TRANSLATING SCIENCE TO BETTER HEALTH:
THE POWER OF DIVERSITY AND MULTICULTURAL ENGAGEMENT

TRAINING WORKSHOP VII
Resource Discovery Training Workshop

ROBERT KIRKEN
University of Texas at El Paso
In the course of a few minutes, using only two direct searches assisted by guided browsing, the researcher has found an excellent set of resources to help translate his initial discovery into a clinical tool.

So, can’t we just use Google?

WWGD (what would Google do!)
**Introduction and Background**

The eagle-i Consortium – founding governance body

- Dartmouth College (NH) - Jason H. Moore, PhD
- Harvard University (MA) - Lee Nadler, MD; Douglas MacFadden
- Jackson State University (MS) - James L. Perkins, PhD
- Morehouse School of Medicine (GA) - Gary M. Gibbons, MD
- Montana State University (MT) - Sara L. Young, MEd
- Oregon Health and Science University (OR) - David W. Robinson, PhD
- University of Alaska Fairbanks (AK) - Bert Boyer, PhD
- University of Hawaii Manoa (HI) - Richard Yanagihara, MD
- University of Puerto Rico (PR) - Emma Fernandez-Repollet

Thank you!

Questions??

---

SOLOMON T. GARNER
Jackson State University
Resource Discovery Tool Demonstration
eagle-i: Overview, Update on Deployment and Multi-Institutional Research Use

Solomon T. Garner, Jr., Ph.D.
Director
Research Resources and Research Networking
RCMI Translational Research Network (RTRN) Data Coordinating Center (DCC)

Demonstration Agenda

– What is eagle-i?
  • Phase I, eagle-i Consortium, Functions
– How does eagle-i work?
  • Resources, Data, Architecture
– How can eagle-i help me?
  • Participation Benefits, Value Created, Connecting Researchers
– What is the RCMI deployment/expansion?
  • Phase II, Collaborative Research, Continuing Activities

What is eagle-i?

A NIH funded project that had the goal of improving biomedical research by:

• Providing a tool through which researchers may find research resources not readily available to him/her
• Reducing the time-consuming and expensive duplication of resources within institutions and/or working groups
• Providing meaningful semantic relationships between resources utilizing an ontology

Supported by Award U24 RR 029825 from the National Center for Research Resources, a part of the National Institutes of Health.
Phase I: The eagle-i Consortium Members

The eagle-i Consortium built a prototype of a national research resource discovery network—One that helps biomedical scientists search for and find previously invisible, but highly valuable resources.

The eagle-i CoreBucks Program:
1. promoted discovery, access, and use of core facilities within the nine eagle-i Consortium institutions;
2. introduced the eagle-i Network search application to the eagle-i Consortium research community; and
3. assessed the functionality and efficacy of the eagle-i Network application to find core resources across the Consortium.

eagle-i Consortium Member Functions

eagle-i Central administration — Teams
- Software and Hardware team:
  - Develop repository
  - Build the network
  - Develop the search function
  - Develop Data Tools
  - User interface
  - Configure and Maintain servers

Data Curation team
- Build data model
- Build biomedical research resource ontology
- Develop ontology to drive front end software

Resource Navigation Team:
- Outreach to Data providers (Researchers, Core facilities, tissue repositories)
- Scientific guidance and consultancy
- Data entry, curation
- User requirements gathering

How does eagle-i work?
eagle-i inventories the many “invisible” RESOURCES generated during the research process which are rarely shared or published. These include:

Reagents, protocols, services, instruments, expertise, organisms, training opportunities, software, human study metadata, biological specimens, etc.
Informational Data Repository

**eagle-i stores data about...**
- Resources whether unique, rare, valuable or invaluable
- NOT refrigerators, Xerox machines, telephone systems, basic computers and cameras, kit instructions, and common chemical reagents such as NaCl

---

**eagle-i Architecture**

---

**How can eagle-i help me?**

**Participation Benefits**
- Find resources and services that are not available at your institution
- Connect to researchers that are interested sharing their resources
- Learn about new techniques relevant to your area of interest
- Potentially incorporate new techniques into future proposals
- Connect to researchers that are interested in utilizing your resources
Participation Benefits

The eagle-i Consortium’s resource repositories will only be as good as the information recorded in them.

- Be part of a groundbreaking experiment that has the potential to change the way researchers find the tools necessary to conduct their research
- Foster biomedical research on a national level by sharing resources and promoting collaborations
- Help reduce time-consuming and expensive duplication of resources by researchers by sharing and reusing existing resources
- Accelerate the development of much needed diagnostics, treatments, and prevention strategies

Value Created via the RDNT eagle-i

Montana Researchers + a Dartmouth Core Laboratory
Chip-sequencing analysis to study microbial communities in pathological tissues

Montana Researchers + a Jackson State Core Laboratory
Analysis of potential biomarkers in different biological systems

Alaska Researchers + a Jackson State Core Laboratory
Froth flotation of minerals to extract gold by using selective and anti-inflammatory compounds

Montana Researchers + a Jackson State Core Laboratory
Fractionation of Moringa leaf extract to assay for anti-oxidant and anti-inflammatory compounds

Morehouse Researchers + a Jackson State Core Laboratory
Analysis of immune response in a model system to assess the effectiveness of existing treatments

Hawaii Researchers + a Harvard Core Laboratory
High throughput iTRAQ proteomics analysis of blood proteins in West Nile virus infected organisms to find markers of susceptibility

PHASE II
The RCMI eagle-i Resource Discovery Networking Tool (RDNT) Expansion
The RCMI Centers that comprise RTRN have established significant scientific resources which are available to support scientific research. Many of these resources are invisible to most of the researchers across the network. The eagle-i resource discovery networking tool provides the opportunity to make these resources available to all interested researchers across the network.
Dr. Jacqueline Hibbert, Associate Professor at Morehouse School of Medicine, used eagle-i to discover the Molecular Magnetic Resonance and Analytical Core facilities at Jackson State University. These core facilities are helping her to extract and identify compounds produced by Moringa oleifera plant leaves, which have been reported to reduce inflammation and assist in wound healing.

Dr. Moti Chapagain, Assistant Professor at the University of Hawaii, used eagle-i to discover a state-of-the-art proteomics core facility that can analyze all the proteins present in blood samples. The researchers will make use of these services to help them predict which kinds of patients are most susceptible to complications from West Nile Virus infection.

Continuing Activities and Potential Outcomes
Research Resources Activities
1. Provide access and training for the eagle-i Resource Discovery Networking Tool (RDNT)
2. To inventory all RCMI core resources and other resources types

Potential Outcomes
- Find experts
- Find resource holders
- Find collaborators
- Find hidden assets
- Establish new relationships
- Achieve research objectives

The expected end-results will be a greater number of translational research outcomes include publications, grant applications, patents, clinical/non-clinical studies and/or new therapies.
How do I access eagle-i data entry?
For Training and Access to the eagle-i Semantic Web Editing and Entry Tool (SWEET) Contact:

Solomon T. Garner, Jr., Ph.D.
Director
Research Resources and Research Networking
RCMI Translational Research Network (RTRN) Data Coordinating Center (DCC)
Solomon.garner@rtrn.net
Solomon.t.garner@jsums.edu
601.979.0332
R3NHelpdesk@rtrn.net
1-877-602-7907

---

Presented at the 13th RCMI International Symposium on Health Disparities | December 9-13, 2012 | San Juan, Puerto Rico

All Rights Reserved - No forms of duplication nor distribution allowed without author's consent
This project was supported by the National Institute on Minority Health and Health Disparities U54MD007584 from the National Institutes of Health.
The placenta and its associated structures are important scientifically and culturally. The placenta is the primary source of tissue whose respective miRNA expression and DNA methylation patterns may prove to be powerful biomarkers possessing predictive capability for a number of diseases or disease progression. Using the placenta as a reference tissue allows researchers to utilize an important residual tissue whose respective miRNA expression and DNA methylation patterns may prove to be powerful biomarkers possessing predictive capability for a number of diseases or disease progression. Maccani MA, Marsit CJ. Epigenetics in the placenta. Am J Reprod Immunol 2009;62:78-89.

The placenta and its associated structures are important scientifically and culturally. The placenta was extended symbolically to all blood-kin. Relatives were sometimes called ‘my piko.’ Pukui MK, Haertig EW, Lee CA. Nānā I Ke Kumu (Look to the Source), Volume I, Honolulu: Queen Lili‘uokalani Children’s Center, 1972:183.

HiBR Specific Aims

1) The primary goal is to provide a biospecimen repository of obstetrical, fetal and neonatal samples combined with existing clinical and experimental data for investigator-initiated research.

2) To facilitate inter-disciplinary collaborations and thus increase the number of high-quality clinical research projects. This includes assisting junior investigators to develop and implement pilot studies.

3) To promote access to and use of HiBR specimens for clinical and translational researches within and outside of Hawaii.
HiBR Participant Ethnic Background

<table>
<thead>
<tr>
<th>Ethnic Background</th>
<th>Number of women self-reporting</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overall</td>
<td>1717</td>
</tr>
<tr>
<td>Hispanic</td>
<td>592</td>
</tr>
<tr>
<td>White European Caucasian</td>
<td>417</td>
</tr>
<tr>
<td>Hawaiian</td>
<td>94</td>
</tr>
<tr>
<td>Japanese</td>
<td>413</td>
</tr>
<tr>
<td>Other Pacific Islanders</td>
<td>553</td>
</tr>
<tr>
<td>Samoan</td>
<td>212</td>
</tr>
<tr>
<td>Latin American or Caribbean</td>
<td>66</td>
</tr>
<tr>
<td>Korean</td>
<td>90</td>
</tr>
<tr>
<td>Other Asian</td>
<td>72</td>
</tr>
<tr>
<td>Black/African American</td>
<td>22</td>
</tr>
<tr>
<td>Native Hawaiian</td>
<td>4</td>
</tr>
<tr>
<td>Hawaiian</td>
<td>12</td>
</tr>
<tr>
<td>Japanese</td>
<td>28</td>
</tr>
<tr>
<td>Other Asian</td>
<td>53</td>
</tr>
</tbody>
</table>

Data Overview

Specimens:
- Umbilical cord (placental)
- Umbilical cord (placenta)
- Umbilical cord (fetal surface)
- Placenta (fetal surface)
- Placenta (center)
- Placenta (edge)
- Placenta (maternal surface)
- Placenta (chunk, frozen)
- DNA (blood)
- RNA (blood)
- Umbilical cord (segment)
- Whole Cord Blood
- Blood

Laboratory Data:
- Placental weight
- Placental dimensions
- Placental shape
- Placental observations
- Placental shape
- Placental observations
- Placenta (center)
- Placenta (maternal surface)
- Placenta (fetal surface)
- Placental shape
- Placental observations
- Maternal plasma (frozen)
- Umbilical cord (frozen)
- Hemoglobin
- Blood

Clinical Data:
- Clinical demographics
- Maternal medical condition
- Pregnancy care
- Pregnancy outcomes
- Delivery information
- Infant care
- Infant characteristics
- Congenital anomalies
- Newborn medical condition
- Hemoglobin

Public Health Indicators:
- Diabetes (ZC-level)
- Diabetes (ZC-level)
- BMI Category
- Blood Pressure Measurements
- Birth Weight
- Gestational Age
- Birth Outcome
- Race/Ethnicity
- Income by category
- Education
- Household size
- Health Insurance

This project was supported by the National Institute on...
Policies

- Access application
  - Local UH facility matter required
  - Local Institutional Review Board
  - Local UH faculty member required as collaborator/local contact
  - Non-commercial use only
  - Unused specimens returned
  - NIH acknowledgement
  - Terminate for any reason
  - No protocol deviation allowed without additional IRB reviews
  - No identifying information available
- Scientific Review
- Sociocultural Ethical Review
- Material Transfer Agreement

HiBR-based research findings emerging

Frederico G. Rocha, Thomas J. Slavin, Dongmei Li, Sandra Yamamoto, Gillian Bryant-Greenwood, "Genetic Susceptibility to Preterm Birth in the Filipino Population in Hawaii" (submitted to SMFM)

SNP rs4742076 was significantly (p<0.0012) associated with PPROM compared to controls. The PPROM patients also had significantly more (p<0.001) dRLN expressed compared to controls. SNP rs375839 was significantly associated (p<0.0025) with both PPROM and PTL compared to the controls.

From Terry Morgan (OHSU) and Gillian Bryant-Greenwood (UH), "Angiotensinogen Thr235 variant is associated with idiopathic preterm labor in Japanese women," OB/GYN Grand Rounds (abstract in development for SGI)

There are baby gender effects with the PTL association becoming stronger if baby is a male; females not significant, perhaps due to interaction between gender, genotype, and birthweight. Notably, most of the PTL cases had histologic evidence of uteroplacental insufficiency (AVM) similar to both our NICHD and Obstetrix network studies.

RM Kawelo; NK Bobbili; RFG Leke; DW Taylor, "The Rate of Transfer of IgG from Mother to Fetus in Hawaii versus Cameroon and the Effect of Maternal Medical Conditions on the Rate of Transfer," (abstract accepted to RCMI)

Preliminary studies show Hawaii samples fall within a standard curve generated by sera from Cameroonians with known total IgG levels, but IgG levels are lower in Hawaiians than Cameroonians.

Luc Rougée and Abby Collier, "Gilbert's Disease and Obesity as Obstetric Risk Factors and Effects on Minority Populations" (award-winning presentation from the Biomedical Research Symposium at JABSOM)

This study is the first to determine the prevalence of clinical Gilbert's disease in Native Hawaiians and Pacific Islanders. Moreover, it is the first to determine effects of Gilbert's disease on pregnancy outcomes.

All Rights Reserved - No forms of duplication nor distribution allowed without author's consent
Biospecimen Repositories in Health Disparities Research: A Technical Assistance Summit
Honolulu, Hawaii (May 15-17, 2012)

- Focused on four phases of biospecimen repository development (community and participant engagement, data/specimen collection and storage, data management and informatics, and data use and access)

- Resulted in one administrative supplement grant application submitted to CTSA between two attendee RCMI institutions and U Michigan on testing reformed consent

- R21 collaboration in process with U Rochester on heavy metals in pregnancy

- R24 grant under development for multi-site study of community engagement and repositories examining molecular markers of stress

- Two collaborative abstracts submitted to RCMI Biennial Conference on best practice in repository informatics, and data use and access

- Presented on topics ranging from best practice in community engagement to technical issues involved in specimen collection, to promoting repositories to stakeholders

- Simultaneously broadcast live through DTCC Webinar (approximately 15 additional participants online)

- Summit attendees: approximately 100 people representing 20+ organizations

Collaboration

- Researchers within and outside Hawaii can request specimens for IRB-approved studies – prioritize disparities-related research

  - [http://rmatix.jabsom.hawaii.edu](http://rmatix.jabsom.hawaii.edu) and click on “Request an RMATRIX Consultation” then “Biospecimen Repository”

  - Email dyet@hawaii.edu
History of CCRTD

- CCRTD was established in 1999 as a part of the RCMI program at Clark Atlanta University.

- Dr. Shafiq Khan was recruited as Scientific Director of CCRTD in 2004 with the help of Georgia Research Alliance support to direct the research activities at CCRTD.

- CCRTD decided to build a prostate cancer research and educational program in 2004.
Goals and Focus of CCRTD defined in 2010

• To establish a world class research center in basic cancer research at Clark Atlanta University.

• To train undergraduate and graduate students and post-doctoral fellows in cancer research in order to prepare the next generation of African-American scientists in biomedical research.

• To establish a community based cancer education and prevention program.

• Selection of Prostate Cancer as the focus area.


The mortality rate from prostate cancer is more than two-fold higher in African Americans compared to Caucasian Americans due to individual differences in:

1) interaction with the health care system
2) diet and biology of the individual; and/or
3) characteristics of the tumor

**Hypothesis**
Research Core Facilities

1. Molecular Biology Core Facilities (MBCF) (Dr. Jaideep Chaudhary)
2. Cell Biology Core Facilities (CBCF) (Dr. Cimona Hinton)
3. Cancer Genomics and Bioinformatics Core Facilities (CGBCF) (Dr. Nathan Bowen)
4. Proteomics Core Facilities (PCF) (Drs. Jin Zou and Myron N.V. Williams)
5. Histology Core Facilities (HCF) (Dr. Valerie Marah)
6. Structural Biology and Drug Discovery Core Facilities (SBDDCF) (Drs. Jin Zou and Xie-Ren Bu)
7. Biospecimen Repository Core Facilities (BRCF) (Dr. Nathan Bowen and TBN)
8. Biostatistics Core Facilities (BCF) (Dr. Fisseha Abebe)

(Significant support for the equipment purchases has come from HHS ARRA, NIMHD)

Collaborative Cancer Genomics Center (CCGC)

Multi-Institutional Collaboration Between:
- Clark Atlanta University
- St. Joseph’s Hospital of Atlanta
- Georgia Institute of Technology

Whole Genome Sequencing to Address Prostate Cancer Disparities and Deliver Personalized Treatment

- Massively parallel DNA sequencing (SOLiD 4 Platform) of individual tumors to identify novel genetic variations contributing to prostate cancer susceptibility, progression, and response to therapy in African American men
- Includes the establishment of a Prostate Cancer Tissue Repository focusing on analysis of African American Tissue and Fluid Samples
Participant Selection, Consents and Waivers

- IRB Approved Study at St. Joseph’s Hospital
- IRB Approved Storage and Study at Clark Atlanta University
- Urologic Oncologists present opportunity to every patient
- Consented by Research RN at St. Joseph’s
  - Consent Form for Study Description, Collection, Storage and Follow Up
  - Consent Form for Long-Term Storage and Future Research
  - HIPAA Waiver for De-Identified Use of Personal Health Information (PHI)

-Patient Privacy and Confidentiality from Researchers is maintained by assigning Unique Numeric Codes to Participants and Samples collected. Key for follow up questioning is held by Urologic Oncologists and Tissue Procurement Specialist.

Tissue and Fluid Samples

The Prostate Cancer Tissue Repository
@ The Center for Cancer Research and Therapeutic Development
Clark Atlanta University, Atlanta, GA

Collaborative Effort with the Oncology Research Department at St. Joseph’s Hospital, Atlanta, GA, and Integrative Cancer Research Center @ Ga Tech to Collect Tissue and Fluids from Prostate and Bladder Cancer Patients.

I. To Date, We’ve Collected and Logged 345 Samples from 123 Prostate Cancer (12 AA) Patients that Include:
- Preoperative Urine, Serum and gDNA from Whole Blood.
- Tissue Biopsies (Jamshidi Needle, Bone Marrow Extraction, 2-3 mm ID, 1-2 cm L) from Concerned Prostate Following Robotic Radical Prostatectomy.
- Location of Biopsies Suggested by Operating Physician and Results from the Preoperative Diagnostic Biopsies.
- Occasional Cuts of Prostate Tissue up to 1 Gram.
- Biopsies and Tissues include Samples of “healthy” Prostate Tissue located away from Tumor regions.
- All samples flash frozen in LN2 following collection and stored at -80°C until transport to CAU for long-term storage in LN2.

II. And 291 Samples of Urine, Serum and gDNA from 97 “healthy” volunteer men.
The Collection Includes:
636 Samples from 210 Men

- Urine and Serum from Cancer Patients and Healthy Volunteers
- Flash Frozen Large Needle Biopsies and Cuts of Fresh Cancer and “Healthy” Areas of Prostate
- Genomic DNA from Whole Blood of Cancer Patients and Healthy Volunteers
- Long Term Liquid Nitrogen Storage

Patient Clinical Database

Specimen Distribution

- CCRTD Review Board Chaired by Valerie Marah, PhD
- Evaluate Proposals submitted to Board for Tissue Usage
  - CAU CCRTD Investigators
  - External Collaborating Institutions (RCMI)
Future Directions

- St. Joseph’s was purchased by Emory Healthcare (Funding for Collection at St. Joe’s was from Mercy Foundation was Discontinued)

- Urologists moved to Piedmont Hospital

- New Funding Opportunity: CAU and Piedmont Hospital included as major Tissue Procurement Facility in Roswell Park Cancer Institute (RPCI) SPORE Application (PI: James Mohler, MD).

CAU/Piedmont as RPCI Spore Member

Radical Prostatectomies
Performed Annually at Piedmont

% African American

Improved Tissue Procurement Protocol with Complete Pathologist Participation

Thank You
Archived Biospecimens for Breast Cancer Research:

“This Treasure Trove of Mine, I’m Going to Let it Shine”

Luisel J. Ricks-Santí, PhD
Assistant Professor
Department of Pediatrics and Child Health
Division of Genetics
Director, National Human Genome Center
Biorepository

How Are Biospecimens Used in Research?

• Biomedical research has moved into the “genomic age”.
• Scientists are also analyzing vast amounts of clinical information from patient records and clinical trials.
• Specifically, human biospecimens can be used to:
  • Identify and validate drug targets
  • Identify disease mechanisms
  • Develop screening tests for “biomarkers” associated with certain sub-types of a disease
  • Group patients based on their genetic characteristics and likelihood of positive response, for testing of new drugs
  • Group patients based on the "biomarkers" of their disease to determine which treatment is appropriate

How Many of Our Freezers Look Like This?

Presented at the 13th RCMI International Symposium on Health Disparities | December 9-13, 2012 | San Juan, Puerto Rico

All Rights Reserved - No forms of duplication nor distribution allowed without author’s consent
NHGC Biorepository: Mission

• To provide centralized infrastructure to collect, handle, process, analyze, and bank valuable samples to improve the availability and quality of biospecimen needed for research.

• To support research at Howard University and beyond by providing access to consistently excellent quality banked biospecimen samples while maintaining patient confidentiality.

  – Charged with implementing harmonized policies and procedures that complement other biorepositories, such as the Howard University Tumor and GHUCCTS Repositories, that will enable the highest quality research while ensuring the ethical integrity of the process and fostering public trust.

National Human Genome Center
Organizational Structure

Biorepository Core
Luisel Ricks-Santi, PhD
Muneer Abbas, PhD
Co-Directors

Collection and Accession
Processing
Storage and Inventory
Distribution

Storage and Inventory
History of the NHGC Biorepository

- 2008-2009 Consulted a LIMS company to assist us in developing a biorepository to inventory and organize archived biospecimens
  - Familial breast cancer study (1990's)
  - African American Hereditary Prostate Cancer Study (AAHPC)
  - African American Diabetes Mellitus Study (AADM)
  - Howard University Family Study (HUFS)

Sample Locator Implementation

- 2009 Implemented the LIMS which included "Sample Locator" and "GeneTell" which links molecular data results with specimen
  - Workstation located in Molecular lab
  - Implemented a centralized Microsoft SQL platform
  - Workstation connects important peripheral devices such as barcode printer, barcode scanner, signature pad, signature card, and signature card reader
  - Strengthened IT security by employing electronic signature technology to better track chain-of-custody, sample movement, storage log, and audit trail
  - Administrator logs into the workstation to organize biorepository and to enter biospecimen information
Inventory and Labeling

• Subsequently, labels were created, affixed to tubes, and systematically reposited.
• Secure 20'x25' room with -20°C and -80°C freezers
  – NL storage on 4th floor

Sample Locator: Reports

• Reports were then generated which describe the exact sample location, sample types, and study names, among other variables.

"Clinical and Genetic Screening of High Risk African American Breast Cancer Families" (1990-2001)

Registry Participants

<table>
<thead>
<tr>
<th>Total enrolled</th>
<th>807</th>
</tr>
</thead>
<tbody>
<tr>
<td>Families enrolled</td>
<td>585</td>
</tr>
<tr>
<td>Population controls enrolled</td>
<td>258</td>
</tr>
<tr>
<td>With consent forms</td>
<td>244</td>
</tr>
</tbody>
</table>

Lymphocytes/ DNA Biorepository (NHGC)

<table>
<thead>
<tr>
<th>Participants with DNA</th>
<th>650</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cancer</td>
<td>128</td>
</tr>
<tr>
<td>Family Members</td>
<td>104</td>
</tr>
<tr>
<td>Students</td>
<td>125</td>
</tr>
<tr>
<td>Population controls</td>
<td>258</td>
</tr>
</tbody>
</table>

Tissue Data

| Total tissues | 218 |
| Total women with tissue | 56 |
### Before Implementation of LIMS

<table>
<thead>
<tr>
<th>Resource Transition</th>
<th>Before Implementation of LIMS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Paper data and only document of Archived resource;</td>
<td>• Paper data and only document of Archived resource;</td>
</tr>
<tr>
<td>No share of identity, no log of sample source or receipt;</td>
<td>• No share of identity, no log of sample source or receipt;</td>
</tr>
<tr>
<td>Evaluation of state of long-term storage (LTS)</td>
<td>• Evaluation of state of long-term storage (LTS)</td>
</tr>
<tr>
<td>• Labels falling off;</td>
<td>• Labels falling off;</td>
</tr>
<tr>
<td>• Samples spread over several locations maintained together with in-process PCR/sequencing samples;</td>
<td>• Samples spread over several locations maintained together with in-process PCR/sequencing samples;</td>
</tr>
<tr>
<td>• Not classified or sorted by project;</td>
<td>• Not classified or sorted by project;</td>
</tr>
<tr>
<td>• Boxes, racks, shelves, trays, wells not labeled;</td>
<td>• Boxes, racks, shelves, trays, wells not labeled;</td>
</tr>
<tr>
<td>• Number of Archived resources is unknown;</td>
<td>• Number of Archived resources is unknown;</td>
</tr>
<tr>
<td>• Identification of Archived resources unknown;</td>
<td>• Identification of Archived resources unknown;</td>
</tr>
<tr>
<td>• Projects unknown;</td>
<td>• Projects unknown;</td>
</tr>
<tr>
<td>• Observed damage of containers because of samples falling on each other;</td>
<td>• Observed damage of containers because of samples falling on each other;</td>
</tr>
</tbody>
</table>

### After Implementation of LIMS

<table>
<thead>
<tr>
<th>Resource Transition</th>
<th>After Implementation of LIMS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Reformed (tide-up)</td>
<td>• Relocated Archived resources from defective freezer to loaner freezer;</td>
</tr>
<tr>
<td>Transfer (tie-up)</td>
<td>• Relocated Archived resources from loaner freezer to repaired freezer;</td>
</tr>
<tr>
<td>Organizational Planning</td>
<td>• Commissions Starfruit Sample Locator;</td>
</tr>
<tr>
<td>• Commissioned Starfruit Sample Locator;</td>
<td>• Commissioned Starfruit Sample Locator;</td>
</tr>
<tr>
<td>• Configured to meet needs of NHGC;</td>
<td>• Configured to meet needs of NHGC;</td>
</tr>
<tr>
<td>• Defined users and biorepository leadership;</td>
<td>• Defined users and biorepository leadership;</td>
</tr>
<tr>
<td>• Group access control;</td>
<td>• Group access control;</td>
</tr>
<tr>
<td>• Storage Equipment access control;</td>
<td>• Storage Equipment access control;</td>
</tr>
<tr>
<td>• Configured equipment location, labels, analyzers, budget type, accession number, category, department, job title, manufacturer, model, serial number, equipment record management;</td>
<td>• Configured equipment location, labels, analyzers, budget type, accession number, category, department, job title, manufacturer, model, serial number, equipment record management;</td>
</tr>
<tr>
<td>• Configured equipment labels: equipment labels: equipment labels: equipment labels;</td>
<td>• Configured equipment labels: equipment labels: equipment labels: equipment labels;</td>
</tr>
<tr>
<td>• Configured biospecimen storage levels;</td>
<td>• Configured biospecimen storage levels;</td>
</tr>
<tr>
<td>• Configured sample types;</td>
<td>• Configured sample types;</td>
</tr>
<tr>
<td>• Configured site (NHGC) information;</td>
<td>• Configured site (NHGC) information;</td>
</tr>
<tr>
<td>• Configured long-gone samples;</td>
<td>• Configured long-gone samples;</td>
</tr>
</tbody>
</table>

### Labeling Biospecimen Samples

- Entry biospecimen data and print labels
- Affix labels onto tubes
- Samples relocated to cardboard boxes that fit into appropriate racks

### Report of Biospecimens

- Several studies, including case-control studies, were logged into the Starfruit Sample Locator
- Biospecimens can be queried by study, sample type, subject ID, etc.
- Starfruit Sample Locator can be readily queried decreasing turn-around time
- Sample locator has resulted in quicker turn-around time

### Recommendations

1. Plan, Plan, Plan
2. Determine the Mission of Biorepository
   - Self-serving
     - For the research/medical community, collaborators, partners
3. Determine Priorities
4. Hire biorepository coordinator or find those with interests in specific projects
5. Identify resources: space, freezers, liquid nitrogen storage, software, hardware
6. If different projects, focus on projects
   - Inventory
   - Annotate
   - Identify associated data

### Acknowledgements

- National Human Genome Center
- RCMI- Howard University
- Howard University Cancer Center
- Howard University College of Medicine
- Grants
  - NCI U54CA0914331 (Hopkins-Howard Partnership)
  - NIGMS S06GM08016 (SCORE)
  - NCRU UL1RR031975 (CTSA)
  - NCRR/ NIMHD G12 RR003048 (RCMI)
OMICS Approaches in Sickle Cell Disease

Sergei Nekhai, Ph.D.
Center for Sickle Cell Disease
RCMI Proteomics Core Facility,
Howard University
NCMBD, NIH
NHBLI, NIH
NIGMS, NIH
NIAID, NIH

Sickle Cell Disease

• Single HBB Glu6 → Val6 mutation
• Affects about 100,000 people in US
• Occurs in about 1 of 500 African American births (~1000 per yr)
• Occurs in 1 of 1,000 to 1,400 Hispanic American births.
**Pathophysiology**

- Sickle erythrocyte membrane damage
- Endothelial cell injury
- Hemolytic vasculopathy
- Chronic inflammatory response
- Chronic hypoxia
- Splenic atrophy

**OMICS for Sickle Cell Disease**

- Transcriptome analysis of monocytes, leukocytes (gene array, RNA-Seq)
- GWAS analysis of monocytes, leukocytes (*HbF* levels and genetic variation at the *HBS1L–MYB*)
- Multiplex analysis of plasma and serum (cytokine profiles)
- Proteomics of RBC, monocytes, plasma

**Gene Expression Profile of SCD Leukocytes**

---

All Rights Reserved - No forms of duplication nor distribution allowed without author's consent
Heme-regulated Gene Expression in Macrophages

Bio-Plex Multiplex System

Technology
- Red laser differentiates bead subsets
- Green laser excites PE reporter
- Beads can have different capture molecules, e.g., antibody, oligonucleotide, etc.

Performance
- Runs in 96-well format
- Uses <50 μL of sample

Applications
- Detect up to 26 Cytokines simultaneously from 50 μL of serum or lysates
- Dynamic ranges of 1 pg/mL to 10,000 pg/mL
- Detect signalling proteins from cell lysates in a multiplex fashion
- Allows SNP Analysis, differential expression, and gene expression as well

| Angiogenic and Inflammatory Markers of Cardiopulmonary Changes in Children and Adolescents with Sickle Cell Disease |
|---------------------------------------------------------------|---|---|---|
| SCD | Control | P |
| RANTES (ng/ml) | 4.0 | 6.9 | 0.0002 |
| IL-8 (pg/ml) | 0.4 | 0.3 | 0.001 |
| IL-10 (pg/ml) | 1.6 | 1.1 | 0.003 |
| IL-6 (pg/ml) | 0.8 | 0.4 | 0.031 |
| TNF (pg/ml) | 25 | 10 | 0.1 |
| IFN-gamma (pg/ml) | 40 | 34 | 0.2 |
| MCP-1 (pg/ml) | 7.0 | 8.1 | 0.4 |
Proteomics in Sickle Cell Disease

- RBC membrane proteomics (2D-DIGE + LC-MS/MS)
- Monocyte proteomic (2D-DIGE + LC-MS/MS)
- Proteomic of plasma (SELDI-TOF, MALDI-TOF, LC-MS/MS)

Change in SCD

Cytoskeletal

- Actin accessory Ankyrin 1 (92 kDa)
- Protein 4.1 (82 kDa); pI: 5.72
- Protein 4.1 (89.2 kDa); pI: 5.98, 6-kDa larger
- Dematin protein 4.9 (44.1 kDa)
- Tropomyosin 3 (30 kDa)
- Anion exchanger band 3 (52 kDa)
- Tropomodulin (40 kDa)
- β-actin (41 kDa)
- Palmitoylated membrane protein p55 (55 kDa)

Membrane Active transport

- ATP synthase α-subunit (48.9 kDa)
- Lipid raft Flotillin-1 (49 kDa)
- Stomatin isoform a (27.4 kDa); pI: 6.5
- Stomatin isoform a (27.4 kDa); pI: 5.56

Cytoplasmic

- Protein turnover Proteasome-β1 subunit (22 kDa)
- Proteasome 26S ATPase subunit 6 (39 kDa)
- Proteasome-α1 subunit, isoform 1 (34 kDa)
- Protein folding Chaperonin containing TCP1 subunit 7 (54 kDa)
- Protein repair Heat-shock protein 8 (68 kDa)
- Peroxiredoxin 3 isoform b (22.2 kDa)
- Peroxiredoxin 1 (22 kDa)
- Catalase (56 kDa)

Glycolysis

- Glyceraldehyde-3-phosphate dehydrogenase (36 kDa)
- Fructose bisphosphate aldolase (39 kDa)

Global Omics Analysis

- Detect major changes by may miss minor changes
- Difficult to develop simple and reliable enrichment procedures
- Need to know what you are looking for

Secretome Analysis

- Reduced number of proteins
- Can focus on smaller subset of targets
- Easier to “translate” your findings

Howard University Proteomics Core Facility

Typical Workflow

- Sample
- Shimadzu HPLC
- NSI
- LTQ Orbitrap XL
- SEQUEST search
- MS/MS
Factors Secreted by Adenovirus-infected Epithelial Cells Maintain Long-term Survival of Primary Endothelial cells

A B C

Factors Secreted by Adenovirus-infected Epithelial Cells

Description GenBank Accession MW Score 1 #Peptides Coverage, %

Pigment epithelium-derived factor (PEDF) P36955 46.3 19.58 2 6.22
Sarcolectin CAB41416 51.3 8.24 3 5.54
Cationic trypsinogen AAG30949 9.1 5.08 1 23.81
Alpha 2 macroglobulin EAW88590 151 0 20 8 1
Apolipoprotein B AAD51759 8.4 2.04 1 26.39
Antithrombin CAA48690 13.8 1.66 1 5.74
sICAM-1 AAB46863 4.3 0 1 50.00
Fibroblast growth factor 17 precursor 060258 10.4 0 2 7.41

Conclusions

- Global OMICS approaches were developed to study SCD-related genes and proteins expression
- Data obtained with plasma and leukocyte profiles are usually limited
- Secretome can provide additional candidate proteins and regulatory proteins
- Newer and faster mass spectrometers and better separations can provide additional data and novel protein candidates

Acknowledgements

Tatiana Ammosova, Howard University
Xiomei Niu, Center for Sickle Cell Disease
Namita Kumari, Yuri Obukhov
Marina Jerebtsova, Children’s National Medical Center
Profiles: Overview, Update on Deployment for RTRN, Support of Multi-Institutional Research

Solomon T. Garner, Jr., Ph.D.; Omar Aldaoud; Andrew Dent, II; Mohamad Malouhi
Director, Research Resources and Research Networking Division
Director, Information Systems and Technology Integration Division
RCMI Translational Research Network (RTRN) Data Coordinating Center
RTRN DCC Research Resources and Research Networking (R^3N) Division

Director
Solomon T. Garner, Jr., Ph.D.

Data Curation Specialist and Resource Navigator
Kathy Caraballo-Gomez

Resource Navigator
Erik Fleming

RTRN Profiles
Research Networking System

Agenda

• About RTRN Profiles
• Profiles Search Demo
• How to Access RTRN Profiles
• How to Add Your profile
• How to edit Your profile
  – Edit Photo, Narrative, Awards and Publications
  – Edit personal information
• How to retrieve your password
• The Posting Process
• Getting Help
Need to find experts and potential collaborators?

Need to discover research connections?

RTRN Profiles is the tool for that!

www.rtrn.net

About RTRN Profiles

• Who benefits?
  – Everyone in the RCMI community

• What is it?
  – A research networking tool that connects people by combining basic directory information with expertise keywords

• Why use it?
  – Find potential collaborators within RCMI community
  – Find Experts within RCMI community
  – Discover research connections
  – Add new expertise to your team
  – reveal new directions for your research

www.rtrn.net

About RTRN Profiles

• Profiles is a tool to speed the process of finding researchers with specific areas of expertise for collaboration and professional networking.

• Profiles is a federated web application that uses the VIVO ontology which standardizes researchers information for sharing

• Profiles allows different institutions to “talk” to each other through federated queries, enabling networks to extend beyond local collaborations while protecting institutional data.

Acknowledgement

RTRN Profiles is a RTRN version of the ground-breaking, open source “Profiles Research Networking Software” that was developed under the supervision of Griffin M Weber, MD, PhD, with support from Grant Number 1 UL1 RR025758-01 to Harvard Catalyst: The Harvard Clinical and Translational Science Center from the National Center for Research Resources and support from Harvard University and its affiliated academic healthcare centers.

www.rtrn.net
RTRN Profiles by the Numbers

- 18 RCMI Institutions
- 1,400+ Profiles in the system
- 16,949+ Publications
- 400 Average unique queries per month

How to Access RTRN Profiles

Profiles on RTRN Website

www.rtrn.net
Profiles on RTRN Website

www.rtrn.net

Click RTRN Profiles

How to Add Your Profile

www.rtrn.net

Add Your Profile

www.rtrn.net

All Rights Reserved - No forms of duplication nor distribution allowed without author's consent
Edit My Profile

www.rtrn.net
Click to LOGIN to edit your Profile information

Select Institution

Enter User Name

Enter Password

Updating Photo, Narrative, Awards and Publications

RTRN Profiles RNS
Edit My Profile

Adding Awards

Edit Narrative

Follow the instructions provided in this section to add awards.
- Users can perform the following actions:
  - Save and add another
  - Save and close
  - Close

Enter a personal narrative that describes your career achievements and research focus.
- Users can perform the following actions:
  - Save
  - Cancel

www.rtrn.net
Add Publications

- Use this section to add publications from PubMed
- Publications can be:
  - Added by manually entering PubMed information
  - Automatically looked up by entering the PubMed ID
  - Added by manually entering custom information based on publication type

Add Publications

- Using this section, PubMed is searched using the information entered about the publication
- Using this section, PubMed is searched using the PubMed ID(s) entered
- Using this section, PubMed is searched using the information entered
- Using this section, multiple publications can be removed

Updating Basic Profile Information

RTRN Profiles RNS
How to Retrieve Your Password

RTRN Profiles RNS

Profiles on RTRN Website

Retrieve Your Password

• Click “Forgot your password” link

• Select Institution

• Enter User Name

• NOTE: The password will be sent to the email address that is currently in the database for a respective user.
The Posting Process

- A newly added profile or updated profile’s basic information (title, cluster, address, phone, email address) will not appear immediately.
- On a frequent basis, the data in RTRN Profiles will be refreshed from staging area with the most current information.

Need Help?
We’re happy to help!

Email us at: R3NHelpdesk@rtrn.net
or
Call us at: 1-877-602-7907

Solomon T. Garner, Jr., Ph.D.
Director
Research Resources and Research Networking
RCMI Translational Research Network (RTRN) Data Coordinating Center (DCC)
Solomon.garner@rtrn.net
601.979.0332
Researchers often struggle to locate and communicate with collaborators across fields and outside rigidly defined organizational confines.

Solution:

- VIVO will help create the collaborations that are crucial in science by facilitating communication and collaboration across interdisciplinary and institutional boundaries NOT ONLY for scientists but also for administrators, students, faculty, donors, funding agencies and the public.
What is VIVO?

An open-source semantic web application that enables the discovery of research and scholarship across disciplines in an institution. Populated with detailed profiles of faculty and researchers; displaying items such as publications, teaching, service, and professional affiliations.

A powerful search functionality for locating people and information within or across institutions.

VIVO harvests data from verified sources

Internal data sources:
- HR Directory
- Office of Sponsored Research
- Institutional Repositories
- Registrar System

External data sources:
- Publication warehouses - e.g. PubMed, Web of Science, and more.
- Grant databases: e.g. NSF/NIH
- National Organizations: AAAS, AMA, etc.

Data stored as RDF triples using standard ontology:
- Faculty and unit administrators can then add additional information to their profile (M).

VIVO data is available for reuse by web pages, applications, and other consumers both within and outside the institution.

A VIVO profile allows you to:

- Find potential colleagues by research areas, scholarship, and collaborations.
- Showcase credentials, expertise, skills, and professional achievements.
- Connect within focus areas and geographic expertise.
- Simplify reporting tasks and link data to external applications - e.g., to generate biosketches or CVs.
- Publish the URL or link the profile to other applications.
- Display visualizations of complex research networks and relationships.
Semantic Search
Community-Wide
Compatible with other software

National Search using a tool called DIRECT
(http://direct2experience.org/) pulls in hits from many institutions from compatible databases (including VIVO)
Research Discovery and Networking Tools

- VIVO search – research discovery and networking
- Duke, Florida – web site plug-ins for reuse of VIVO data
- Digital Enterprise Research Institute – analytics for VIVO data
- VIVO Search Light – find experts related to any page on the world wide web
- UCSF – find investigators "like me" across the network
- Harvard – visualize publication collaboration patterns
- Northwestern – C-Know Recommender for team building
- AIA society portal – identity management
- CTSA consortium portal
- Pittsburgh – Digital Vita – produce vita and biosketches
- Direct2Experts – get counts of researchers matching criteria and link to them
- Community of Science – use VIVO data for faculty interests, route opportunities to faculty
- Federal Researcher Profile System – avoid duplication of entry, simplify administration
- OpenPhacts (EU) – provide provenance for assertions
- NRN visualization – show data sources and their inventory of data
- VIVO concept – what topic areas are covered by people, departments, universities

vivo.sourceforge.net  vivoweb.org  vivo.sourceforge.net
More Information...

How can you get involved and learn more about the project, the code, adoption at your site and more?

Contact Form: http://vivoweb.org
Mailing List: http://vivoweb.org/archives

Panel Discussion / Q&A

Thank you!
Thank you for participating!