the group has one outstanding question concerning the sharing of information from deceased research participants. Ongoing workgroup discussion includes the development of joint surveys of physicians, asking permission to put results in medical records and handling refusals, dealing with patient and clinician ELSI concerns, and writing the case study requested from the eMERGE Phase II paper authors. The group suggested that lab experts be invited to join the conversation at the next Steering Committee meeting. The co-chairs also mentioned that there is much overlap within the CERC group and other related groups such as CSER, CTSA, and RoR. Co-chairs and workgroup members are actively involved in these other groups on site specific terms since these groups, particularly CSER and RoR, are just getting started and are not ready for a formal liaison from eMERGE.

Input-Feedback from ESP

ESP Members provided brief comments to the Network. The Network, specifically the CERC workgroup, should plan for systematic feedback and evaluation on many current efforts. There are so many good things being implemented and discussed that should be distributed beyond the eMERGE Network. Collaborations between workgroups and other institutions were also encouraged, specifically for EMR capabilities. Potential stakeholders also need to be brought into the conversation to discuss implementation and evaluation. eMERGE investigators were actively encouraged to contribute to the current standards efforts from implementation into the EMR. There is much knowledge and experience within this group that can be leveraged to move this conversation along in the greater community. The sharing of phenotypes was mentioned; once a phenotype is defined, implemented, and linked to clinical decision support, this computational knowledge will also be necessary to share with a broader audience than eMERGE.
eMERGE has continued to be a valuable platform for many people and continues to jump start the careers of junior faculty. Junior faculty at the meeting were encouraged to take advantage of all that eMERGE has to offer. The Network was praised for retaining Phase I leadership as the Network transitioned to Phase II, is which is essential to the Network continuing to flourish. The ESP complimented the project management for the Network on many of the behind the scenes tasks that will continue to keep the Network moving. The ESP was enthusiastic about the number of white papers being composed and thought a broader dissemination through seminar series or webinars would ensure that individuals outside of eMERGE learn from the Network. The Network was encouraged to stay focused on output.

Action Items:

1. CC will schedule a small PGx meeting between NHGRI, eMERGE PGx co-chairs and CIDR.
2. Steve Scherer will send the PGRN Seq reagent ordering information to the Network.
3. PGx pilot study timelines will be discussed on the workgroup's call in October.
4. A discussion concerning the PGx repository will be added to the workgroup's call in October.
5. Dan will speak with PGRN and inquire about the type of information that would be useful to get back from the eMERGE Network.
6. Lab staff from each institute's CLIA labs will need to be brought into the conversation concerning implementing the PGRN Seq platform.
7. The phenotype workgroup will explore the possibility of collaborating with PHENX concerning LOINC codes.

8. CERC and EHRI need to decide on their "Case Study" for the eMERGE Phase II Paper.
9. Authors for the eMERGE Phase II paper need to be confirmed.
10. All sites need to describe their eMERGE activities and send this text to Omri and Helena.