

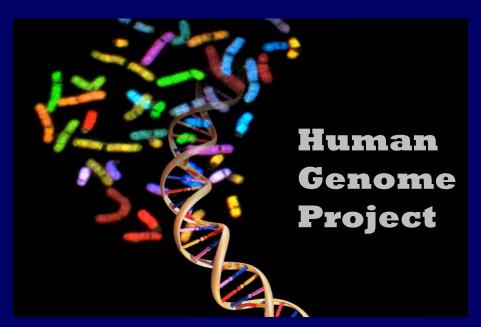
# Genomics and Undiagnosed Disease

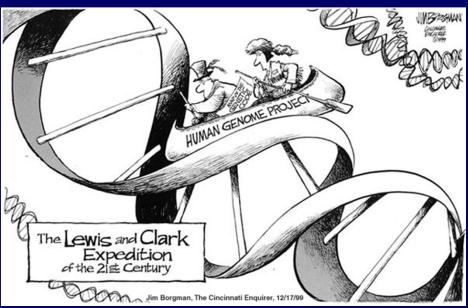


Eric Green, M.D., Ph.D. Director, NHGRI



## ~21 Years Ago

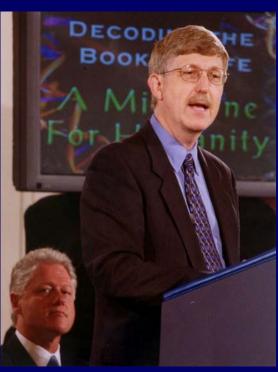


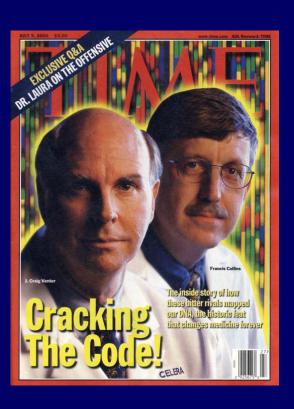


# October 1990 Human Genome Project Begins

## ~11 Years Ago



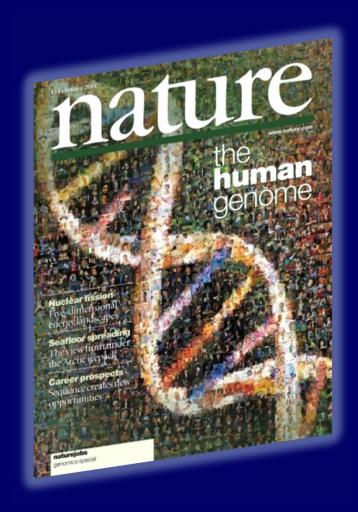




June 2000

Draft Human Genome Sequence Announced

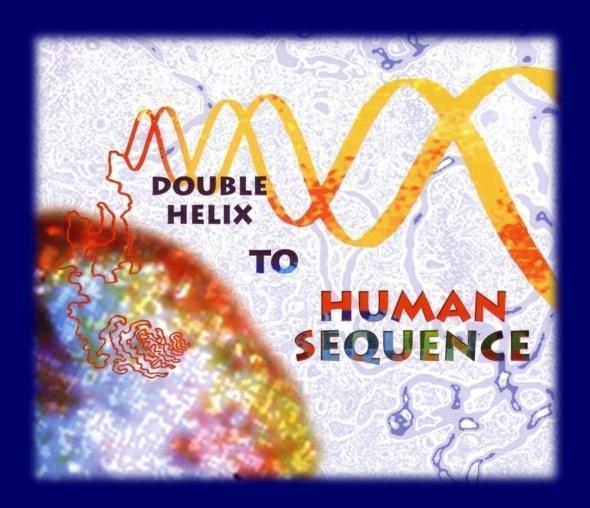
## ~11 Years Ago



February 2001

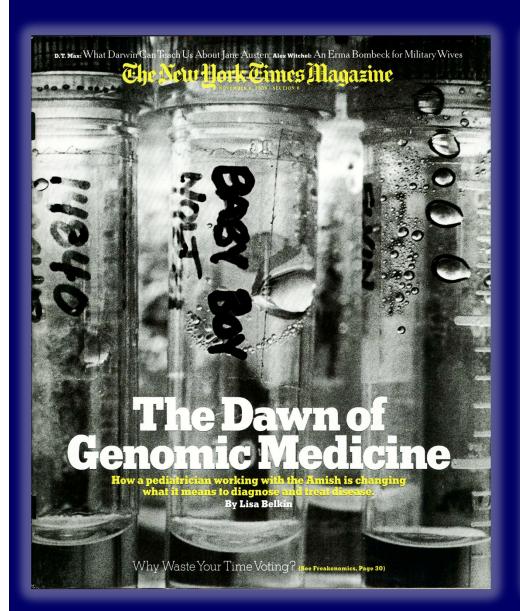
Draft Human Genome Sequence Published

## ~9 Years Ago



April 2003

Human Genome Project Ends





### **Genomic Medicine**

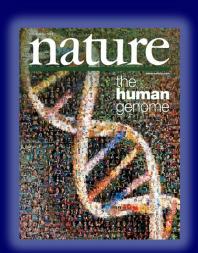
# Healthcare tailored to the individual based on genomic information



















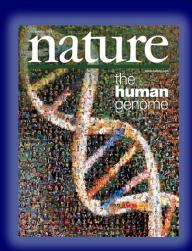
Realization of Genomic Medicine



"Fulfilling the Promise"



Function of the Human Genome Sequence

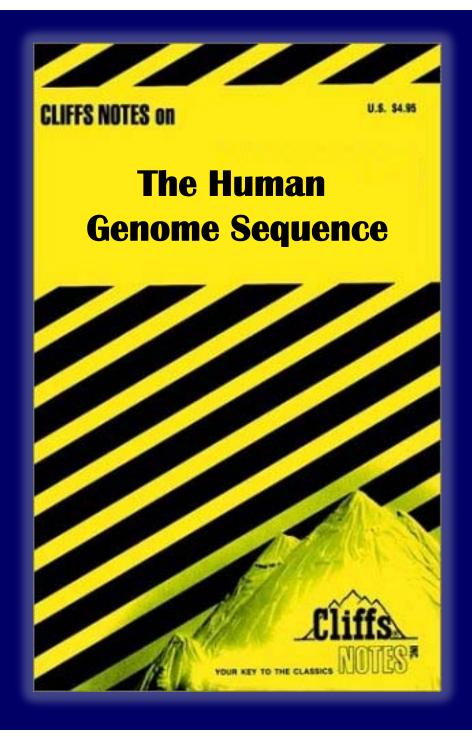


Human Genome Project

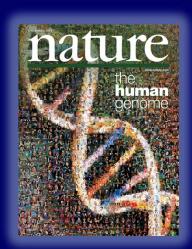


Realization of Genomic Medicine

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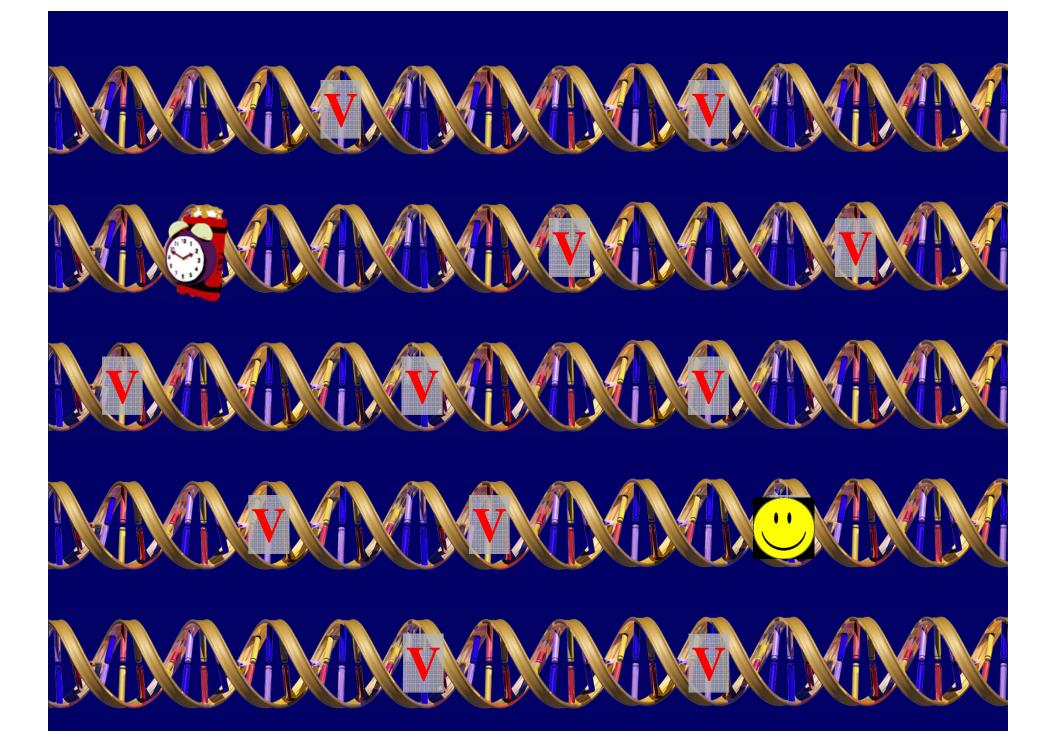
Human Genomic Variation



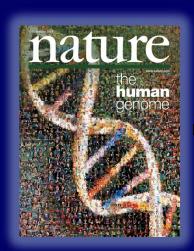
Human Genome Project



Realization of Genomic Medicine



Genomic Basis for Human Diseases

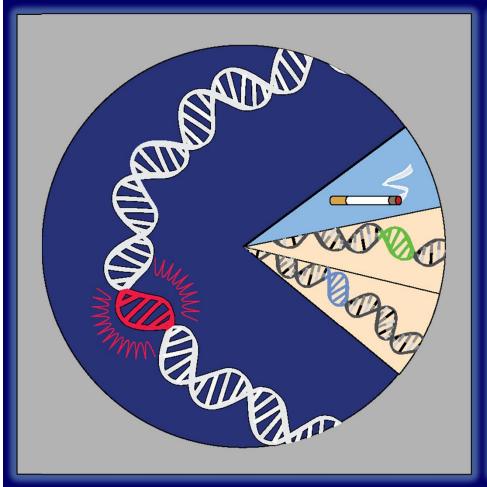


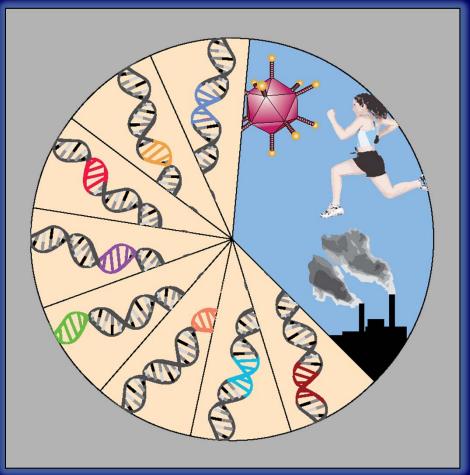
Human Genome Project



Realization of Genomic Medicine

#### **Genomic Architecture of Genetic Diseases**





Rare, Simple, Monogenic, Mendelian...

Common, Complex, Multigenic, Non-Mendelian...

#### **Mendelian Diseases/Traits**

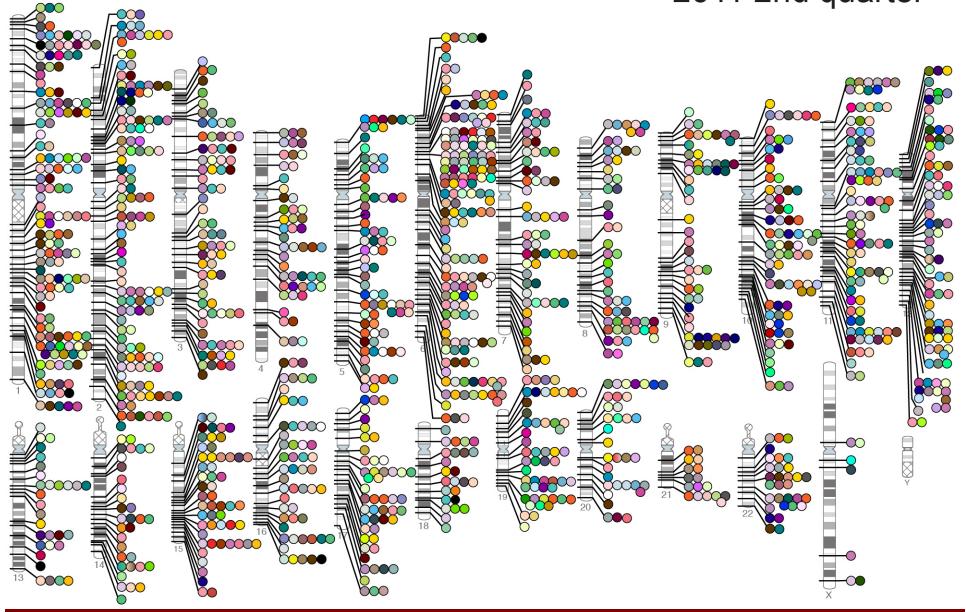
Suspected Mendelian Disease/Trait (~1900)

Molecular Basis Unknown (~1800)

Molecular Basis Known (~3500)

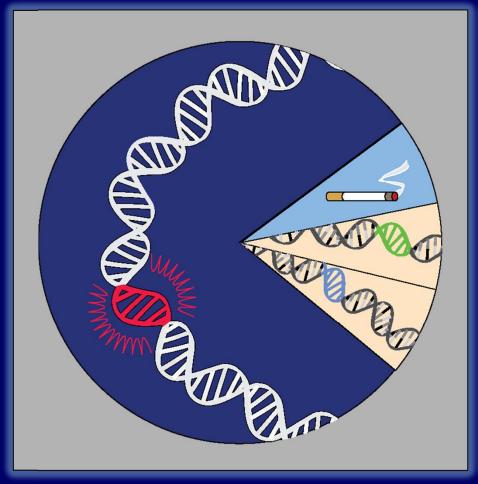
Source: Online Mendelian Inheritance in Man (www.ncbi.nlm.nih.gov/omim)

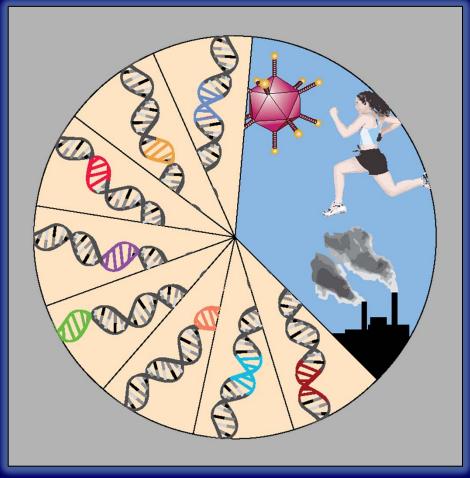
#### 2011 2nd quarter



genome.gov/gwastudies

#### **Genomic Architecture of Genetic Diseases**





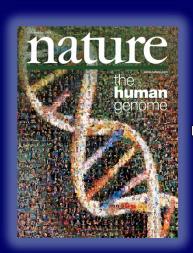
Rare, Simple, Monogenic, Mendelian...

Common, Complex, Multigenic, Non-Mendelian...

**Mostly Coding Mutations** 

**Mostly Non-Coding Mutations** 

Routine Whole-Genome Sequencing



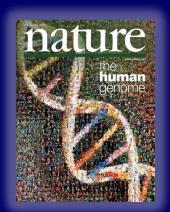
Human Genome Project



Realization of Genomic Medicine

# **Human Genome Sequence**

~\$1,000,000,000





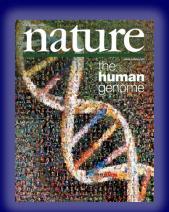
~\$1,000

"The \$1000 Genome"



# **Human Genome Sequence**

~\$1,000,000,000

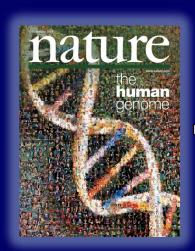




~\$1,000

"The \$1000 Genome"

Routine Analysis of Genome Sequences

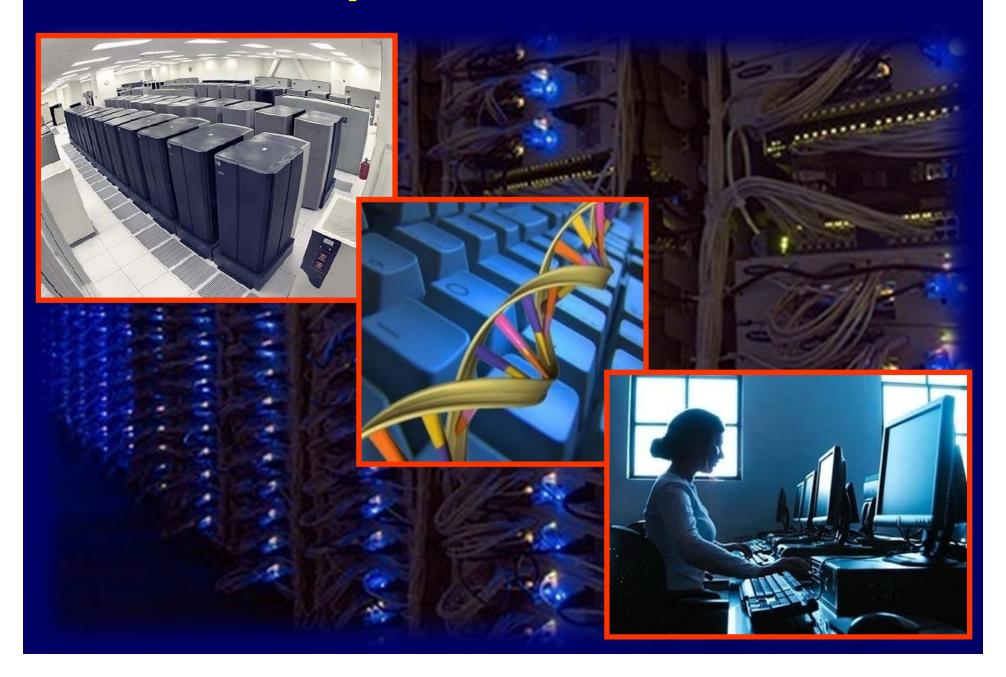


Human Genome Project



Realization of Genomic Medicine

# **The Computational Bottleneck**



#### **The Informational Bottleneck**

GAACCCGACTAGGAT( CGCGAA GGGGTCT CCGCGACTGTCGCCC AGAATCGGGAAAGGG GAAAGCCGCTAGAGC TGTGCGGAGTAGGGG GTCTTTGGCATTAGG TGTCTCCAAACTTTT' TGGGGTAAAGGAATA AGAAGAGATGGAAGA ATGCACTTGTTTTAT' ACACTTGATT TTOTT TTGGGGTAGGTAGAA AAAGCAAATTTGTTG CTGACATTTAATAAA' AATCTTAGGCAAAGT( ATGAATGAATAGGTA TATAAATAGCTCATA' TCCGGTGCTAAGGAG TGATGTTATCCACCT' AAATTA TAGACTTTT GTTCTAAATACTAAT( AATATAGGTTAAAAA **AAAATATTTCATAAG** TTACAAACTTCCTTC' GTGGTAGGCTTTGGA TGTGACTTGACCTTT ATGGATTACCATATT' CTGGATA (GCAATGAC TTTCTATTGTATGTT( TTACAAACTTCCTTC' GTGGTAGGCTTT



GTCTGGCGGACCCTGA TGGACCTAAAGAGAGG AGGGAGGCTGGGAGTC **GTGCGTAGTGGGTGGA** CAAAA GGAAGGGTGG GCACCCAGAGTAGTAG TGGAAAAGGCCAGCGT GTGTATGGGTTGGGTT AAAACAGAAAGCATTA ACTCAAGTACGCTACT CCCCTTCATGCCTTGG TCAGCCAACAAAATT GAT (C) TCAAAAATTG CCGAAGTTATATCCAA TAGCATCTAAGTTCGG TATTATACTGGTGTGA AAAAAGTCAAATATGT CAGTTAATCCTGGAAC AATTATCTTTTTGTGT AAATGTTAATTGGCAT GAATATT (CATGGATA ATCACCTGACACATTT CTCATTTCTGTTCTCC CCTAAAATACCAATGA TTGCTTAGTTTTCAAA CCTTAACATCTCTGTG GTT----CTATTATT TTTTGTGACTCTCAAT GGAAACACGTCACATG AAAATTATTATGGTAT TTGCTTAGTTTTCAAA CCTTAL CATCTCTGTG

#### Ten Years On — The Human Genome and Medicine

Harold Varmus, M.D.

the United States and the United Kingdom, accom- fected the health care of most individuals."2 panied by the leaders of the public and private teams deciphering the human genome, announced of articles on genomic medicine.3 Is it approprithat a draft sequence had been completed. That ate for the Journal to be taking stock so soon? It occasion was rich with promises of new and more is, and for the following reasons. powerful ways to understand, diagnose, prevent,

On a June day nearly 10 years ago, the leaders of Human Genome Project has not yet directly af-

In this issue, the Journal begins another series

First, readers will want to know the state of

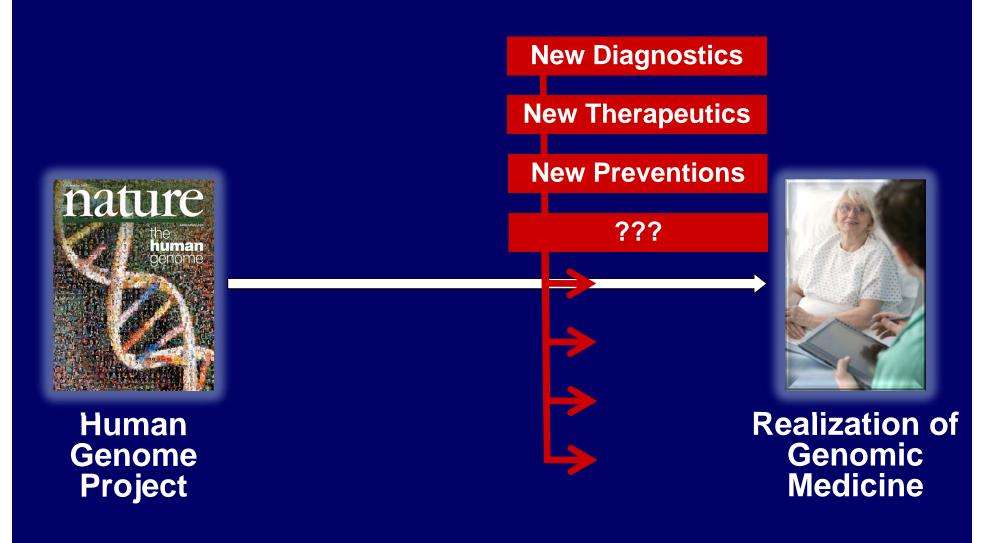
Physicians are still a long way from submitting their patients' full genomes for sequencing, not because the price is high, but because the data are difficult to interpret.

some strong genetic markers for assessing drug influential haplotypes, and in general, other imresponsiveness, risk of disease, or risk of disease progression — have entered routine medical practice. And most of these can be traced to discoveries that preceded the unveiling of the human genome. As Francis Collins, formerly the leader of the publicly funded sequencing efforts, recently commented: "the consequences for clinical medi-

plicated susceptibility haplotypes collectively account for only a small fraction of the apparent heritable risk. Clearly, more than one decade of genomics will be required to understand the inborn risks of most common disorders, such as diabetes and hypertension.

Second, readers will enjoy learning from these cine . . . have thus far been modest . . . the articles how rapidly the engines of genomics and

N ENGL J MED 362;21 NEJM.ORG MAY 27, 2010





# ~11 Months Ago



#### **PERSPECTIVE**

doi:10.1038/nature09764

#### Charting a course for genomic medicine from base pairs to bedside

Eric D. Green<sup>1</sup>, Mark S. Guyer<sup>1</sup> & National Human Genome Research Institute<sup>4</sup>

There has been much progress in genomics in the ten years since a draft sequence of the human genome was published. Opportunities for understanding health and disease are now unprecedented, as advances in genomics are harnessed to obtain robust foundational knowledge about the structure and function of the human genome and about the genetic contributions to human health and disease. Here we articulate a 2011 vision for the future of genomics research and describe the path towards an era of genomic medicine

ince the end of the Human Genome Project (HGP) in 2003 and the quickly. Although genomics has already begun to improve diagnostics publication of a reference human genome sequence<sup>12</sup>, genomics has a milestry of a reference human genome sequence<sup>12</sup>, genomics has an an interaction of a reference human genome sequence<sup>12</sup>, genomics has a milestry of himself and the attended in the second of the se become a mainstay of biomedical research. The scientific commu-(see rollfold). Optimism about the potential contributions of genomics for improving human health has been fuelled by new insights about cancer<sup>4-7</sup>, the molecular basis of inherited diseases (http://www.ncbi.nlm.nih.gov/ omim and http://www.genome.gov/GWAStudies) and the role of structural variation in disease<sup>8</sup>, some of which have already led to new therapies<sup>9-15</sup>. Other advances have already changed medical practice (for example, microarrays are now used for dinical detection of genomic imbalances and pharmacogenomic testing is routinely performed before administration of certain medications 15). Together, these achievements (see accompanying paper16) document that genomics is contributing to a better understanding nan biology and to improving human health.

As it did eight years ago<sup>17</sup>, the National Human Genome Research Institute (NHGRI) has engaged the scientific community (http://www. genome.gov/Planning) to reflect on the key attributes of genomics (Box 1) and explore future directions and challenges for the field. These discussions have led to an updated vision that focuses on understanding human biology and the diagnosis, prevention and treatment of human disease including consideration of the implications of those advances for society (but these discussions, intentionally did not address the role of genomics in agriculture, energy and other areas). Like the HGP, achieving this vision is broader than what any single organization or country can achieve realizing the full benefits of genomics will be a global effort.

This 2011 vision for genomics is organized around five domains extendng from basic research to health applications (Fig. 2). It reflects the view that, over time, the most effective way to improve human health is to understand normal biology (in this case, genome biology) as a basis for understanding disease biology, which then becomes the basis for improving health. At the same time, there are other connections among these domains. Genomics offers opportunities for improving health without a thorough understanding of disease (for example, cancer therapies can be selected based on genomic profiles that identify tumour subtypes 18,19), and clinical discoveries can lead back to understanding disease or even basic biology.

The past decade has seen genomics contribute fundamental knowledge about biology and its perturbation in disease. Further deepening this

effectiveness of healthcare cannot realistically be expected for many years nity's foresight in launching this ambitious project' is evident in the broad (Fig. 2). Achieving such progress will depend not only on research, but range of scientific advances that the HGP has enabled, as shown in Fig. 1 strated the kinds of achievements that can be anticipated with a few examples (Box 2) where a confluence of need and opportunities should lead to major accomplishments in genomic medicine in the coming decade. Similarly, we note three cross-cutting areas that are broadly relevant and fundamental across the entire spectrum of genomics and genomic medicine: bioinformatics and computational biology (Box 3), education and training (Box 4), and genomics and society (Box 5).

#### Understanding the biology of genomes

Substantial progress in understanding the structure of genomes has revealed much about the complexity of genome biology. Continued acquisition of basic knowledge about genome structure and function will be needed to illuminate further those complexities (Fig. 2). The contri bution of genomics will include more comprehensive sets (catalogues) of data and new research tools, which will enhance the capabilities of all researchers to reveal fundamental principles of biology

#### Comprehensive catalogues of genomic data

Comprehensive genomic catalogues have been uniquely valuable and widely used. There is a compelling need to improve existing catalogues and to generate new ones, such as complete collections of genetic variation functional genomic elements, RNAs, proteins, and other biological molecules, for both human and model organisms

Genomic studies of the genes and pathways associated with disease related traits require comprehensive catalogues of genetic variation, which provide both genetic markers for association studies and variants for identifying candidate genes. Developing a detailed catalogue of variation in the human genome has been an international effort that began with The SNP Consortium<sup>20</sup> and the International HapMap Project<sup>21</sup> (http://hapmap. nchi.nlm.nih.gov), and is ongoing with the 1000 Genomes Project2 (http://www.1000genomes.org).

Over the past decade, these catalogues have been critical in the discovery of the specific genes for roughly 3,000 Mendelian (monogenic) disease

understanding will accelerate the transition to genomic medicine (clinical care based on genomic information). But significant change rarely comes

<sup>1</sup>National Human Genome Research Institute, National Institutes of Health, 31 Center Dr., Bethesda, Maryland 20892-2152, USA \*Usts of participants and their affiliations appear at the end of the paper.

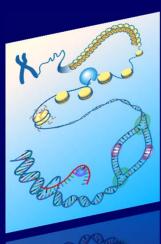
February 2011 NHGRI Published New Vision for Genomics

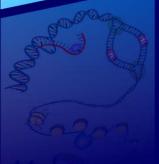
# **Five Domains of Genomics Research**

Understanding the Structure of Genomes Understanding the Biology of Genomes Understanding the Biology of Disease

Advancing the Science of Medicine Improving the Effectiveness of Healthcare













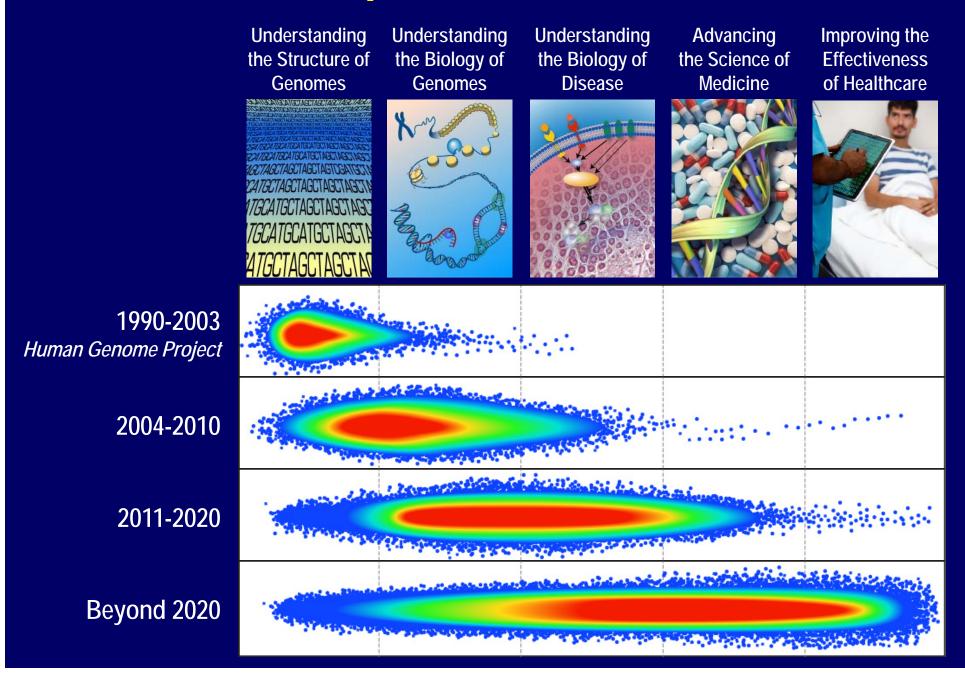


**Base Pairs to Bedside** 



**Helix to Health** 

#### **Genomic Accomplishments Across Domains**



### 2011 NHGRI Strategic Plan for Genomics

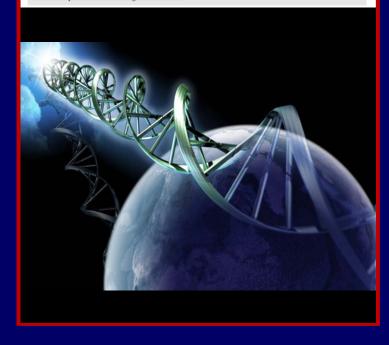


doi:10.1038/nature0976

#### Charting a course for genomic medicine from base pairs to bedside

Eric D. Green<sup>1</sup>, Mark S. Guyer<sup>1</sup> & National Human Genome Research Institute\*

There has been much progress in genomics in the ten years since a draft sequence of the human genome was published. Opportunities for understanding health and disease are now unprecedented, as advances in genomics are harnessed to obtain robust foundational knowledge about the structure and function of the human genome and about the genetic contributions to human health and disease. Here we articulate a 2011 vision for the future of genomics research and describe the path towards an era of genomic medicine.





#### ROY 2

#### Imperatives for genomic medicine



Opportunities for genomic medicine will come from simultaneously acquiring foundational knowledge of genome function, insights into disease biology and powerful genomic tools. The following imperatives will capitalize on these opportunities in the coming decade.

Making genomics-based diagnostics routine. Genomic technology

development so far has been driven by the research market. In the next decade, technology advances could enable a clinician to acquire a complete genomic diagnostic panel (including genomic, epigenomic, transcriptomic and microbiomic analyses) as routinely as a blood chemistry panel.

Defining the genetic components of disease. All diseases involve a genetic component. Genome sequencing could be used to determine the genetic variation underlying the full spectrum of diseases, from rare Mendelian to common complex disorders, through the study of upwards of a million patients; efforts should begin now to organize the necessary sample collections.

Comprehensive characterization of cancer genomes. A comprehensive genomic view of all cancers<sup>4–7</sup> will reveal molecular taxonomies and altered pathways for each cancer subtype. Such information should lead to more robust diagnostic and therapeutic strategies and a roadmap for developing new treatments<sup>74,75</sup>.

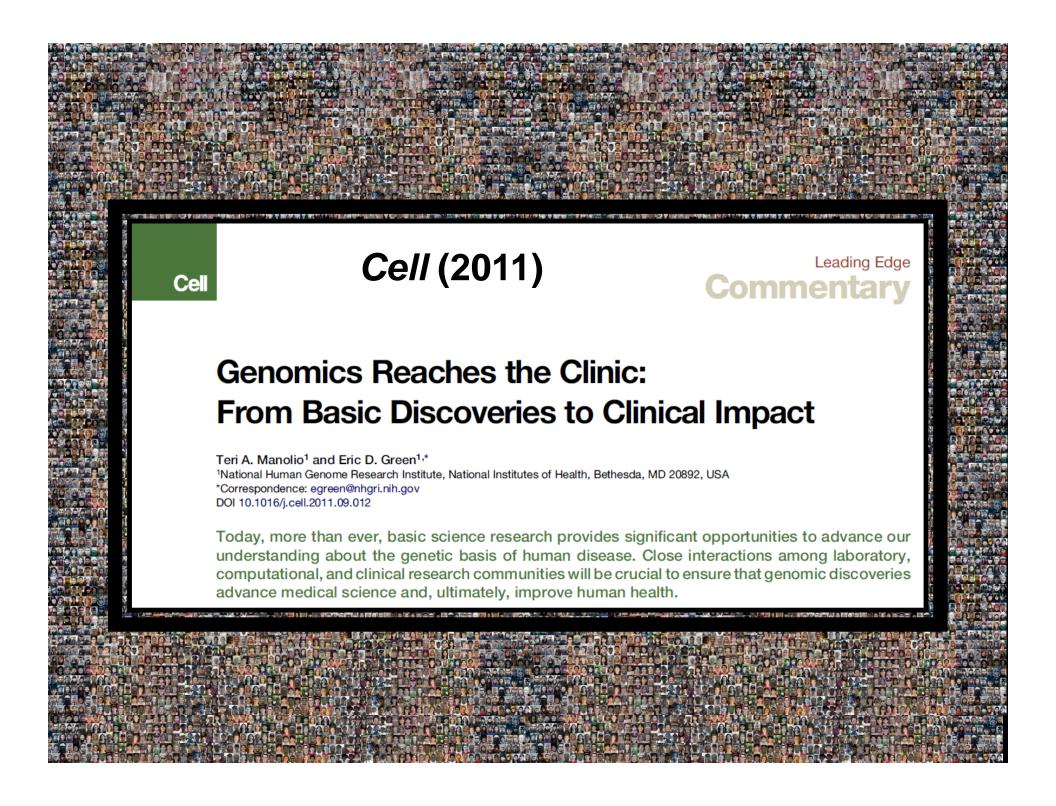
Practical systems for clinical genomic informatics. Thousands of genomic variants associated with disease risk and treatment response are known, and many more will be discovered. New models for capturing and displaying these variants and their phenotypic consequences should be developed and incorporated into practical systems that make information available to patients and their healthcare providers, so that they can interpret and reinterpret the data as knowledge evolves.

The role of the human microbiome in health and disease. Many diseases are influenced by the microbial communities that inhabit our bodies (the microbiome)<sup>101</sup>. Recent initiatives<sup>102,103</sup> (http://www.human-microbiome.org) are using new sequencing technologies to catalogue the resident microflora at distinct body sites, and studying correlations between specific diseases and the composition of the microbiome<sup>104</sup>. More extensive studies are needed to build on these first revelations and to investigate approaches for manipulating the microbiome as a new therapeutic approach.

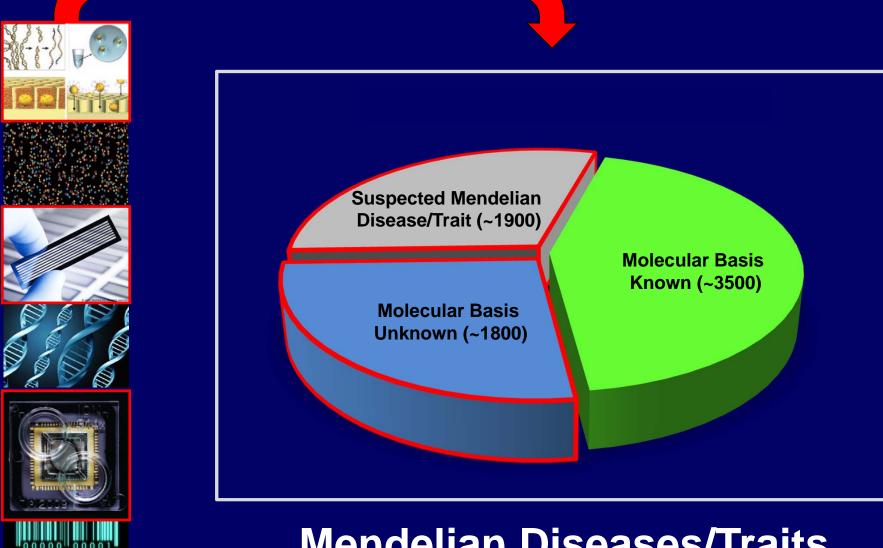








#### The Future: Genome Sequencing

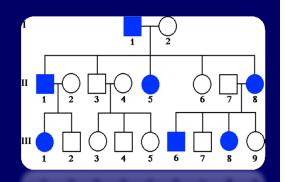


**Mendelian Diseases/Traits** 

#### **Mendelian Disorders Genome Centers**

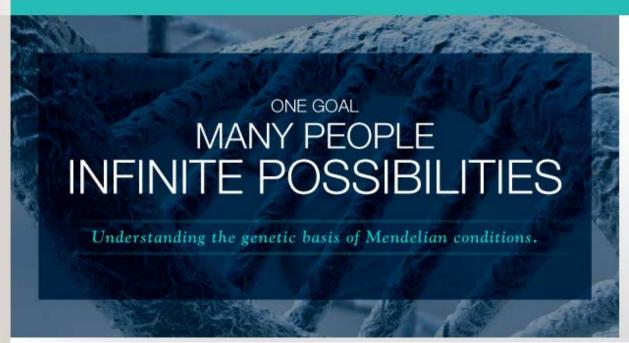
- Discover genetic basis of as many Mendelian disorders as possible (sample solicitation, sequencing, and data analysis)
- Establish and disseminate study designs and methods for the elucidation of the genetic basis of Mendelian phenotypes
- Create and maintain a public list of human samples as a point of coordination for broad-based discovery efforts





#### Mendelian Genome Centers Hill MININGTO

Finding the genes underlying human Mendelian conditions



The Mendelian Genome Centers will apply next-generation sequencing and computational approaches to discover the genes and variants that underlie Mendelian conditions.

Our vision is to discover new genes that cause Mendelian conditions. As a result, we will expand our understanding about their biology to facilitate their diagnosis, and potentially indicate new treatments.



University of Washington Center for Mendellan Genomics (coordinating center)



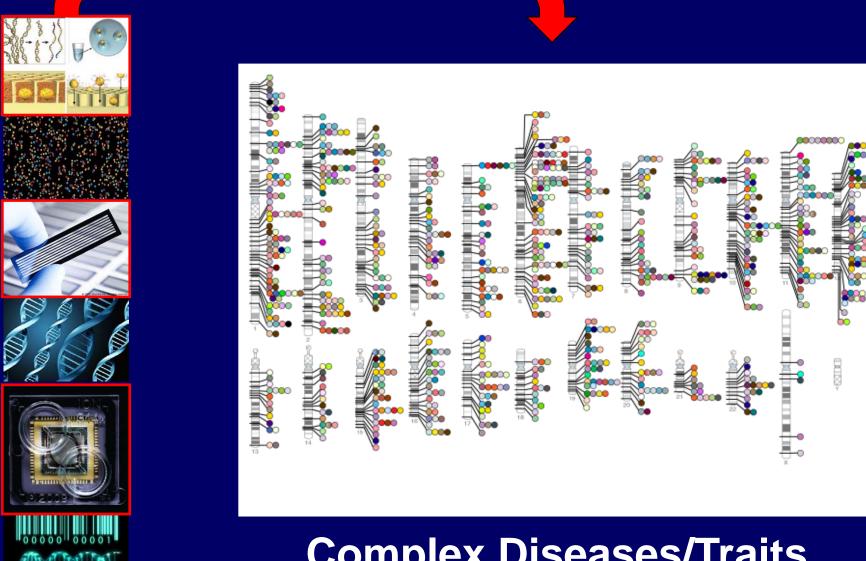
Yale Center for Mendelian Disorders





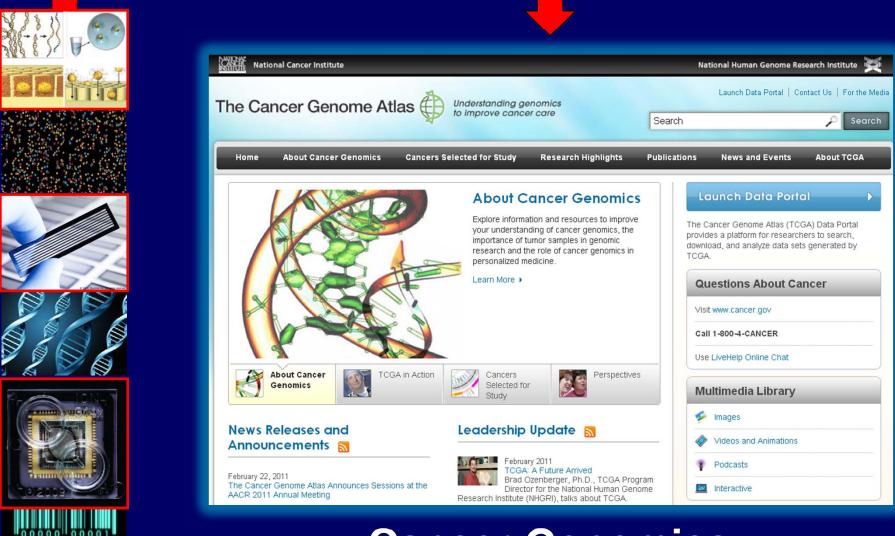
Baylor-Johns Hopkins Center for Mendelian Genetics

### The Future: Genome Sequencing



**Complex Diseases/Traits** 

#### The Future: Genome Sequencing



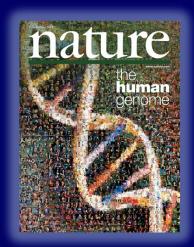
**Cancer Genomics** 

# Clinical Genomic Information Systems









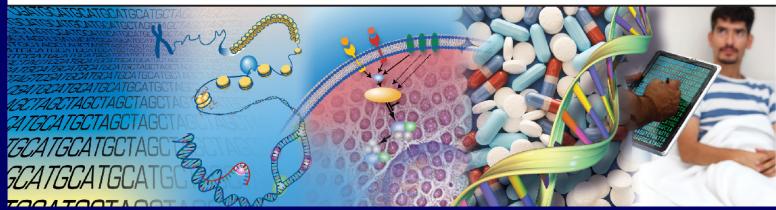


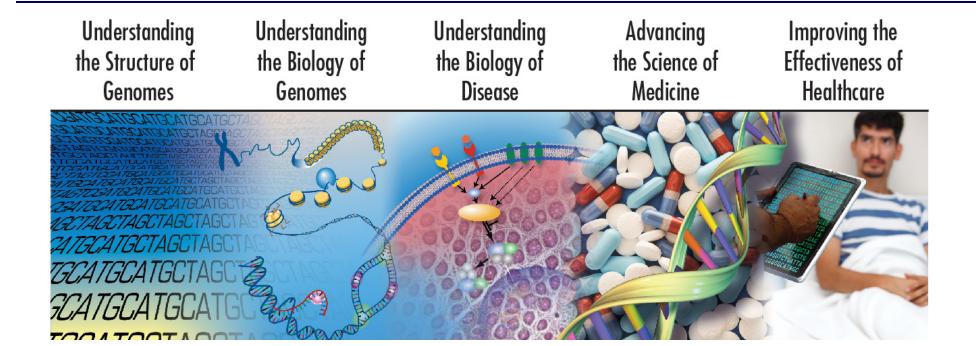
#### Human Genome Project

# Realization of Genomic Medicine

Understanding
the Structure of
Genomes

Understanding the Biology of Genomes Understanding the Biology of Disease Advancing the Science of Medicine Improving the Effectiveness of Healthcare





A pessimist sees the difficulty in every opportunity. An optimist sees the opportunity in every difficulty.

--Winston Churchill

