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Translation of genomic discoveries to primary care – A role for the PA?

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Translating Genomics...

- Genomic discoveries relevant to common disease diagnosis and management are coming at an increasing rate.
- Basic discoveries are leading to the development of clinical applications.
- Ergo, improved healthcare is around the corner!



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Translating Genomics...

- Genomic discoveries relevant to common disease diagnosis and management are coming at an increasing rate.
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Mind the gap!

- Ergo, improved healthcare is around the corner!



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Translating Genomics...

Filling the gap

- » Does the application address a clinical need?
- » Does the application meet a clinical need?
- » Is the application acceptable to patients?
- » Is the application acceptable to health care providers?
- » Is the application acceptable to insurers?
- » Is the application acceptable to society?
- » How are patients best educated about the application?
- » How are providers best educated about the application?



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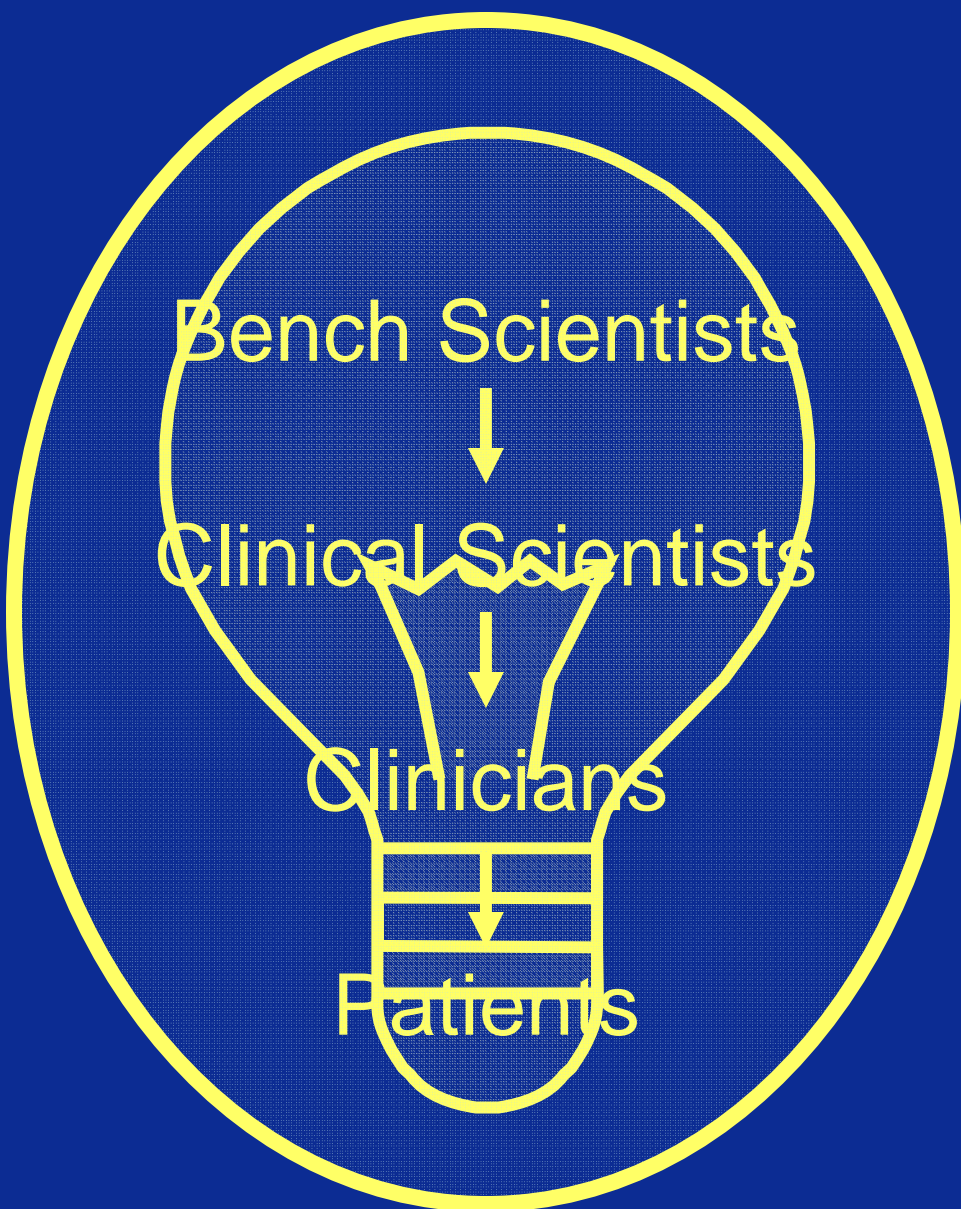
Who will fill the gap?



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Multiplex ClinSeq

PUHGV



Multiplex Genetic Susceptibility Testing:

*A prototype for applied research to inform
personalized medicine*

Colleen M. McBride, PhD. & Larry Brody, Ph.D.

Research Partners:

National Human Genome Research Institute
Henry Ford Health System
Group Health Cooperative
Cancer Research Network (NCI)





Multiplex Project Aims

To develop a prototype for multiplex genetic susceptibility testing

- Multiple markers of susceptibility for multiple diseases
- Provide risk feedback to target populations

To create an infrastructure to facilitate public health research

- Decide upon “standard of care” for consent, feedback & support services
- Identify optimal study population(s) & recruitment approach

Clinic-based population

➤ Cancer Research Network (NCI-funded)

- Full complement of preventive services
- Patient bases geographically distributed with racial-ethnic & SES diversity
- Henry Ford Health System clinical recruitment site
- Group Health Cooperative (HMO Research Network), Survey coordination

➤ Sample size: 5000+ touched ~ 1000 tested

➤ Healthy adults

- Ages 25-40
- Without diseases included on test batter

Study Design

Baseline screening survey



Mail invitation to website
to consider genetic testing



Web-based
decision process re: testing
w/financial incentives



Consent process
In-clinic blood draw



Test feedback provided directly to subject
by mail + telephone follow-up

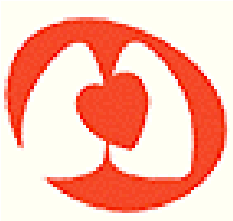


3 month follow-up telephone survey

ClinSeq: A translational research project in clinical genomics



Medical & Statistical
Genetics



NHLBI
□



NIH Clinical Center



NIH Intramural
Sequencing Center

Specific Aims

1. Develop a robust infrastructure for the generation and use of LSMS in a clinical research setting
2. Use LSMS data to develop novel approaches to clinical biomedical research
3. To understand how to interact with subjects re LSMS

Approach

- Phenotype 1,000 subjects
- Sequence 200-400 candidate genes
- Follow-up studies
- Interpret variants and validate *some*
- Return results

Clinical evaluation

- Family history (semiautomated)
- Medical history (form-driven)
- Blood pressure
- Coronary calcium score (MDCT)
- Echo/electro-cardiography
- Clinical & research bloods

Prior to NIH visit:

- Verbal consent via phone communication
- Family history tool (online)



Initial visit to NIH:

- Sample collection for fasting labs (cholesterol, etc)
- General consent
- Family history if unable to complete this information prior to visit
- Medical history intake
- Clinical evaluation
- Second sample collection (non-fasting)



Visit to Suburban Hospital:

- Multidetector computed tomography (MDCT) to assess coronary artery calcification



Initial follow-up (regular mail):

- Assessment of clinically validated test results (labs, MDCT)



Contact by phone or regular mail to find out if participant is interested in (a) undergoing further phenotyping AND/OR (b) learning genotyping results

AND/OR

Participant may "OPT OUT" of learning results
AND
still remain part of study

NOTE 1



Follow-up visit to the NIH:
Genetic education & counseling for results from genome sequencing

Follow-up visit to the NIH:
Further phenotyping

Health Professionals' Genetics Education Needs Exploration (HP GENE) Survey



National Human Genome Research Institute

National Institutes of Health

Health Professionals' Understanding of Human Genetic Variation Study

Vence Bonham, JD
Associate Investigator
Social and Behavioral Research Branch
Principal Investigator



Project Aim

To investigate health professionals' **knowledge** of human genetic variation, **beliefs** about biological and genetic differences based upon their patients' race and ethnicity and its **use** in clinical practice.



Health Professionals' Genetics Education Needs Exploration (HP GENE) Survey



National Human Genome Research Institute

National Institutes of Health



7. Random mutations cause all of the genetic variation in the human genome.

- | | | | |
|-----------------------|-----------------------|--|-----------------------|
| true | false | scientific
evidence
inconclusive | don't
know |
| <input type="radio"/> | <input type="radio"/> | <input type="radio"/> | <input type="radio"/> |

8. The variation in the human genome includes both disease causing gene variants and variants that have no effect on health and disease.

- | | | | |
|-----------------------|-----------------------|--|-----------------------|
| true | false | scientific
evidence
inconclusive | don't
know |
| <input type="radio"/> | <input type="radio"/> | <input type="radio"/> | <input type="radio"/> |

STUDY DESIGN

Phase I Qualitative Study

Dimensional analysis and qualitative content analysis were used to explore physicians' perceptions of and experiences with racial factors in clinical decision-making, determining the racial background of a patient, and perceptions of the race-related causes of health differences.

Phase II Scale Development

Focus groups were used to assist in question development. The process of scale development occurred in an iterative fashion. Thirty-two cognitive interviews with physicians were used to refine the instrument and scale. Two panels of experts, geneticists with expertise in human genetic variation and social scientists with expertise in survey methodology provided input.

Phase III National Physician Survey

A pilot survey of 400 physicians will be conducted fall 2007 to examine psychometrics of the scale. The scale will be revised based upon the findings. In 2008 a National Survey of 3000 Primary Care Physicians will be conducted using the final HGVB scale.

Phase IV National Physician Assistants Survey ????





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- Colleen McBride Ph.D., DIR, NHGRI
Multiplex
- Les Biesecker, M.D., DIR, NHGRI
ClinSeq
- Vence Bonham, J.D., ECIB, NHGRI
PUHGV



Possible discussion topics:

- To what extent will these sorts of research questions interest the PA community?
- What unique perspectives could the PA community bring to this type of research?
- To what extent do PA training centers participate in research? Independent? Part of a larger academic center?
- Do PA's have a research society? NAPCRG? How to engage PA's with interest?



Possible discussion topics:

- What other factors need to be considered to facilitate the translation of genomic discoveries to primary care?