Will Genomics Widen or Help Heal the Schism Between Medicine and Public Health?

Muin J. Khoury MD, PhD

National Office of Public Health Genomics

SAFER • HEALTHIER • PEOPLE™

Outline

- The Challenges of Translation
- What is the Schism?
- The Translation Highway in Genomics
  - T1 through T4
- Medicine-Public Health Collaboration in Genomics Translation: A Population Health Approach
  - Four Areas of Emphasis

Historical Perspectives From the Double Helix to Personal Genomics: Where is Translation?

- 1953: Double Helix
- 1990: Human Genome Project started

- 2003: Human genome project completed
- 2005: HapMap Project completed

- 2007: GWAS
- 2007: HHS Personalized Healthcare initiative
- 2007: Personal Genomics

"The Genomics Gold Rush"

Topol EJ et al. JAMA 2007;298:218-221

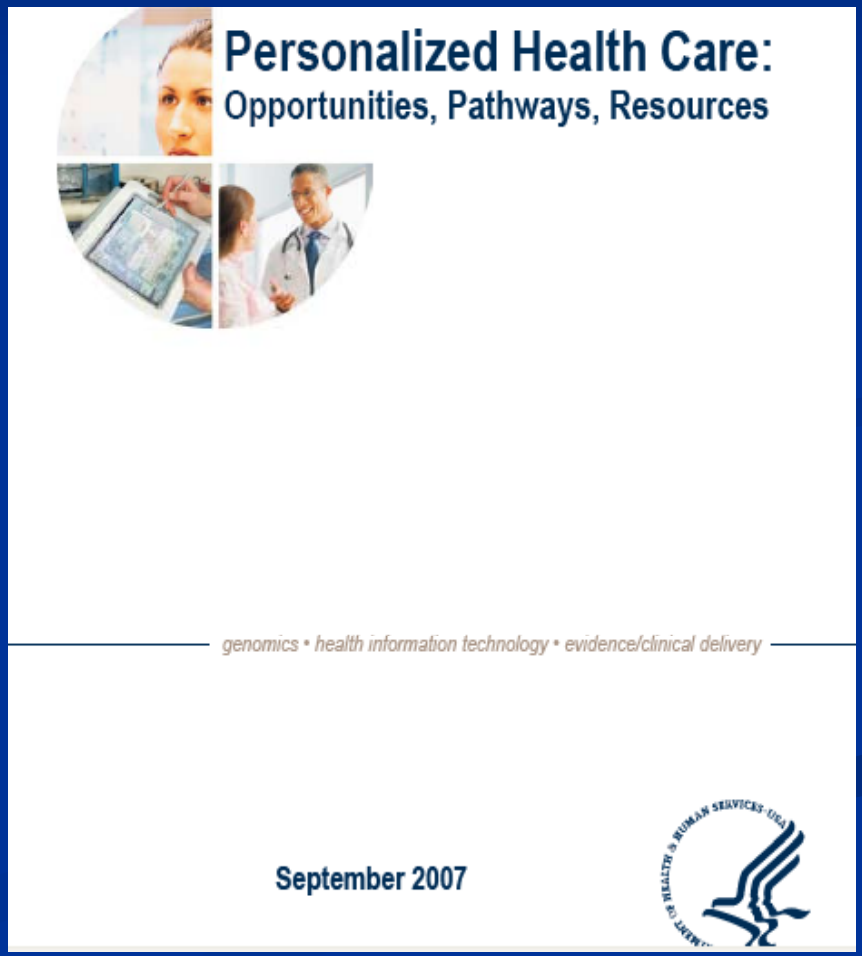
Table. Pertinent Details of Findings of Recent Whole-Genome Association Studies (All From 2007)

Disease	Source	Gene/Locus[a]	No. of SNPs	Primary Study Cases/Controls	Replication Study Cases/Controls	OR_{het}	OR_{hom}	*P* Value	PAR, %
Breast cancer	Easton et al[1]	*FGFR2*	528 000	1145/1142	1776/2072	1.20	1.64	1×10^{-10}	16
	Hunter et al[2]	*FGFR2*	228 000	4398/4316	21 860/22 578	1.23	1.63	2×10^{-26}	NR
		TNRC9				1.23	1.39	1×10^{-36}	NR
		MAP3K1				1.13	1.27	2×10^{-20}	NR
		LSP1				1.06	1.17	3×10^{-9}	NR
		8q24				1.06	1.18	5×10^{-12}	NR
	Stacey et al[3]	2q35	311 000	1600/11 536	4533/17 513	1.11	1.44	5×10^{-14}	14
		TNRC9				1.27	1.64	6×10^{-19}	13
CAD	McPherson et al[4]	Chromosome 9p21	73 000	322/312	3989/18 805	1.20	NR	4×10^{-6}	13
MI	Helgadottir et al[5]	Chromosome 9p21	306 000	1607/6728	4587/12 769	1.25	1.64	1×10^{-20}	21
Obesity	Frayling et al[6]	*FTO*	490 000	1924/2998	3757/5346	1.32	1.67	3×10^{-35}	20
Diabetes	Sladek et al[7]	*TCF7L2*	393 000	1380/1323	2617/2894	1.65	2.77	1×10^{-34}	28
		SLC30A8				1.18	1.53	6×10^{-9}	24
		HHEX				1.19	1.44	3×10^{-6}	19
		EXT2				1.25	1.50	1×10^{-4}	16
	Steinthorsdottir et al[8]	*CDKAL1*	339 000	1399/5275	4739/9379	1.25	1.50	8×10^{-9}	16
	Scott et al[9]	*IGF2BP1*	315 000	1161/1174	1215/1258	1.14	NR	9×10^{-16}	NR
		CDKN2A/B				1.20	NR	8×10^{-15}	NR
		11p12				1.25	NR	4×10^{-7}	NR
	Zeggini et al[10]	*KCNJ11*	490 000	1924/2998	3757/5346	1.14	NR	5×10^{-11}	NR
		PPARG				1.14	NR	2×10^{-14}	NR
	Saxena et al[11]	Multiple	386 000	1464/1467	14 586/17 968				
Prostate cancer	Yeager et al[12]	8q24	550 000	1772/1157	4290/4299	1.26	1.58	9×10^{-13}	21
	Gudmundsson et al[13]	8q24	316 000	1453/3064	1583/2817	1.71	NR	2×10^{-14}	13[b]

Abbreviations: CAD, coronary artery disease; het, heterozygotes; hom, homozygotes; MI, myocardial infarction; NR, not reported; OR, odds ratio; PAR, population-attributable risk;

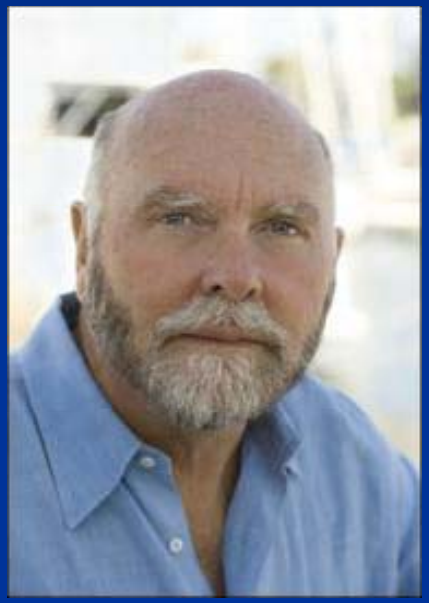
HHS Personalized HealthCare Initiative

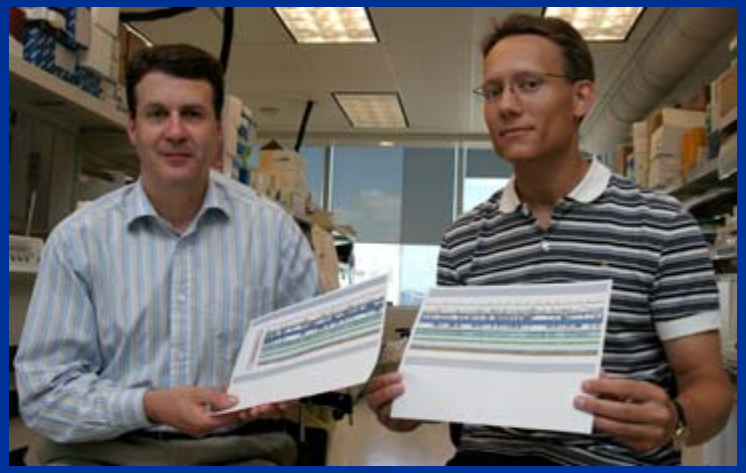
- The Personalized Health Care Initiative will improve the safety, quality and effectiveness of healthcare for every patient in the US. By using “genomics”, or the identification of genes and how they relate to drug treatment, personalized health care will enable medicine to be tailored to each person’s needs.



"First Individual Human Genome Decoded"

The Diploid Genome Sequence of an Individual Human
PLoS Biology, Sept 3, 2007





Toronto researchers Steve Scherer, left, and Lars Feuk show the map of Craig Venter's genetic code. (Jorge Uzon for The Globe and Mail)

'We have developed a framework that can serve as a model for the emerging field of en masse personalized genomics"

CVS

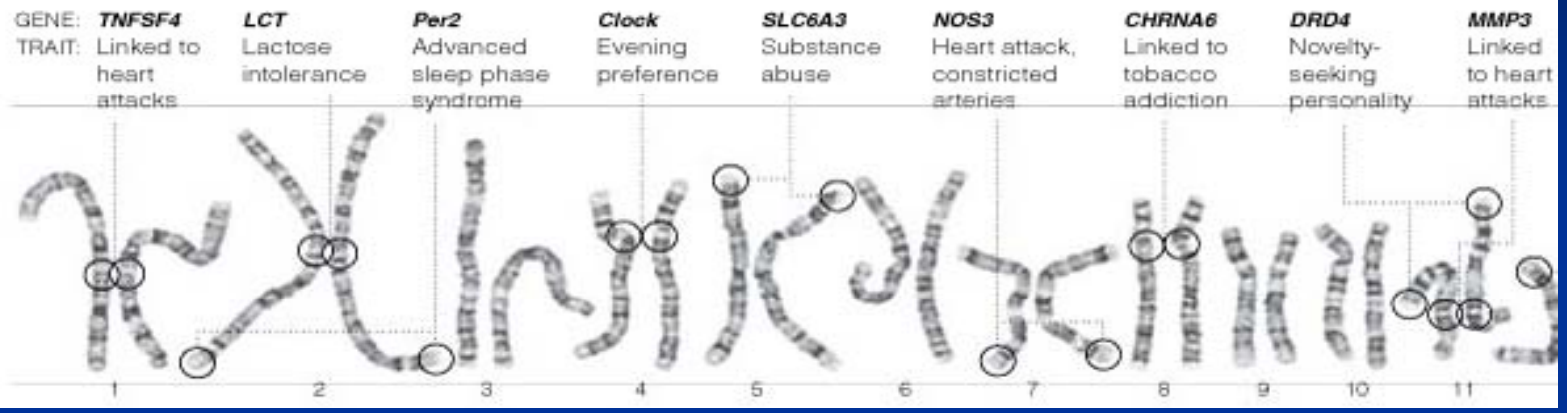
The Diploid Genome Sequence of J. Craig Venter

http://journals.plos.org/plosbiology/suppinfo/pbio.0050254/pbio.0050254.sd001.htm

http://www.nytimes.com/imagepages/2007/09/03/science/04vent.genomegraphic.html

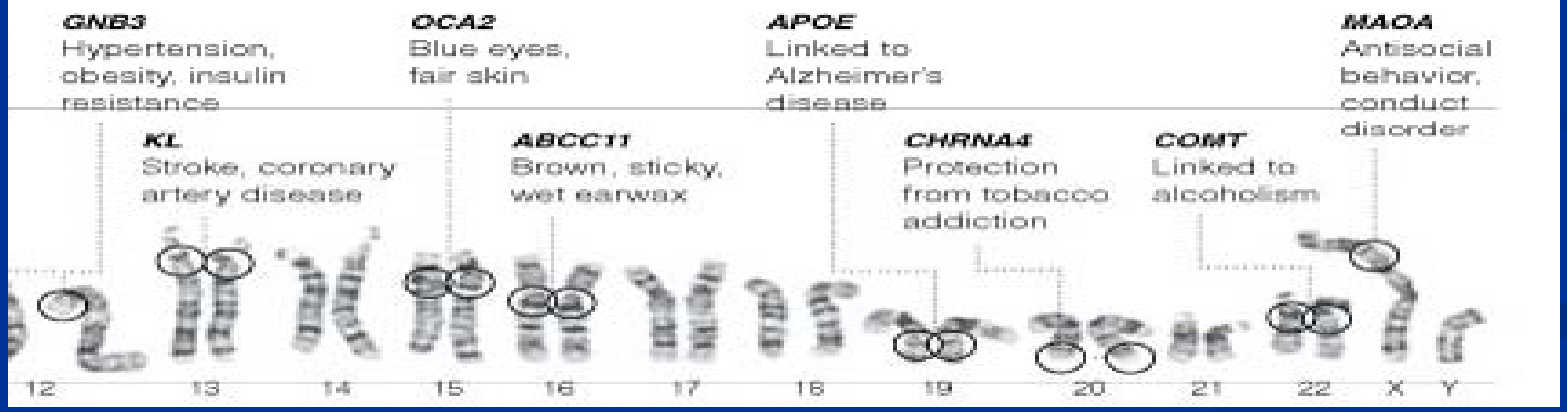
The New York Times

DECODING HIMSELF A team led by J. Craig Venter, above, has finished the first mapping of a full, or diploid, genome,



September 3, 2007

made up of DNA inherited from both parents. The genome is Dr. Venter's own.



"My Genome, Myself: Seeking Clues in DNA"
A. Harmon, New York Times, Nov 17, 2007

TRACKING SNPS

Using the Web site of 23andMe, a company that queried 550,000 SNPs in a sample of her DNA, the reporter determined that her genotype for adult lactose intolerance is **GG** (she is lactose intolerant). Some of her other genotypes are below:

SNP	Location	Genotype	Genotype associated with
rs662799	APOA5	AA	Tendency to gain weight when eating fatty foods
rs174575	FADS2	CC	Higher I.Q. if breast fed for nine months as infant
rs6920220	6q23	GG	Low risk of rheumatoid arthritis
rs17070145	KIBRA	CC	Relatively poor verbal memory
rs1801260	CLOCK	AA	Early rising
rs1953558	OR11H7P	CC	Sensitivity to smell of sweat
rs17822931	ABCC11	CC	Wet earwax

"Genetic counselors cannot deprive people of the right of genetic Self determination" K. Stefansson, Nov 17, 2007

What Do You Do With a Gene When You Find One?

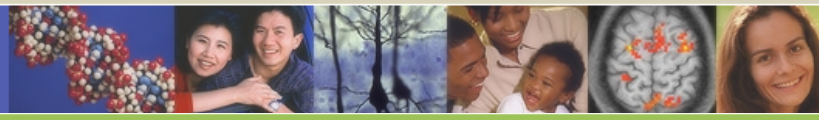
Two Challenges for
"Translation" into Practice and
Population Health Benefits?

Challenge 1: Premature or Inappropriate Translation

NATIONAL INSTITUTES OF HEALTH

Print this page | Topic Finder | Search NIMH: GO

NIMH National Institute of Mental Health
Reducing the burden of mental illness and behavioral disorders through research on mind, brain, and behavior



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Press Release
September 27, 2007

Genes Linked to Suicidal Thinking During Antidepressant Treatment

Specific variations in two genes are linked to suicidal thinking that sometimes occurs in people taking the most commonly prescribed class of antidepressants, according to a large study led by scientists at the National Institutes of Health's (NIH) National Institute of Mental Health (NIMH). Depending on the particular mix inherited, these versions increased the likelihood of such thoughts from 2- to15-fold, the study found. About 1 percent of adult patients were deemed to be at high genetic risk, 41 percent at elevated risk and 58 percent at lower risk.

If confirmed, the findings may hold promise for genetic testing, as more such markers are identified.

Risk increased proportionately if a participant had two, as opposed to just one of the suspect versions. Both genes code for components of the brain's glutamate chemical messenger system, which recent studies suggest is involved in the antidepressant response.

Overall, about 6 percent of 1,915 patients with depression reported that they started to have suicidal thoughts while taking an antidepressant. This rate soared to 36 percent among the few patients with both of the suspect gene versions; 59 percent of the patients who had suicidal thoughts had at least one of the versions.

Francis J. McMahon, M.D., Gonzalo Laje, M.D., NIMH Mood and Anxiety Disorders Program, and colleagues at the National Human Genome Research Institute (NHGRI), Mount Sinai School of Medicine, and the University of Texas Southwestern Medical Center, report on their findings in the October, 2007 issue of The American Journal of Psychiatry.

"These data suggest that genetics may soon help us in our quest to individualize treatments for depression," said NIMH Director Thomas R. Insel, M.D.

"In the future, we hope that genetic testing will help doctors identify those few patients who are at high risk for suicidal thinking during antidepressant therapy and need close monitoring or alternative treatments," said McMahon. "This should help allay concerns for the vast majority of patients. The best way to prevent suicide is to treat depression."

Press Contact(s)

Jules Asher
NIMH Press Office
301-443-4536
NIMHpress@nih.gov

More NIMH Science News about:

- Depression
- Suicide Prevention
- Children & Adolescents
- Medications

Press Resources

- NIMH Mental Health Information
- Statistics on Mental Disorders
- Scientific Meetings
- Information about NIMH
- CRISP: NIH research database of current and completed research

NIH press release, Sept 27, 2007: genetic association study published in Am J Psych implicates two genes: *GRIK2, GRIA3*

Public release date: 27-Sep-2007
[Print Article | E-mail Article | Close Window]

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Contact: Suzanne Lane
slane@thelcgroup.com
212-757-6880
The Lane Communications Group

Genetic test announced for suicidal ideation in patients using antidepressant drugs

Safer prescribing anticipated

Boulder, CO, October 1, 2007 – NeuroMark, a Boulder, Colorado company, announced today the immediate availability of a genetic test to identify people at risk of suicidal ideation—thoughts of committing suicide—when prescribed an antidepressant drug. The test, called the Mark-C™ test, is expected to help restore public confidence in antidepressant medication and help to reduce a recently announced spike in suicide rates among U.S. youth. "This is an exciting example of the power of genetics to address a critical need and make important drugs safer for patients worldwide," stated Kim Bechthold, NeuroMark's CEO.

In September 2007, the Centers for Disease Control (CDC), announced that in 2004 there was a 8% rise in suicide rates among 10-19 year olds, the year that the FDA issued public health warnings linking antidepressant drugs with suicidal ideation and behavior. "The largest percentage increase in rates from 2003 to 2004 was among females aged 10—14 (75.9%), followed by females aged 15—19 years (32.3%) and males aged 15—19 years (9%)," according to the CDC.

In a statement, the company said, "We feel a sense of responsibility, given the current climate, to provide the test to physicians immediately so that they may identify patients who would benefit from closer monitoring or even a change in therapy. It is our hope that this early test will encourage more people to consider antidepressant drug treatment who would benefit from it."

"Before the NeuroMark test, we couldn't differentiate between the subset of patients who were at risk of suicidal ideation and those who could more safely take an antidepressant drug," stated NeuroMark president Dr. Peter Tolias. "The Mark-C test is highly predictive and identifies citalopram-treated patients who are at high risk for suicidal ideation. The test also identifies people at low risk, giving the physician more confidence in prescribing citalopram," he added.

A Nation-Wide Confirmatory Study

In a unique move, the company is inviting physicians and patients across the country to participate in prospectively collecting data to confirm and extend the predicted risk of the Mark-C test. The data will be compiled in the Mark-C Outcomes Database and participating physicians and patients will be notified as new data they submit confirms and extends the predictive value and clinical utility of the test.

Patients can participate by filling out a short QUIDS-SR "self-described" inventory at each appointment with their doctor. The inventory is submitted by their doctor to the database where scientists will study the results and extended information. In this way each patient is contributing to further developing the test for other patients. The patient's identity is not disclosed and each patient will be advised when the database is updated and expanded. This is the first nationwide prospective gathering of data conducted in partnership with patients and families and their physicians.

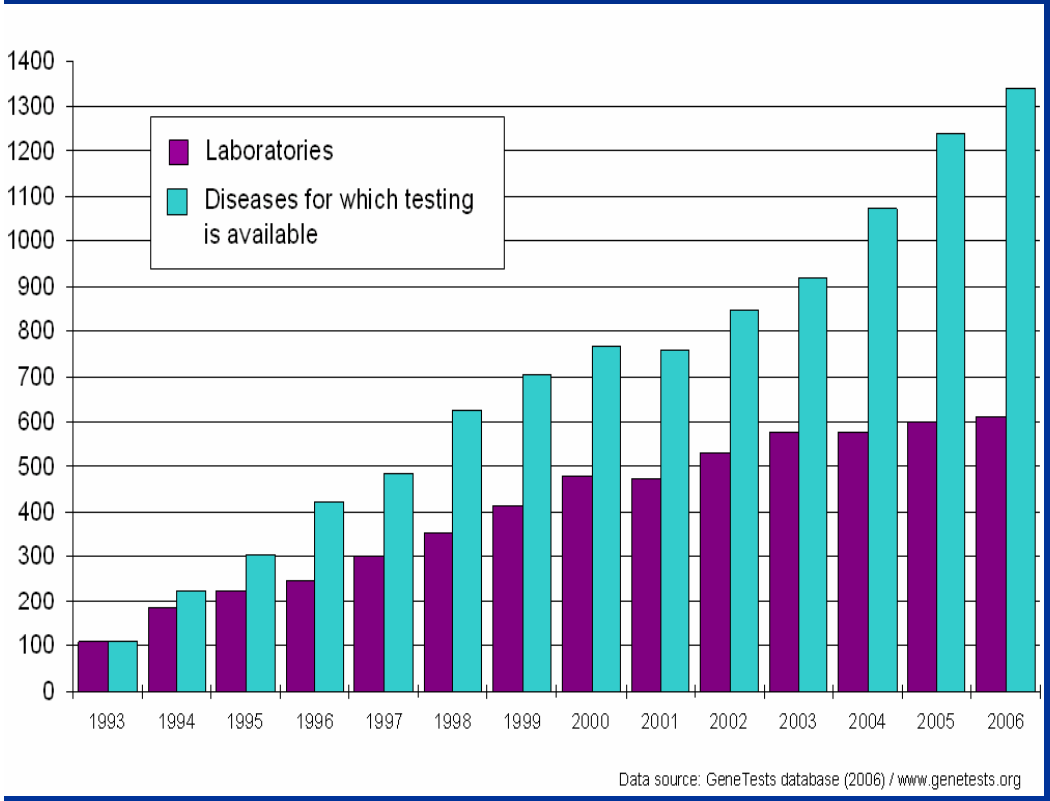
NeuroMark press release, Oct 1, 2007: genetic test available for suicidal ideation in patients treated with SSRIs

"For more information visit www.neuromark.com "

Population level Questions are Important for Using Genetic Information in Practice

- How many people have this genetic variant?
- Is prevalence different in subgroups of the population?
- What is the magnitude of risk (with or without the variant)
- How much of the population burden of disease does it explain?
- Does the variant interact with other genes and modifiable risk factors?

Genetic Testing as a Public Health Issue

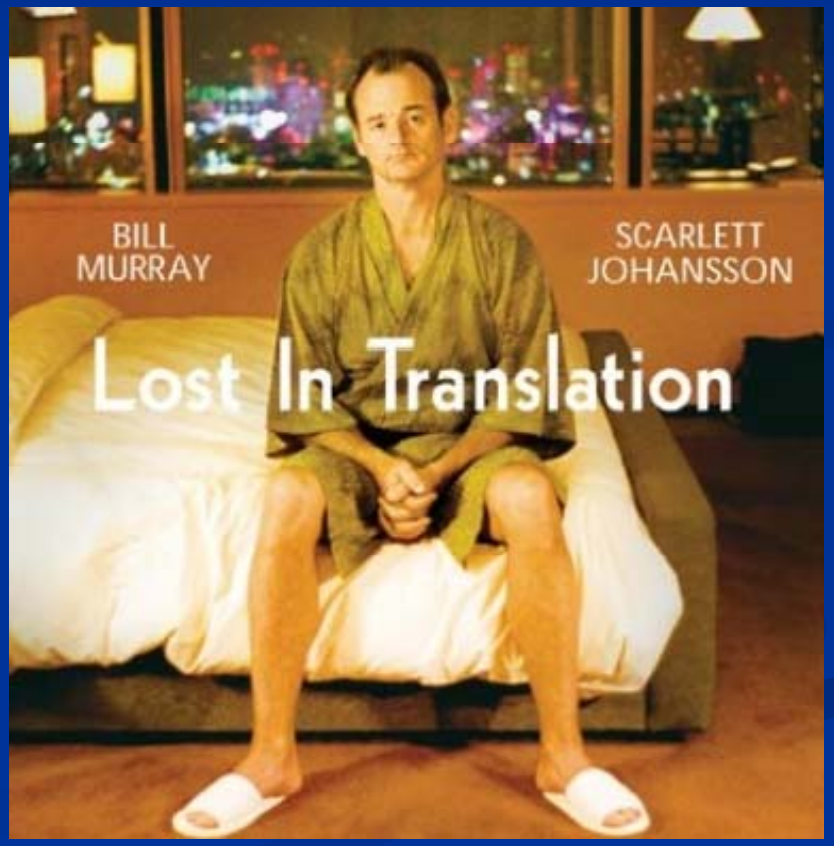


- How good is the genetic test (analytic validity)?
- How predictive or diagnostic is the test (clinical validity)
- What are the benefits and harms (clinical utility)
- How can we ensure quality testing and access?
- How can we educate providers and consumers?
- How can we monitor use and evaluating health impact in the real world (post market surveillance)
- How can we address complex social and ethical tissues?

Challenge 2:
"Lost in Translation"

C. Lenfant NEJM 2003;349:868

< 33% of patients with coronary artery disease are prescribed aspirin



”Lost in Translation”

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< 33% of patients with coronary artery disease are prescribed aspirin

“Let's be realistic: If we didn't do it with aspirin, how can we expect to do it with DNA?”

"Lost in Translation"

C. Lenfant NEJM 2003;349:868

- **It takes an estimated average of 17 years for 14% of new scientific discoveries to reach day to day clinical practice**
- **JM Westfall JAMA 2007;297:403**

"Let's be realistic: If we didn't do it with aspirin, how can we expect to do it with DNA?"

Outline

- The Challenges of Translation
- What is the Schism?
- The Translation Highway in Genomics
  - T1 through T4
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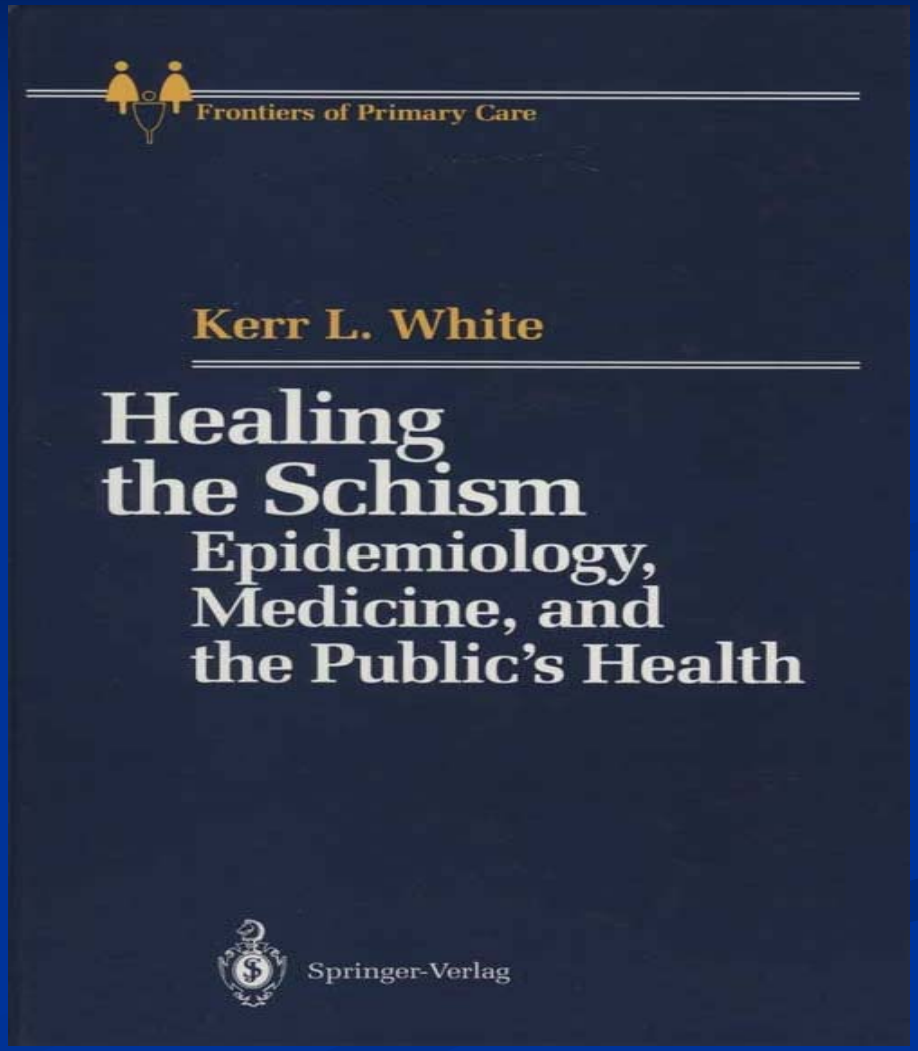
  - Four Areas of Emphasis

The "Schism" Between Medicine and Public Health (K. White, 1991)

- "Today, the two cultures "medicine" and "public health" seem to live in different, often unfriendly worlds"



"Sick Individuals and Sick Populations"

G Rose (1986)

- Population approach vs. high risk approach

- "Realistically, many diseases will long continue to call for both approaches, and fortunately competition between them is usually unnecessary"

Who needs genomics research when it is obvious what we need to do to prevent common chronic diseases?

Exercise more

Eat a healthier diet

Stop smoking

Drink alcohol in moderation

Take an aspirin per day

See your doctor

Get mammography

Get colorectal cancer screening

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THERE ARE MAJOR DISPARITIES IN HEALTH BEHAVIORS & OUTCOMES

"Dissecting Complex Disease: the Quest for the Philosopher's Stone?"

A. Buchanan et al. (Int J Epidemiol 2006;35:562)

- "If a minor fraction of the billions spent on technological research were spent instead on simpler things like, yes, early health education to improve diet and promote exercise, the benefits could grossly dwarf even the greatest plausible genetic successes"

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Int. J. Epidemiol. Advance Access published September 19, 2006

International Journal of Epidemiology
doi:10.1093/ije/dyl214

Letter to the Editor

Genomics, epidemiology, and common complex diseases: let's not throw out the baby with the bathwater!

From MUIN J KHOURY and MARTA GWINN

American Journal of EPIDEMIOLOGY

Volume 161
Number 9
May 1, 2005

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Published by Oxford University Press

SPECIAL ARTICLE

Do We Need Genomic Research for the Prevention of Common Diseases with Environmental Causes?

Muin J. Khoury, Robert Davis, Marta Gwinn, Mary Lou Lindegren, and Paula Yoon

From the Office of Genomics and Disease Prevention, Coordinating Center on Health Promotion, Centers for Disease Control and Prevention, Atlanta, GA

The "Schism" between Medicine and Public Health

- **Medicine**
- Health care
- Individuals
- Treatment
- Biomedical research
- Genes

Khoury MJ et al. Am J Prev Med 2007

The "Schism" between Medicine and Public Health

- **Medicine**
  - Health care
  - Individuals
  - Treatment
  - Biomedical research
  - Genes
- **Public Health**
  - Health
  - Populations
  - Prevention
  - Behavioral/Social/Policy
  - Environment

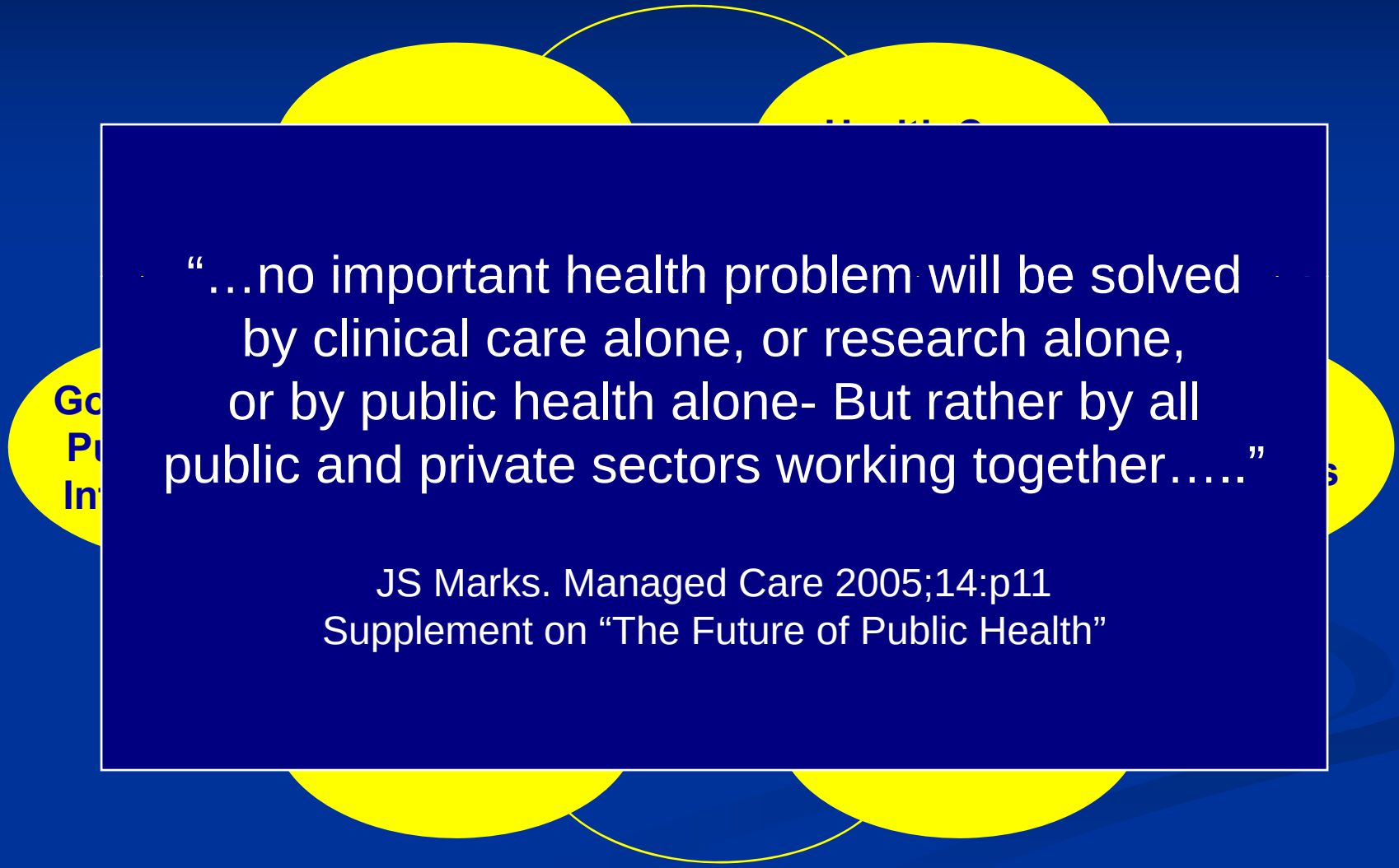
Khoury MJ et al. Am J Prev Med 2007

Who Will Keep the Public Healthy? (IOM, 2002)

New Definition of "Public Health" as "Population Health"

"Can Public Health and Medicine Partner in the Public Interest?"

JM McGinnis. Health Affairs 2006;25:1044



"…no important health problem will be solved by clinical care alone, or research alone, or by public health alone- But rather by all public and private sectors working together….."

JS Marks. Managed Care 2005;14:p11
Supplement on "The Future of Public Health"

The Emergence of Public Health Genomics

The population health approach provides the best strategy for the appropriate applications of genomics in health practice in the 21st century

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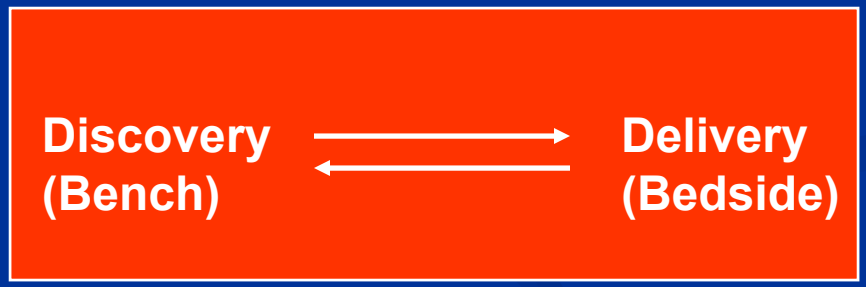
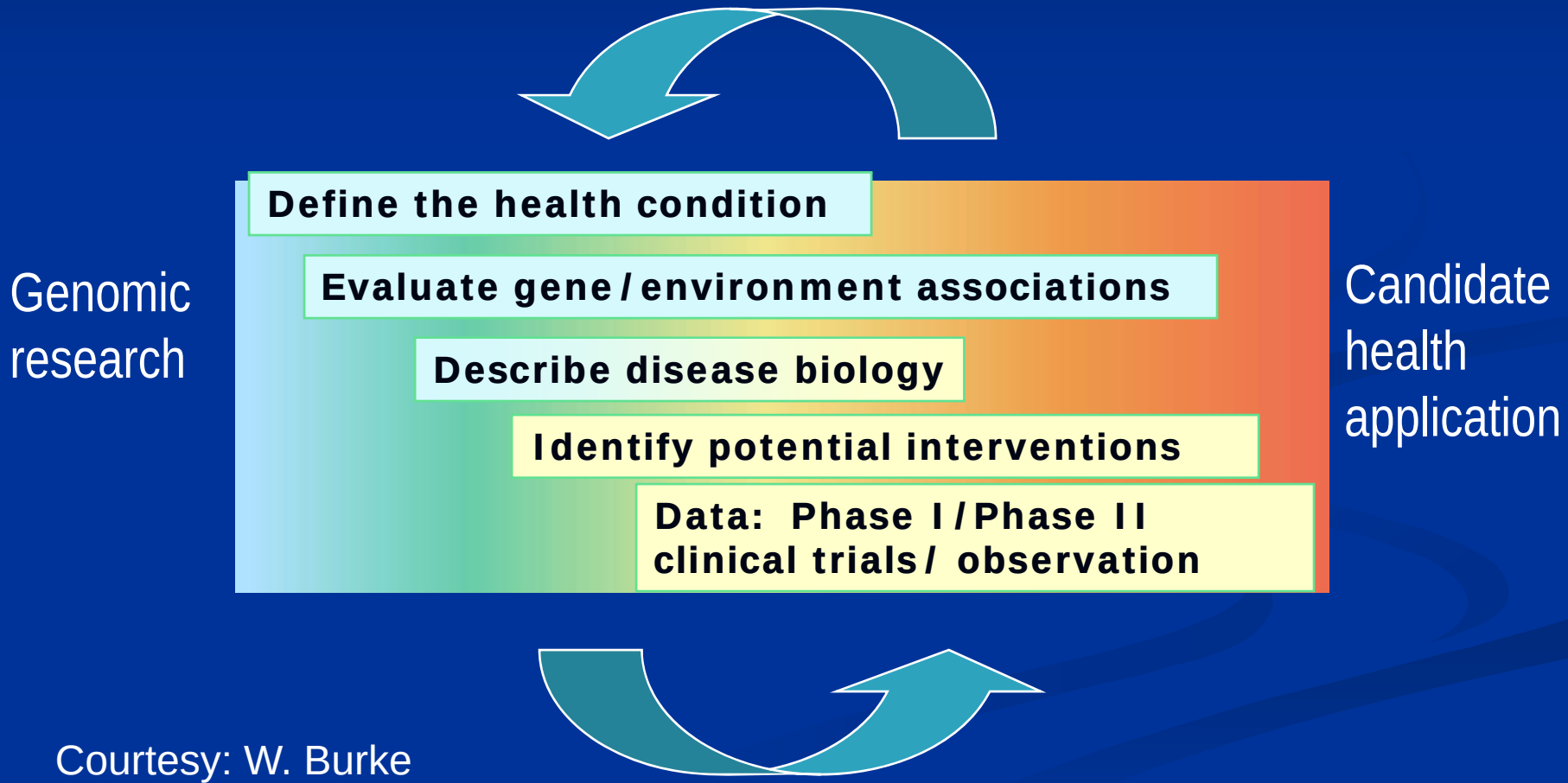
NIH Road Map- "Time for a New Vision"



E. Zerhouni NEJM 2005;353:15

T1
Discovery to Candidate Health Application



Courtesy: W. Burke
Based on Khoury et al. Genet Med 2007

The "Second" Translational Block

"The Roadmap Less Traveled" L. Green

T1: First block:

Translation from concept into first human studies

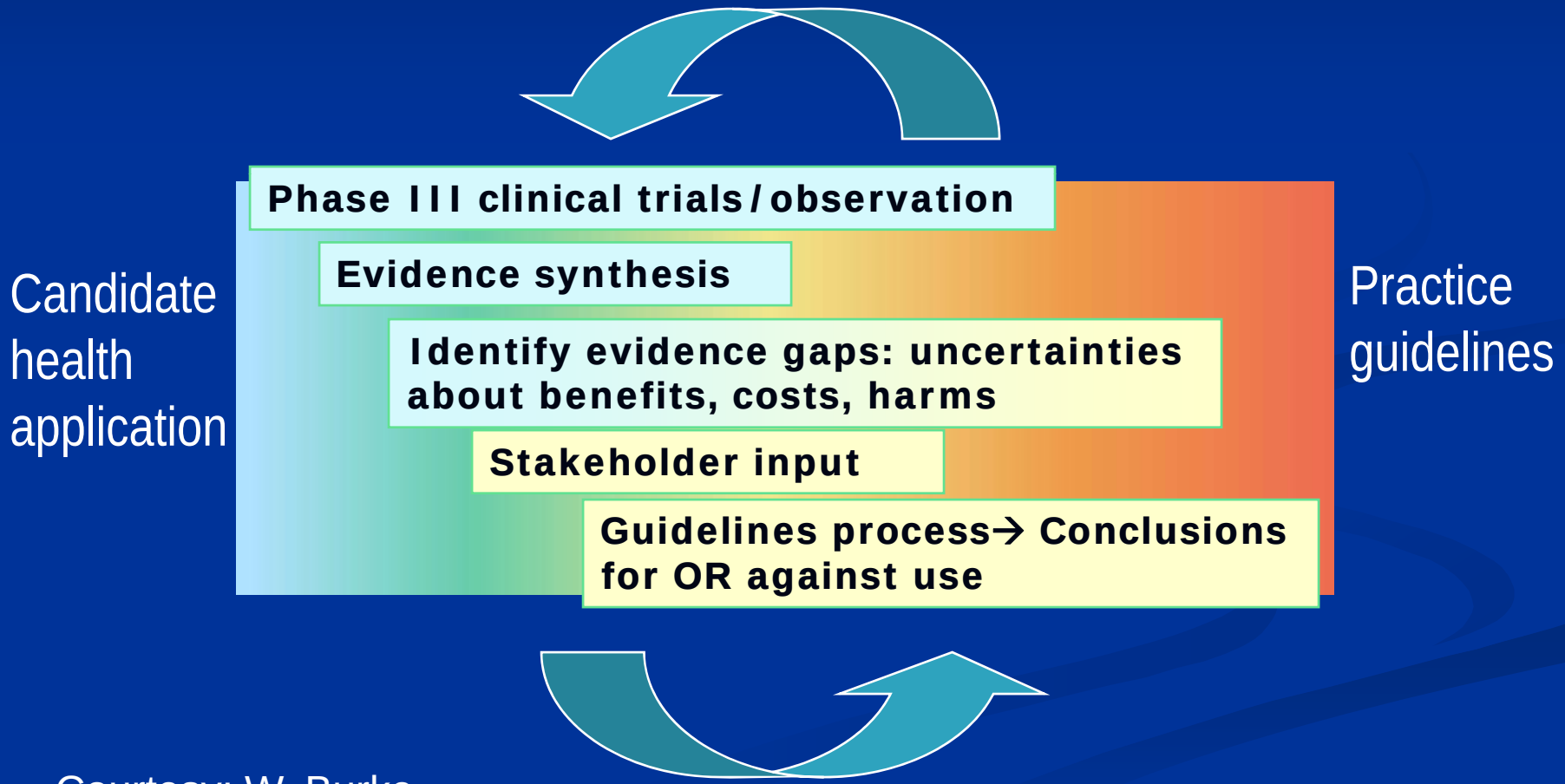
T2: Second block:

Translation from human studies into practice

Courtesy:
G Ginsberg

IOM Clinical Research Roundtable, Sung et al JAMA, 2003

T2
Health Application to Evidence-based Practice Guidelines

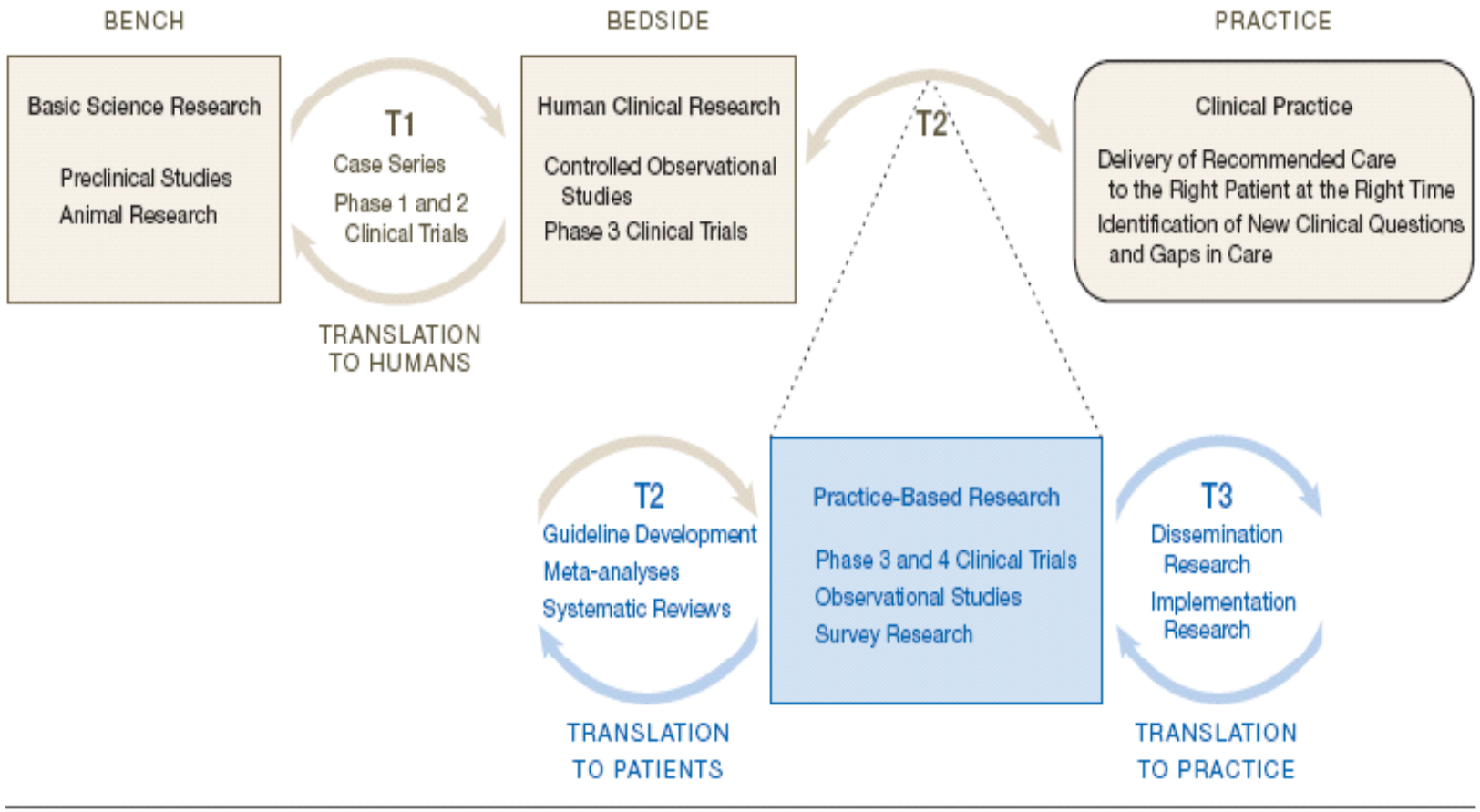


Courtesy: W. Burke
Based on Khoury et al. Genet Med 2007

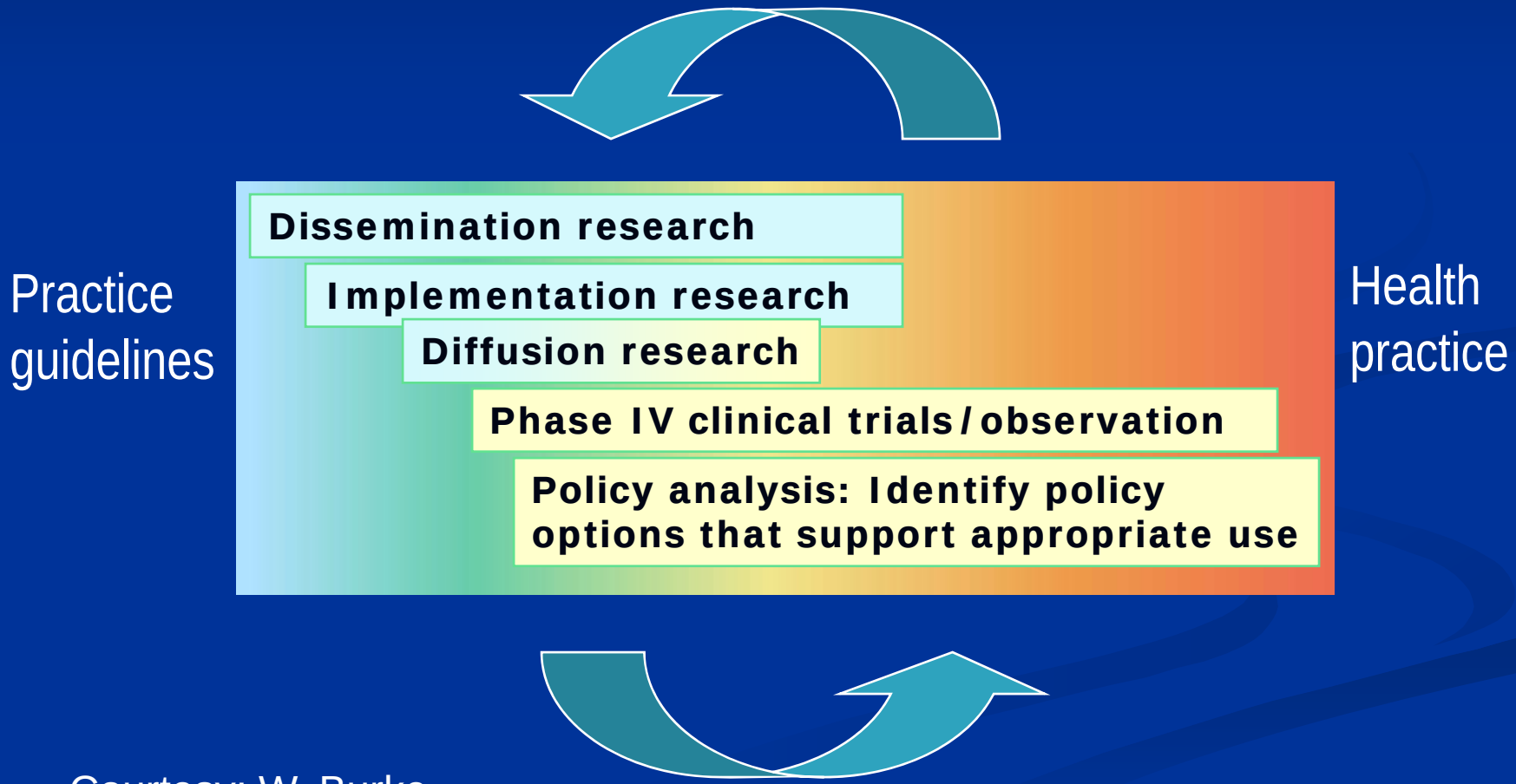
The "Third" Translation Block

JM Westfall et al JAMA 2007;2007;297:403.

Figure. "Blue Highways" on the NIH Roadmap

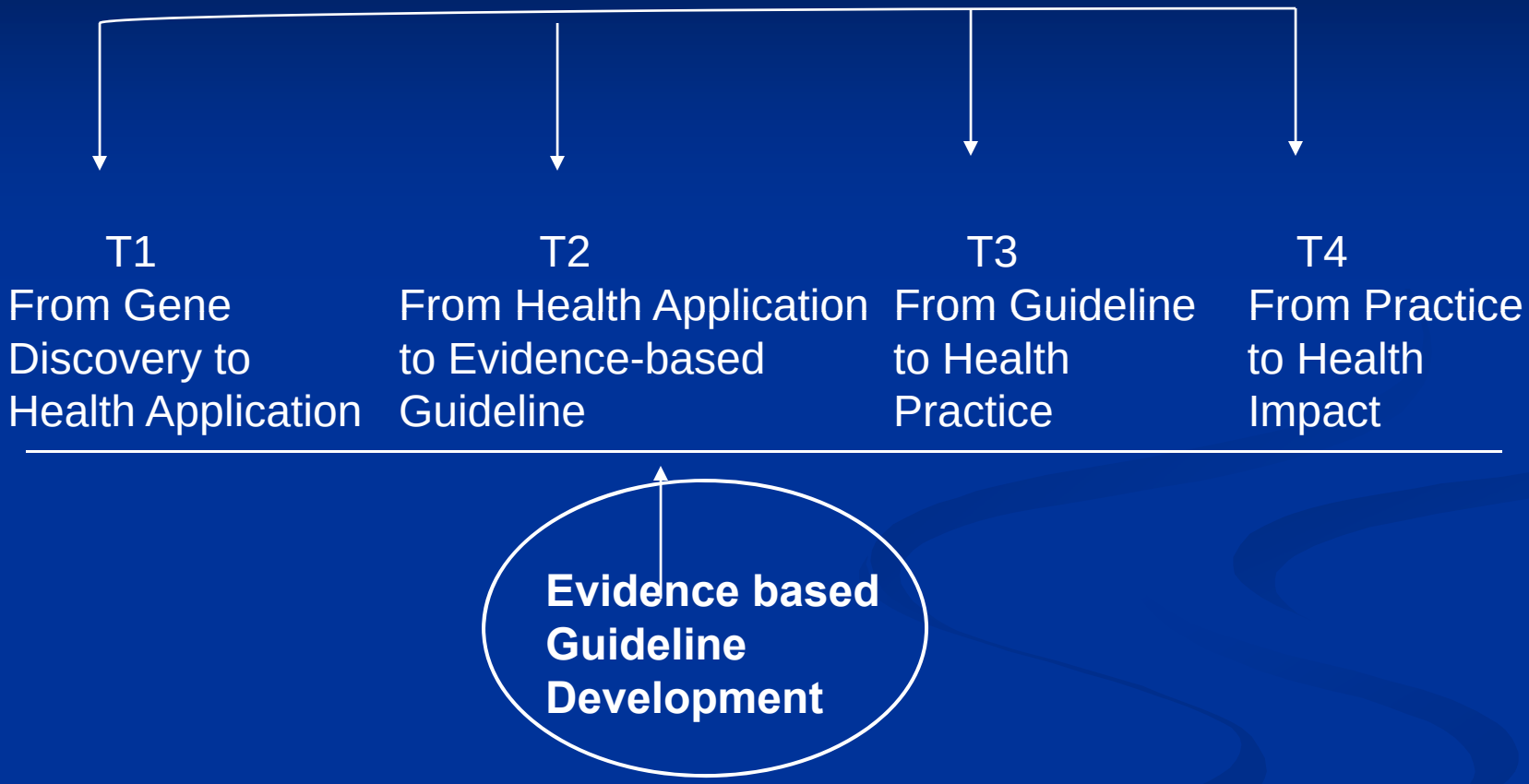


T3
Practice Guidelines to Health Practice



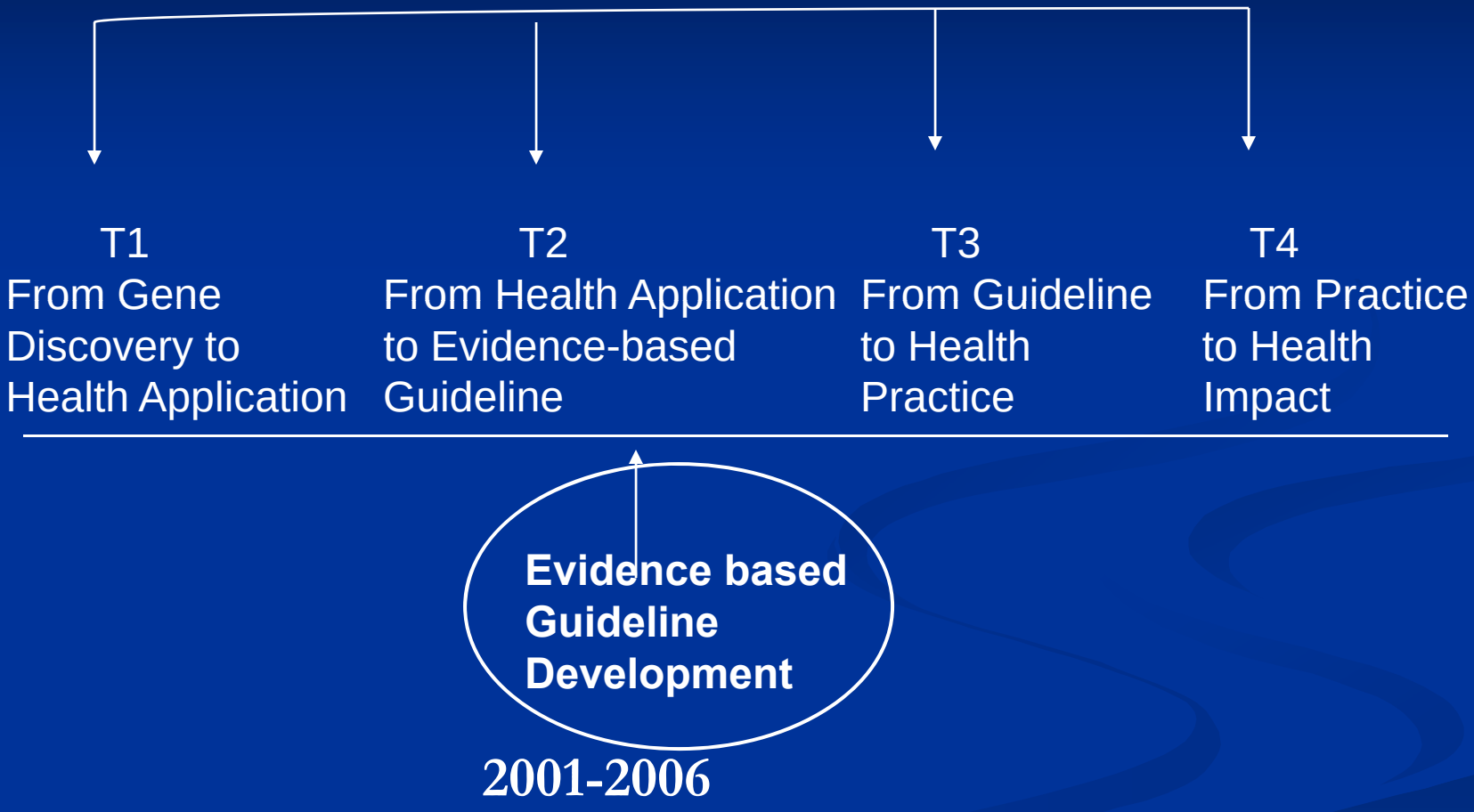
Courtesy: W. Burke
Based on Khoury et al/ Genet Med 2007

The Four Phases of Translation For Genomic Applications in Population Health



Khoury MJ et al. Genet Med 2007

The Four Phases of Translation For Genomic Applications in Population Health

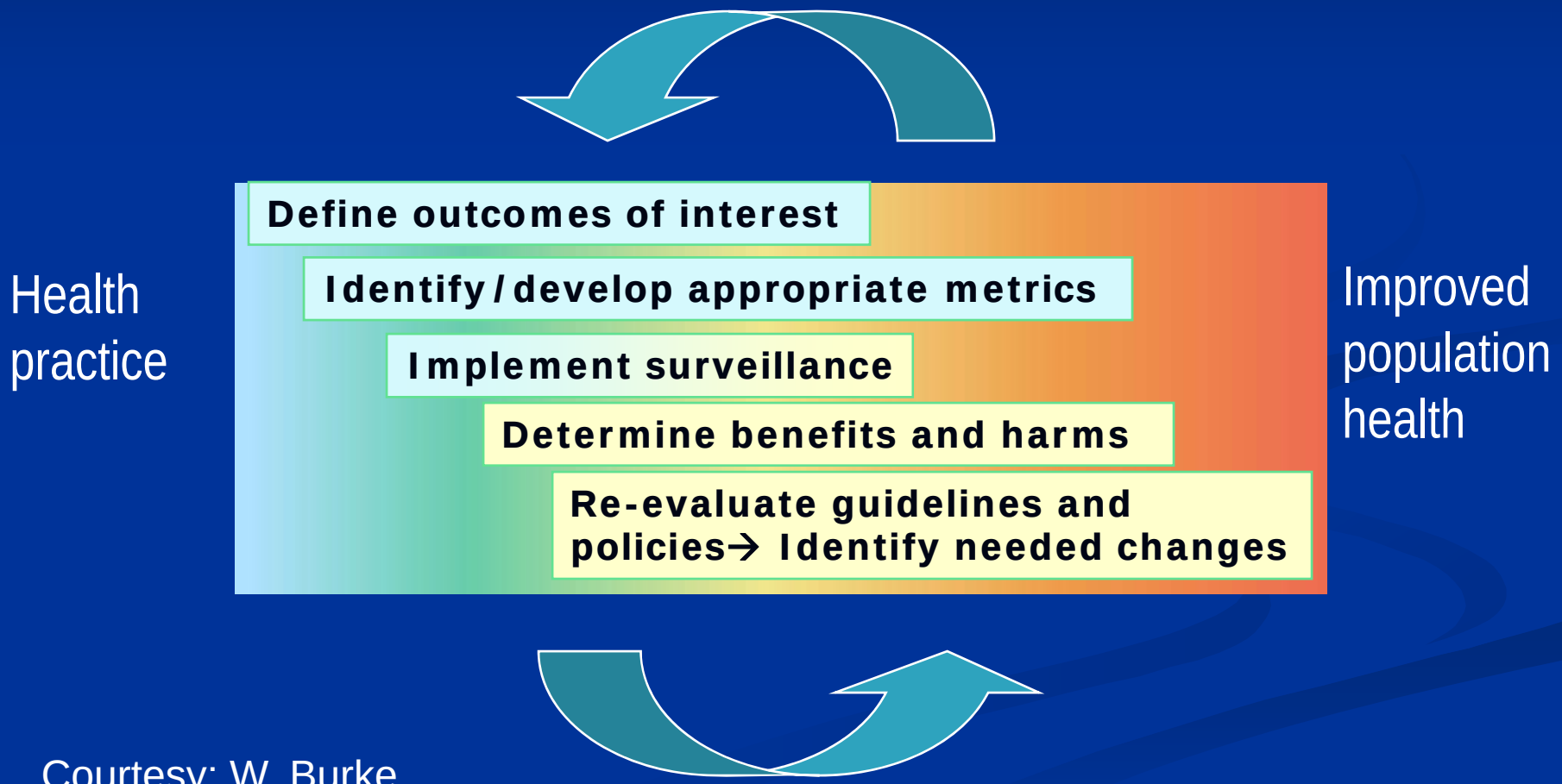


Less than 3% of published genomics research is T2 and beyond

Only 2 USPSTF evidence based guidelines (BRCA1 & HFE)

Khoury MJ et al. Genet Med 2007

T4
Health Practice to Health Impact



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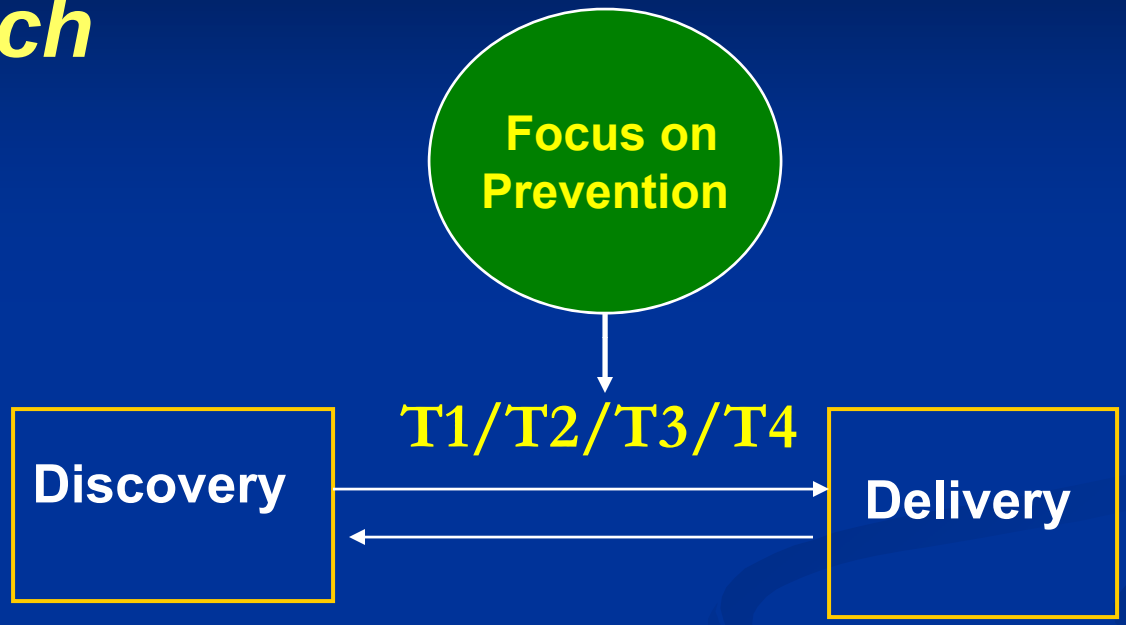
Medicine-Public Health Collaboration in Genomics Translation: A Population Approach



Khoury MJ et al. Am J Prev Med 2007

Gene-Based Medicine in 2010?

Condition	Genes	RR	Lifetime
Prostate Ca	HPC1, 2, 3	0.5	7%
Alzheimer's	APOE,FAD3,XAD	0.3	10%
Heart disease	APOB,CETP	2.5	70%
Colon Cancer	FCC4,APC	4.0	23%
Lung Cancer	NAT2	6.0	40%

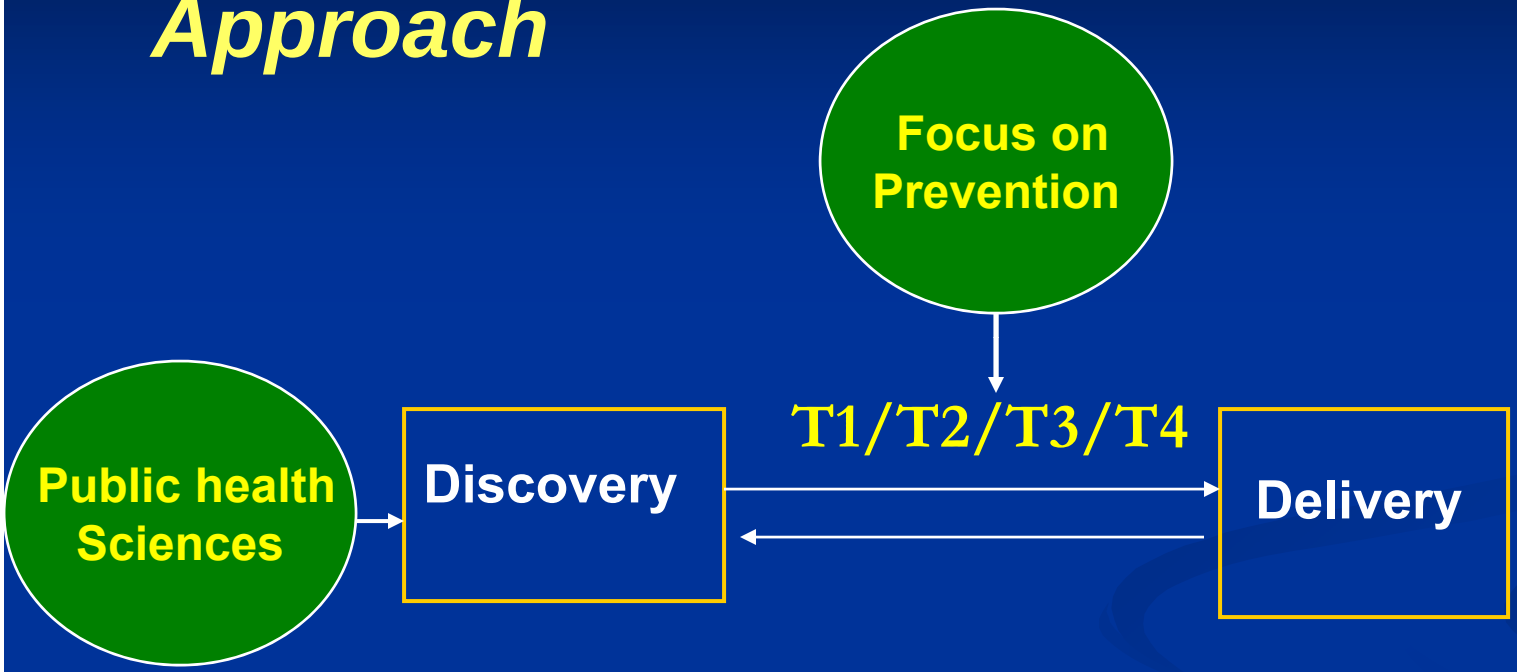
- **(PS. It is happening today but without the Data to Support it!)**

Collins FC, New Engl J Med 1999;341:28-37.

Gene-Based Medicine in 2010?
Prevention Strategies Based on Gene-Environment Interaction

- Increased Risk for
  - Heart disease
  - Colon Cancer
  - Lung Cancer
- Prevention Strategies
  - Tertiary: Cholesterol drugs + Lifestyle changes
  - Secondary: Increased surveillance for early detection
  - Primary: Behavior modification for smoking cessation

Medicine-Public Health Collaboration in Genomics Translation: A Population Approach



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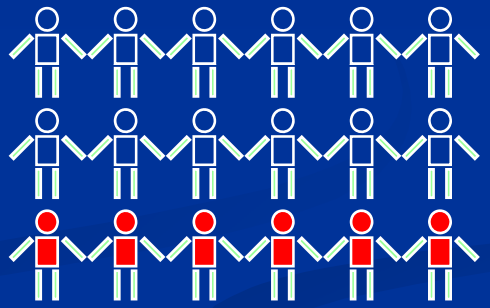
National Profile of Genome Variation

Benefit: Population Data for Health Impact

- NHANES: representative sample of U.S. population



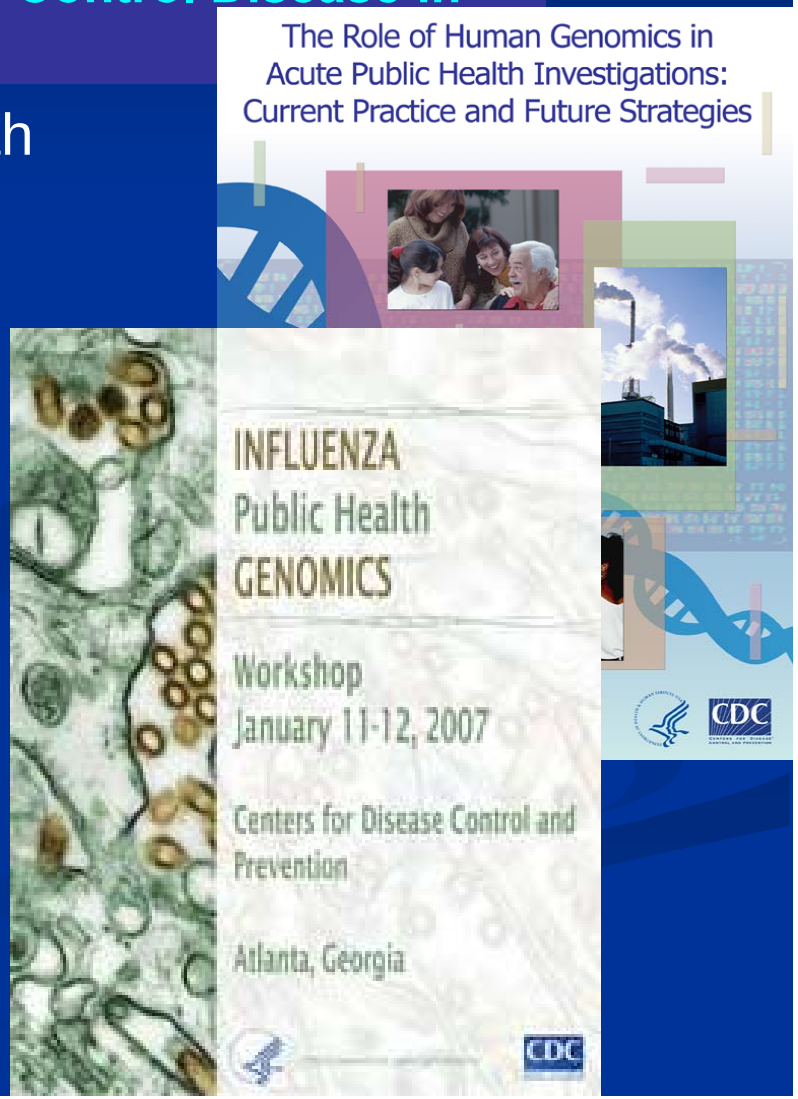
- Needed for research and practice
- Basis for estimating numbers of people at risk and who could benefit from interventions (health impact)

- From studying 100 genetic variants to studying 1,000,000 variants

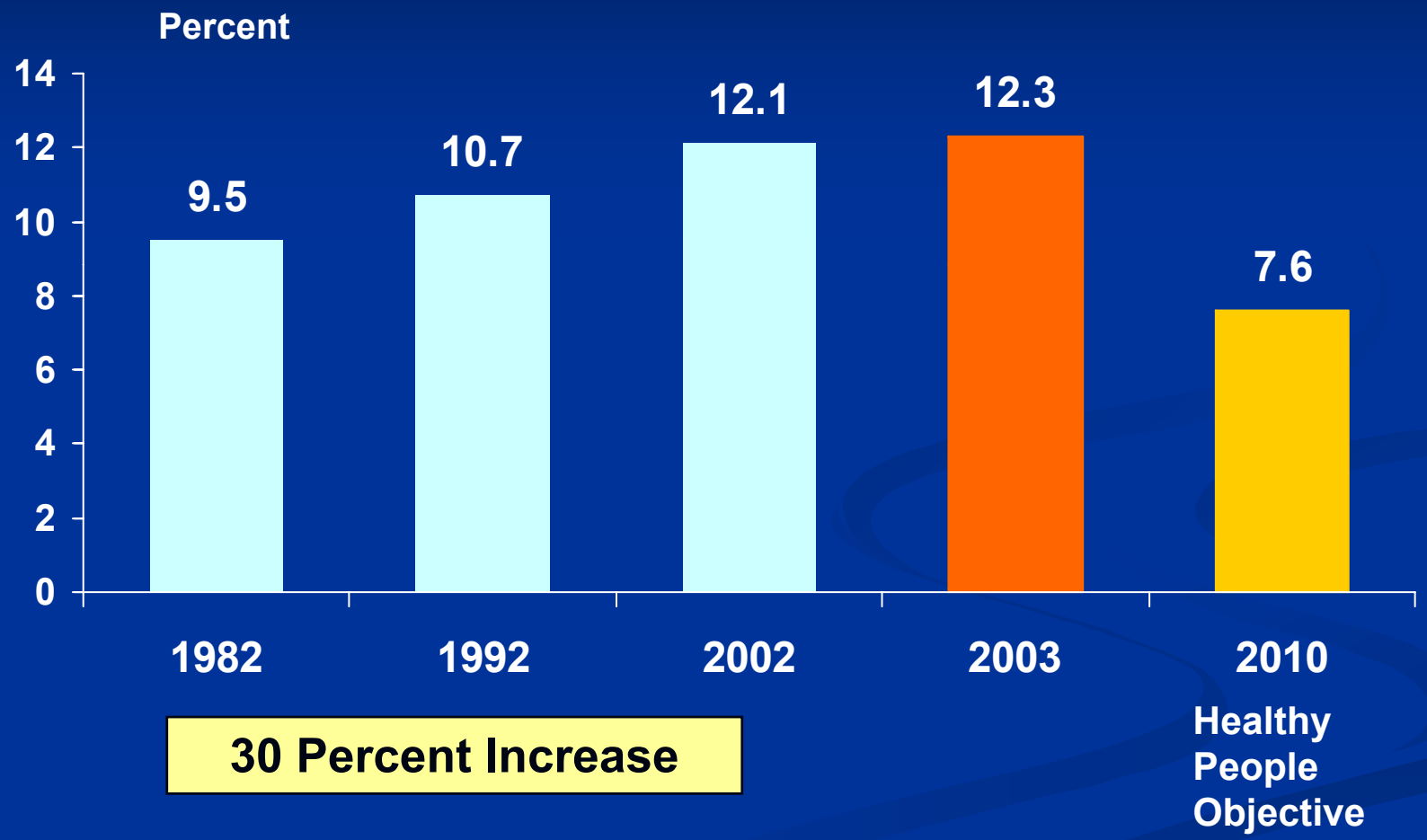
Genomics in Population Investigations

Benefit: Understand, Prevent and Control Disease in Communities

- Pathogen genomics a key public health tool
- Human genomics: susceptibility, vaccine and drug response, adverse effects
- Identify environmental factors for intervention
- Integration across CDC and public health programs

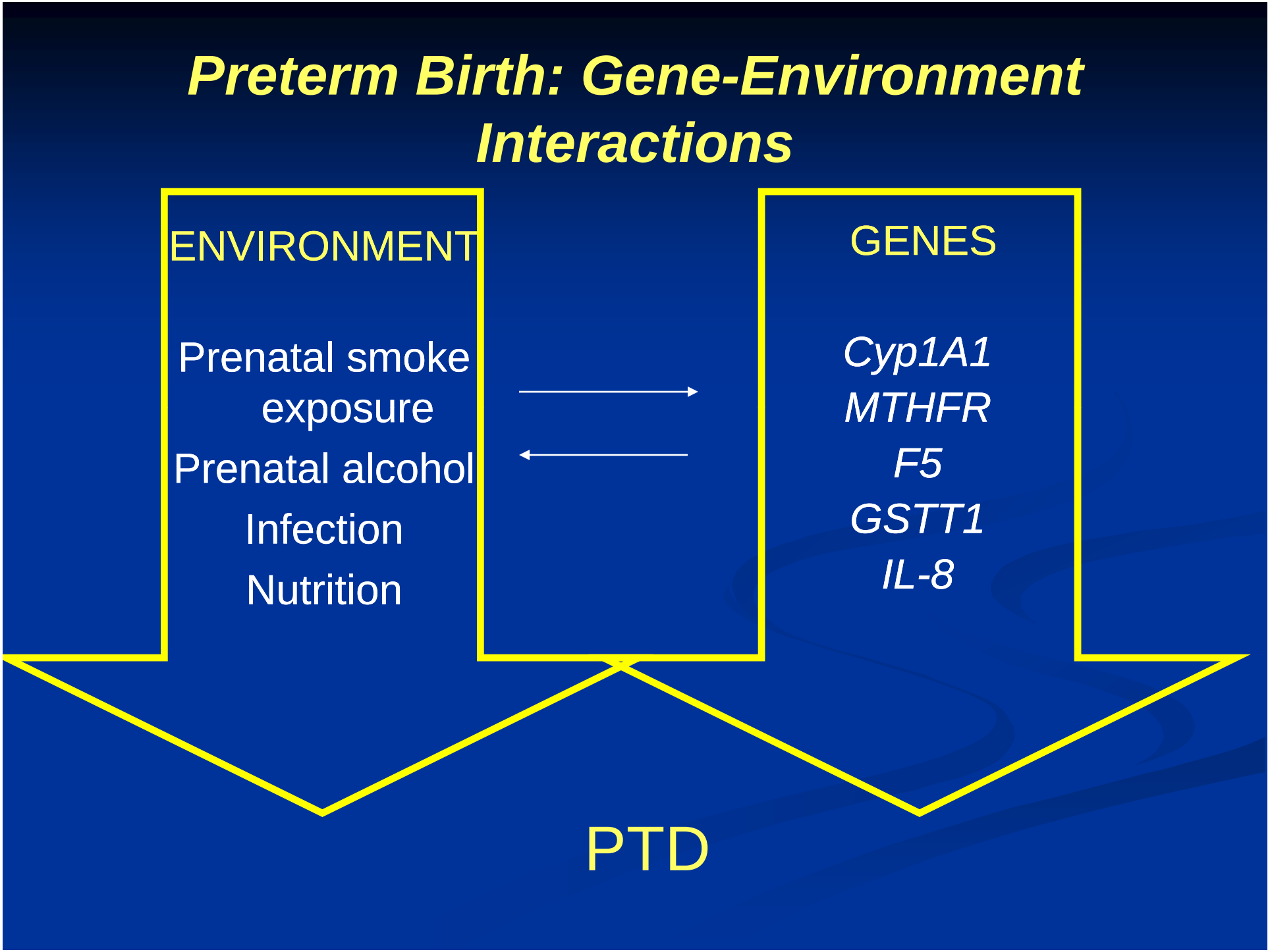


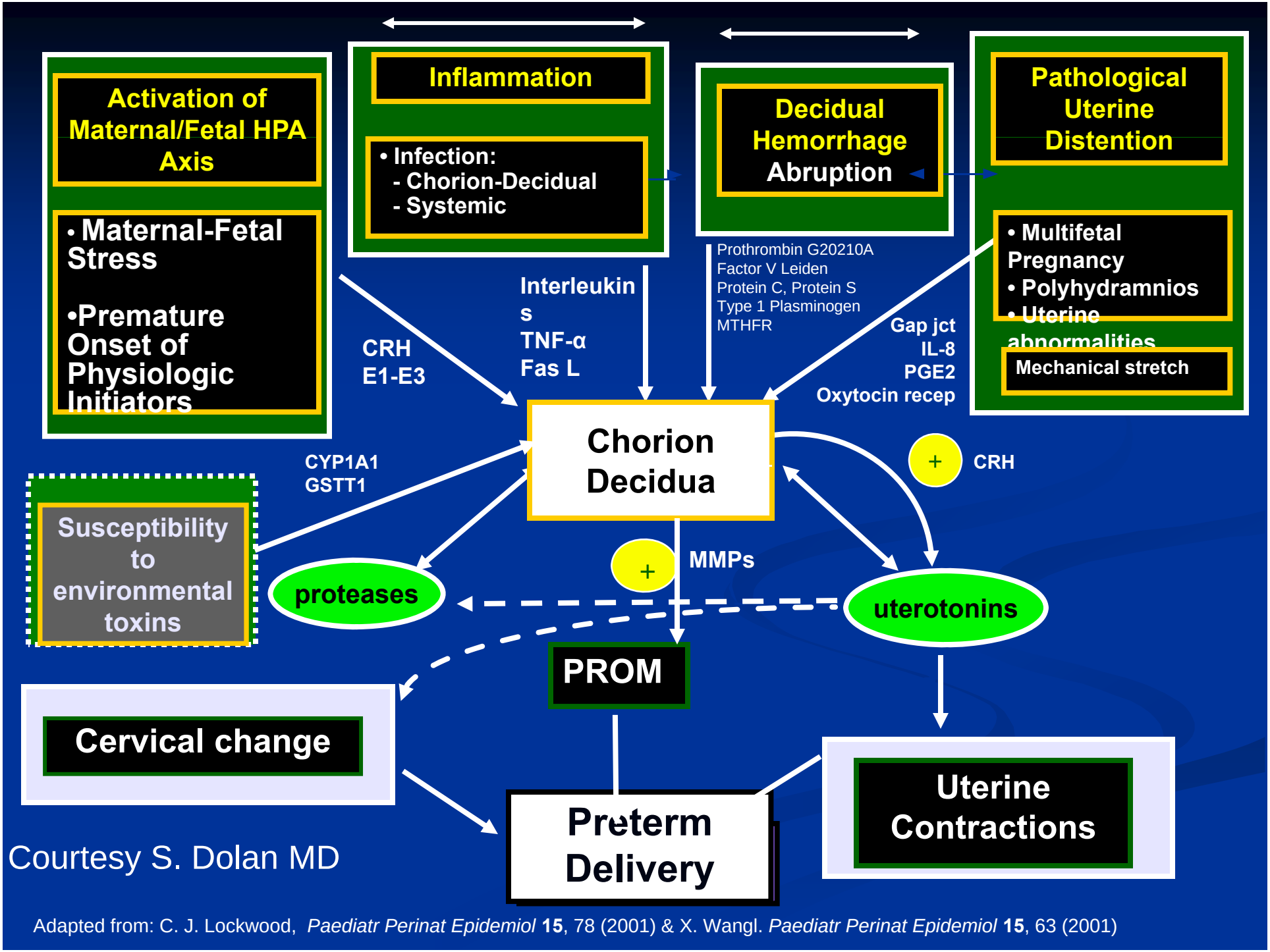
The Increasing Rate of Preterm Birth in the United States



* Preliminary Data, NCHS, 11/23/04.
Preterm is less than 37 completed weeks gestation.
Source: National Center for Health Statistics, final natality data
Prepared by March of Dimes Perinatal Data Center, 2004

Preterm Birth: Gene-Environment Interactions





Adapted from: C. J. Lockwood, *Paediatr Perinat Epidemiol* **15**, 78 (2001) & X. Wangl. *Paediatr Perinat Epidemiol* **15**, 63 (2001)

What Will it Take to Bring Down the Rate of Preterm Birth?

"Successful prevention needs to include newly focused research, incorporating new technologies and recognition that genetic, environmental, social, and behavioral factors interact in complex pathogenesis and multiple pathways leading to PTB."

American Journal of Obstetrics and Gynecology (2005) 193, 626–35

ELSEVIER

American Journal of Obstetrics & Gynecology

www.ajog.org

CLINICAL OPINION

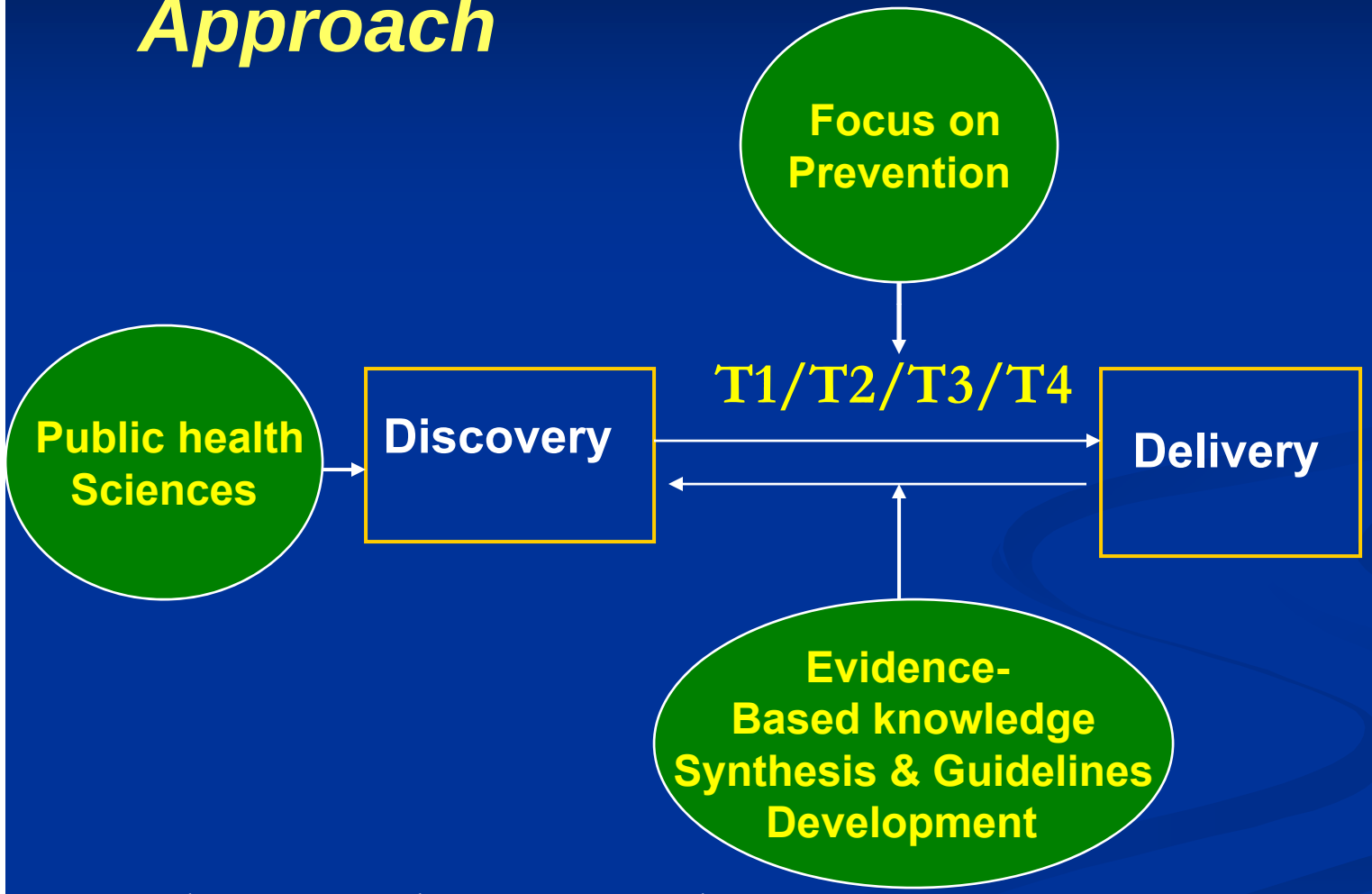
Research agenda for preterm birth: Recommendations from the March of Dimes

Nancy S. Green, MD,[a,b,*] Karla Damus, RN, PhD,[a,c] Joe Leigh Simpson, MD,[d] Jay Iams, MD,[e] E. Albert Reece, MD, PhD, MBA,[f] Calvin J. Hobel, MD,[g] Irwin R. Merkatz, MD,[c] Michael F. Greene, MD,[h] Richard H. Schwarz, MD,[i] and the March of Dimes Scientific Advisory Committee on Prematurity

March of Dimes, White Plains, NY[a]; Departments of Pediatrics and Cell Biology,[b] and Department of Obstetrics & Gynecology and Women's Health,[c] Albert Einstein College of Medicine, Bronx, NY; Department of Obstetrics and Gynecology and Molecular and Human Genetics, Baylor College of Medicine, Houston, TX[d]; Department of Obstetrics and Gynecology, Ohio State University, Columbus, OH[e]; Department of Obstetrics and Gynecology, Dean's Office, University of Arkansas for Medical Sciences, Little Rock, AR[f]; Departments of Obstetrics, Gynecology and Pediatrics, Cedars-Sinai Medical Center, University of California Los Angeles School of Medicine, Los Angeles, CA[g]; Department of Obstetrics and Gynecology and Reproductive Biology, Harvard Medical School, Boston, MA[h]; Department of Obstetrics and Gynecology, Maimonides Medical Center, Brooklyn, NY[i]

Am J Ob Gyn 2005;193:626

Medicine-Public Health Collaboration in Genomics Translation: A Population Approach



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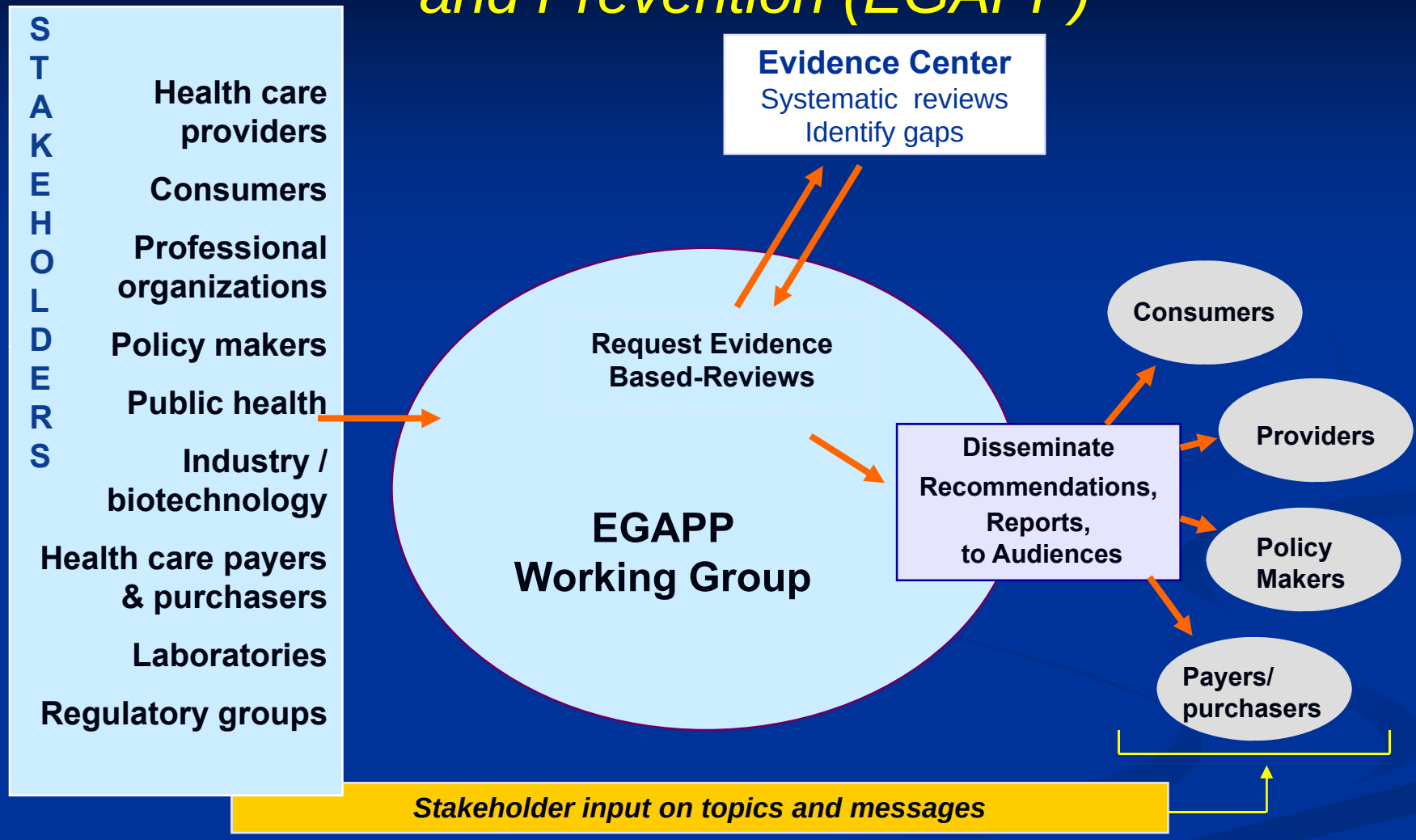
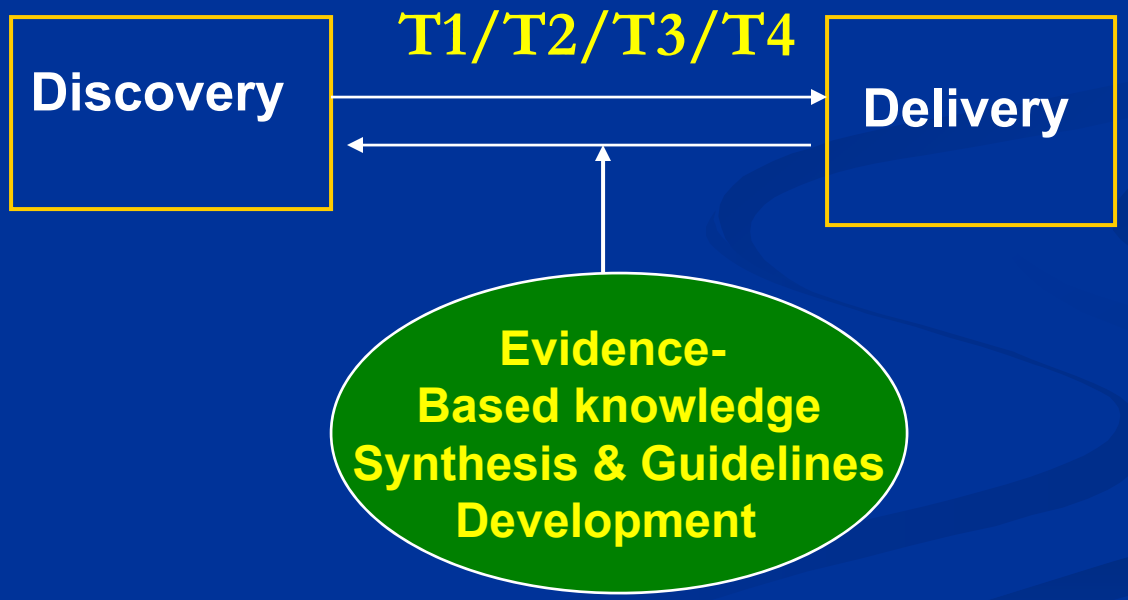
Evaluation of Genomic Applications in Practice and Prevention (EGAPP)



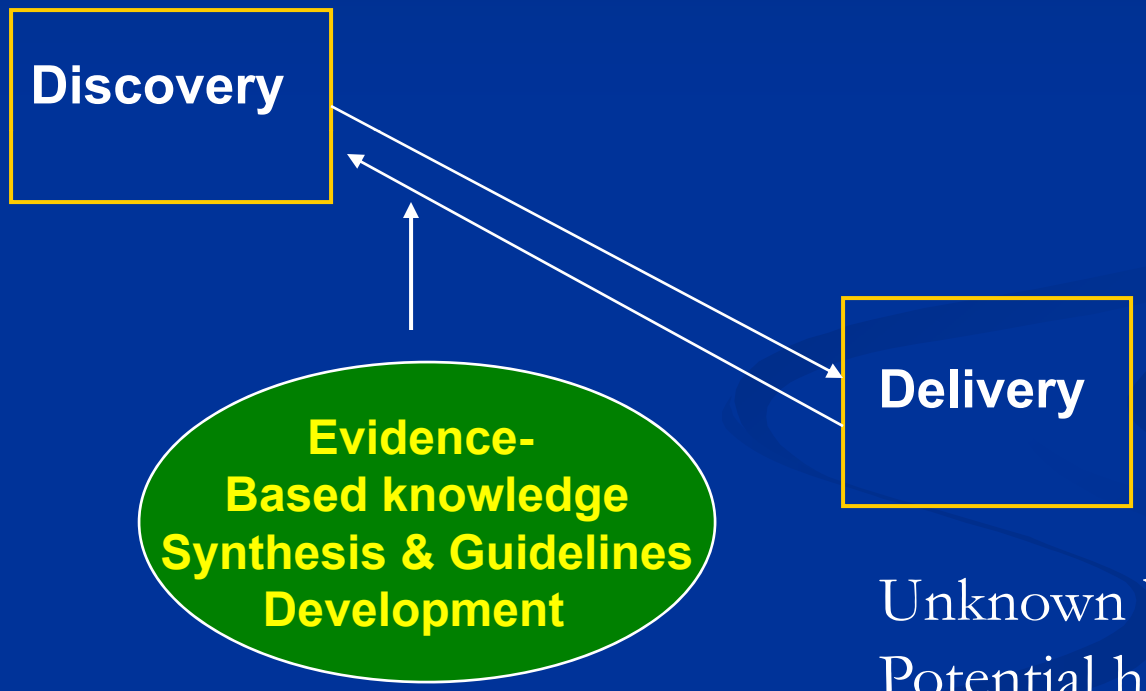
EGAPP Topics 2007

- Proteomic tests for ovarian cancer detection and management
- Hereditary nonpolyposis colorectal cancer (HNPCC) screening
- Cyp450 Polymorphisms testing in adults with depression
- UGT1A1 testing in colorectal cancer patients treated with Irinotecan
- Impact of gene expression profiles on breast cancer outcomes
- Use of genomic profiling to assess cardiovascular risk and identify individualized prevention strategies
- Cyp450 testing to predict response to pain Management with codeine

Genomic Medicine Meets Evidence-Based Medicine: Where is the Right Threshold Between Research and Practice?

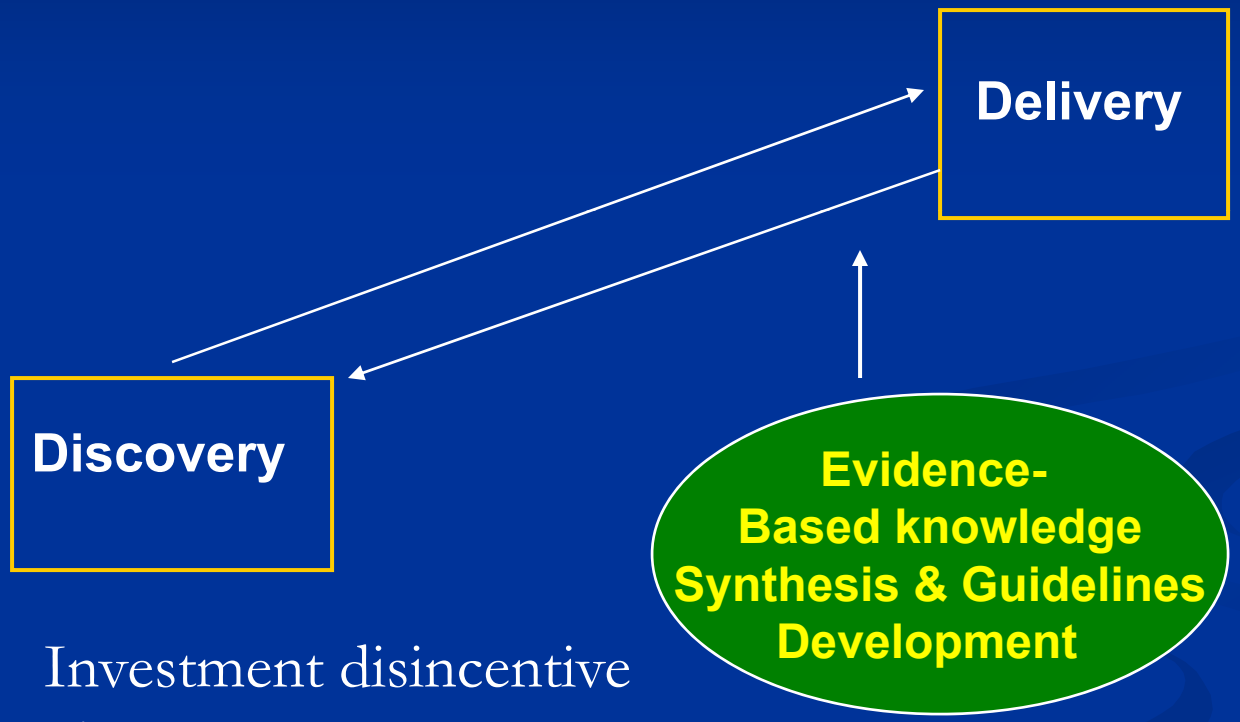


Genomic Medicine Meets Evidence-Based Medicine: Problems with Low Threshold



Unknown benefits
Potential harms
Expensive technologies
Lack of coverage
Disparities

Genomic Medicine Meets Evidence-Based Medicine: Problems with High Threshold

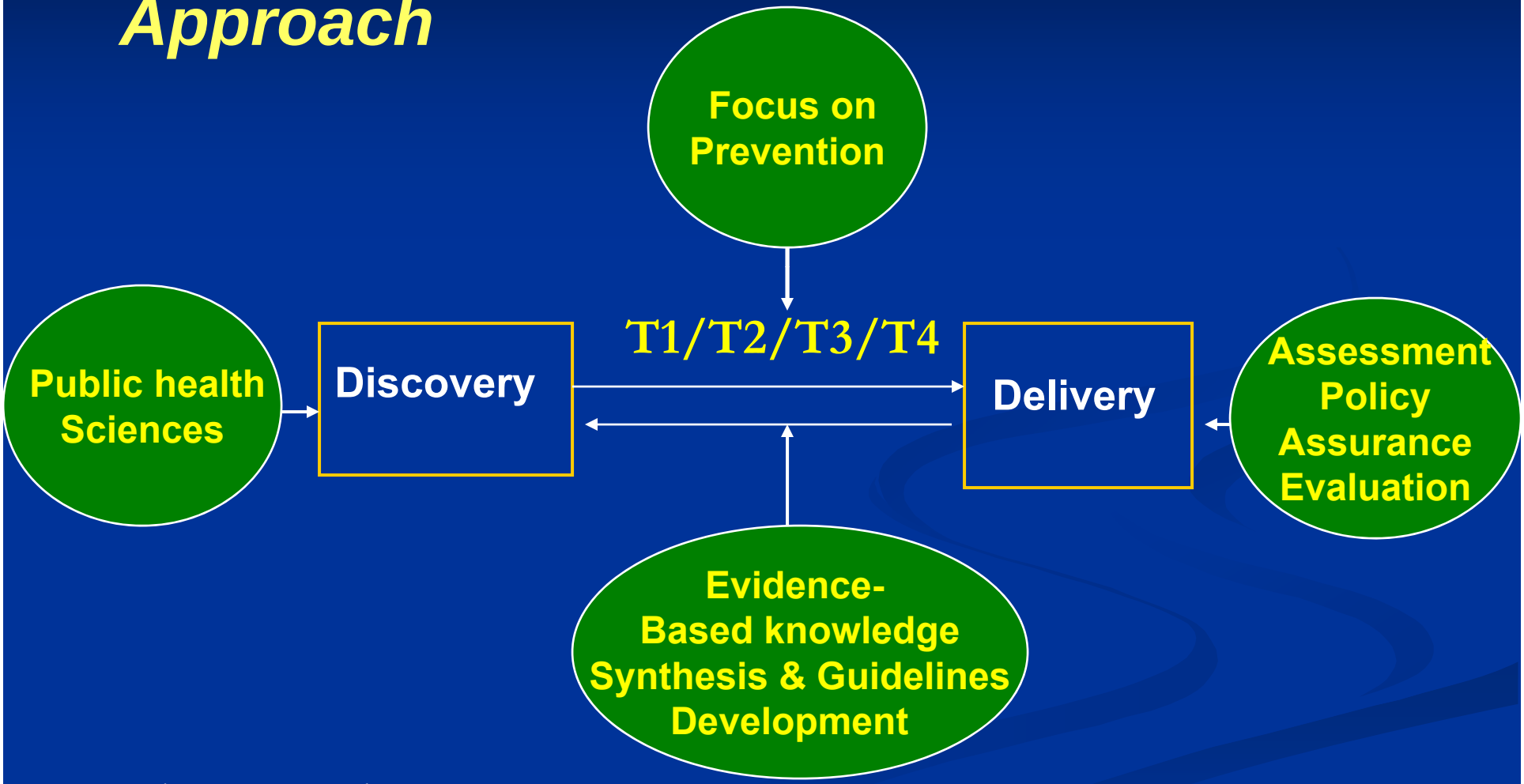


Investment disincentive
Slow integration
Delay access
Lack of coverage
Disparities

Is there a Solution to the Current Evidence Dilemma in Genomic Medicine?

- Explore the concept of “Coverage with Evidence Development (CED)”
- Clinical and public health data collection for certain tests that meet minimal evidentiary standards
- Post market data collection as a prerequisite
- Different thresholds for different types of tests or applications

Medicine-Public Health Collaboration in Genomics Translation: A Population Approach



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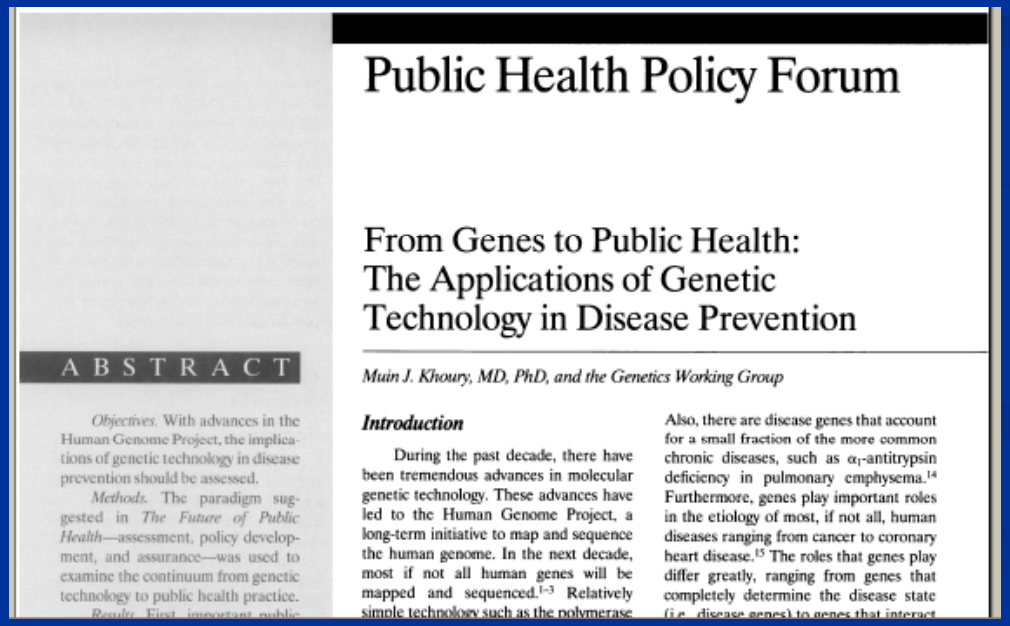
Genomics and Public Health Functions
(Khoury et al, 1996)

- Public Health Functions
  - Assessment
  - Policy Development
  - Assurance



Public Health Policy Forum

From Genes to Public Health: The Applications of Genetic Technology in Disease Prevention

Muin J. Khoury, MD, PhD, and the Genetics Working Group

ABSTRACT

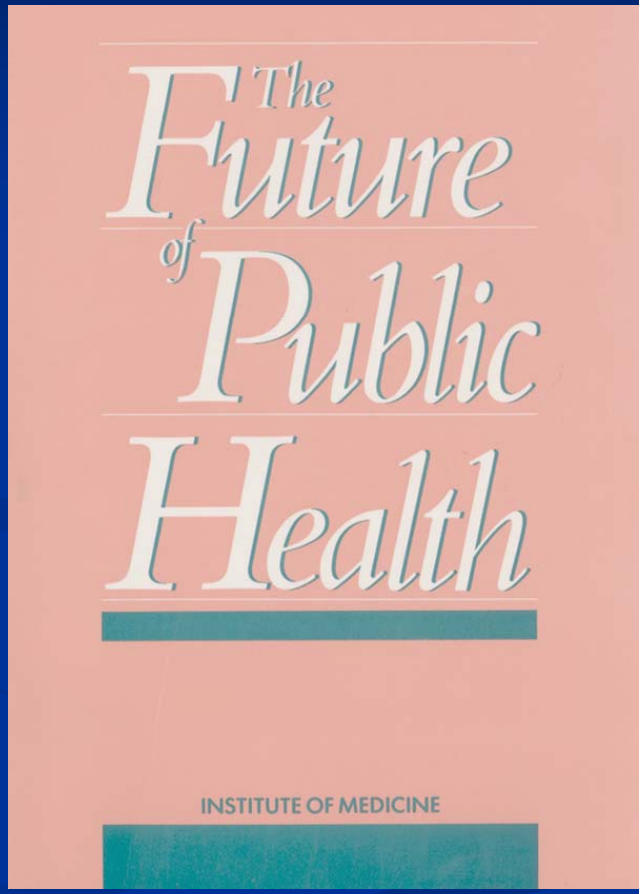
Objectives. With advances in the Human Genome Project, the implications of genetic technology in disease prevention should be assessed.

Methods. The paradigm suggested in *The Future of Public Health*—assessment, policy development, and assurance—was used to examine the continuum from genetic technology to public health practice.

Introduction

During the past decade, there have been tremendous advances in molecular genetic technology. These advances have led to the Human Genome Project, a long-term initiative to map and sequence the human genome. In the next decade, most if not all human genes will be mapped and sequenced.[1–3] Relatively simple technology such as the polymerase

Also, there are disease genes that account for a small fraction of the more common chronic diseases, such as α_1-antitrypsin deficiency in pulmonary emphysema.[14] Furthermore, genes play important roles in the etiology of most, if not all, human diseases ranging from cancer to coronary heart disease.[15] The roles that genes play differ greatly, ranging from genes that completely determine the disease state



Genomics and the Population Health Approach

- ASSURANCE: Ensure that validated genetic information is used to improve health, especially in underserved populations (“Lost in Translation”)

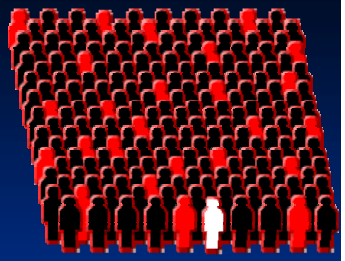
- ASSESSMENT: Provide population level information that can prevent premature and inappropriate use of genetic information through information, guidelines education, policy and legislation (Premature or Inappropriate Translation)

Family History Public Health Initiative

Benefit: Tools for Prevention

- Family history captures shared genes, behaviors, and environment
- Use to target screening, prevention
- CDC tool (6 diseases) & validation study in collaboration with NIH, academic centers
- Partnership with US Surgeon General

Family History is a better Genomic-Environmental Tool than Individual Genetic Risk Factors



	Relative Risk
Heart disease	2.0 – 5.4
Breast cancer	2.1 – 3.9
Colorectal cancer	1.7 – 4.9
Prostate cancer	3.2 – 11.0
Melanoma	2.7 – 4.3
Type II diabetes	2.4 – 4.0
Osteoporosis	2.0 – 2.4
Asthma	3.0 – 7.0

Am J Prev Med - February 2003

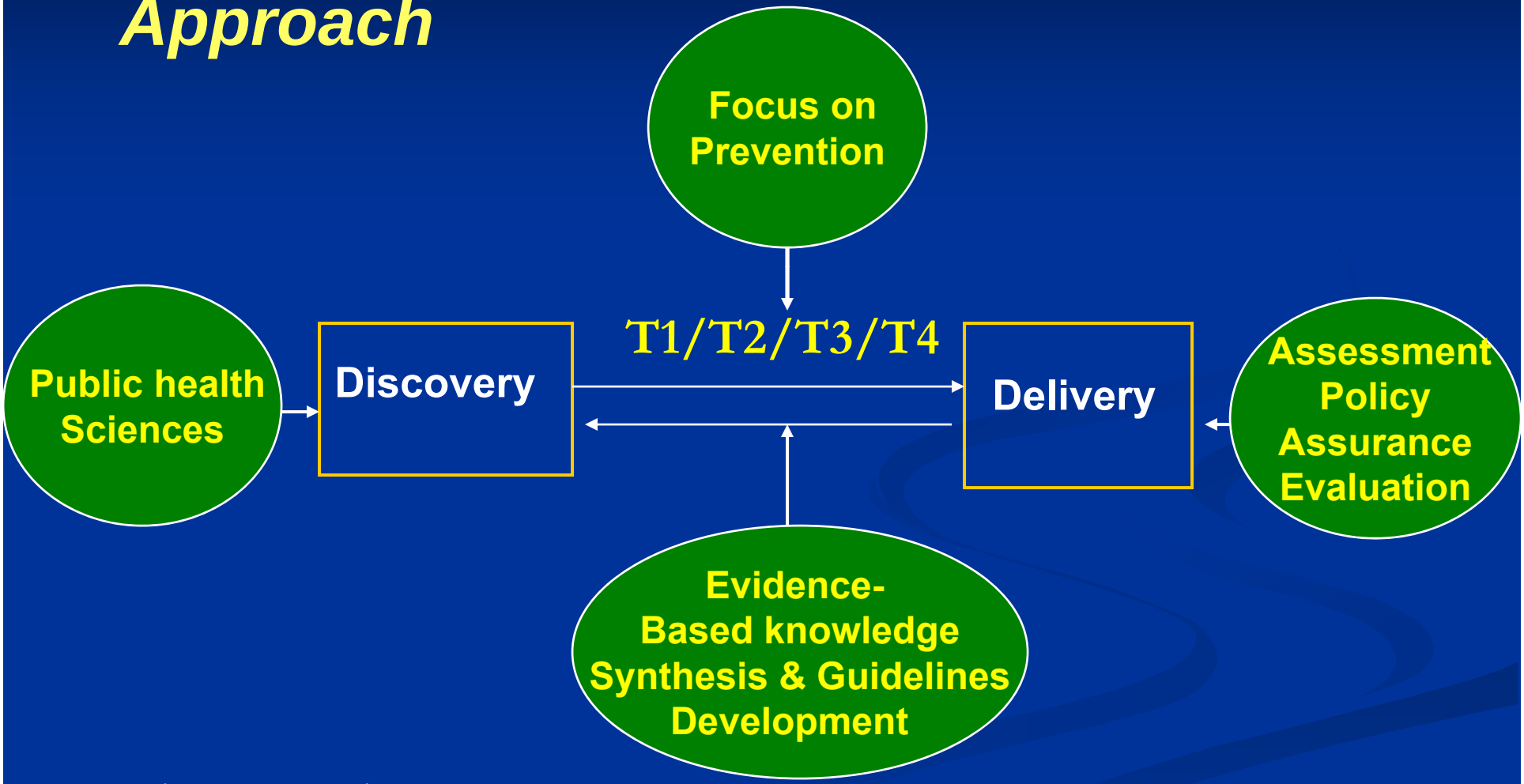
CDC
SAFER·HEALTHIER·PEOPLE

Public Health Surveillance of DTC Genetic Tests

	Oregon	Michigan	Utah	National
Total Sample Size	1867	5499	2441	5250
Awareness of DTC Tests (% Yes, CI)	24.4% [22.2%,26.7%]	7.6% [6.8%,8.4%]	19.7% [17.7%,22%]	14% [12.7%,14.6%]
Use of DTC Tests (% Yes, CI)	0.3%	0.9%	-	0.6% [0.4% - 0.8%]

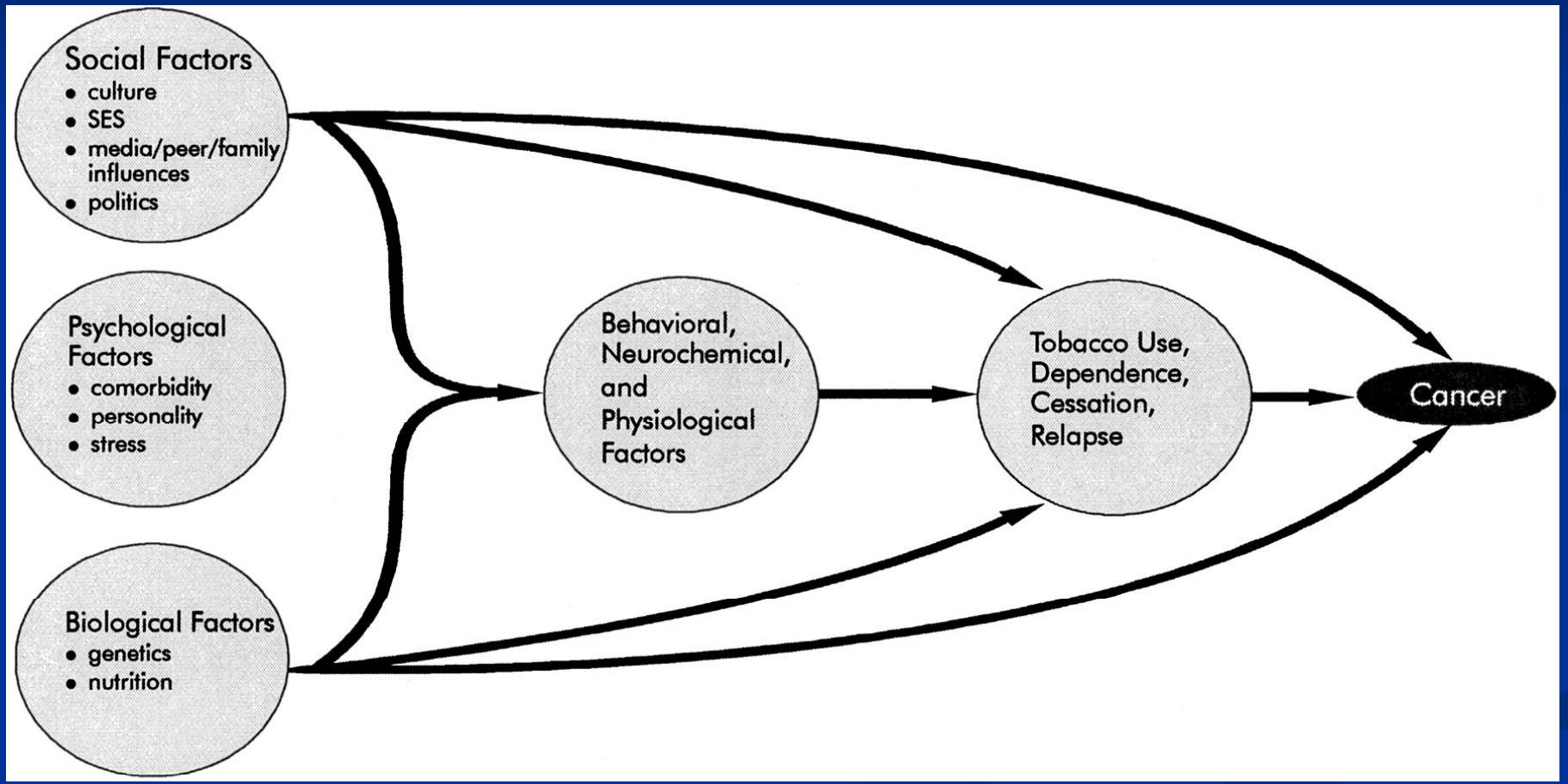
Goddard K et al. Genetics in Medicine 2006

Medicine-Public Health Collaboration in Genomics Translation: A Population Approach



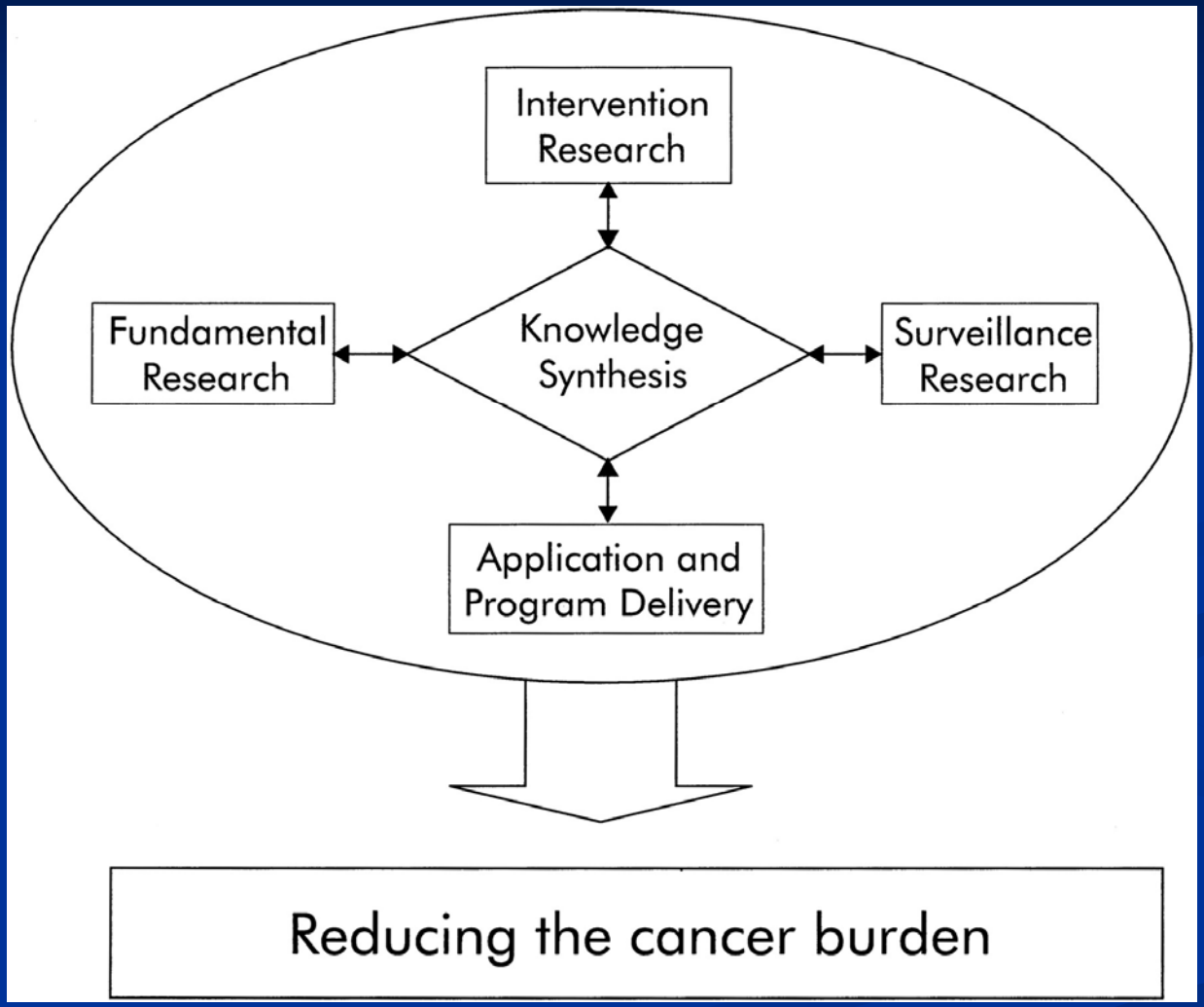
Khoury MJ et al. Am J Prev 2007

A New Strategy for Cancer Control Research Biobehavioral Model for Nicotine Addiction Allowing Interplay Among Numerous Factors



Hiatt, R. A. et al. Cancer Epidemiol Biomarkers Prev 1999;8:957-964

A Framework for Cancer Control Research (from 1994 Advisory Committee on Cancer Control. Canada



Hiatt, R. A. et al. Cancer Epidemiol Biomarkers Prev 1999;8:957-964

Framework for Integrating Genomics and Related Fields into Multidisciplinary Cancer Control: A Population Translation Approach