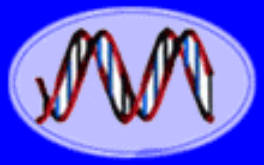
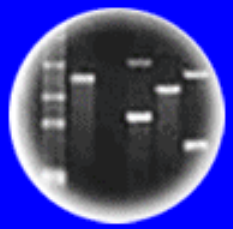


DNA
Genetic Code of Life

Entire Genetic Code
of a Bacteria



DNA Fingerprinting

Cloning: Ethical Issues
and Future Consequences

Plants of Tomorrow

HC70A & SAS70A Winter 2013
Genetic Engineering in Medicine, Agriculture, and Law

Professors Bob Goldberg, Channapatna Prakash & John Harada

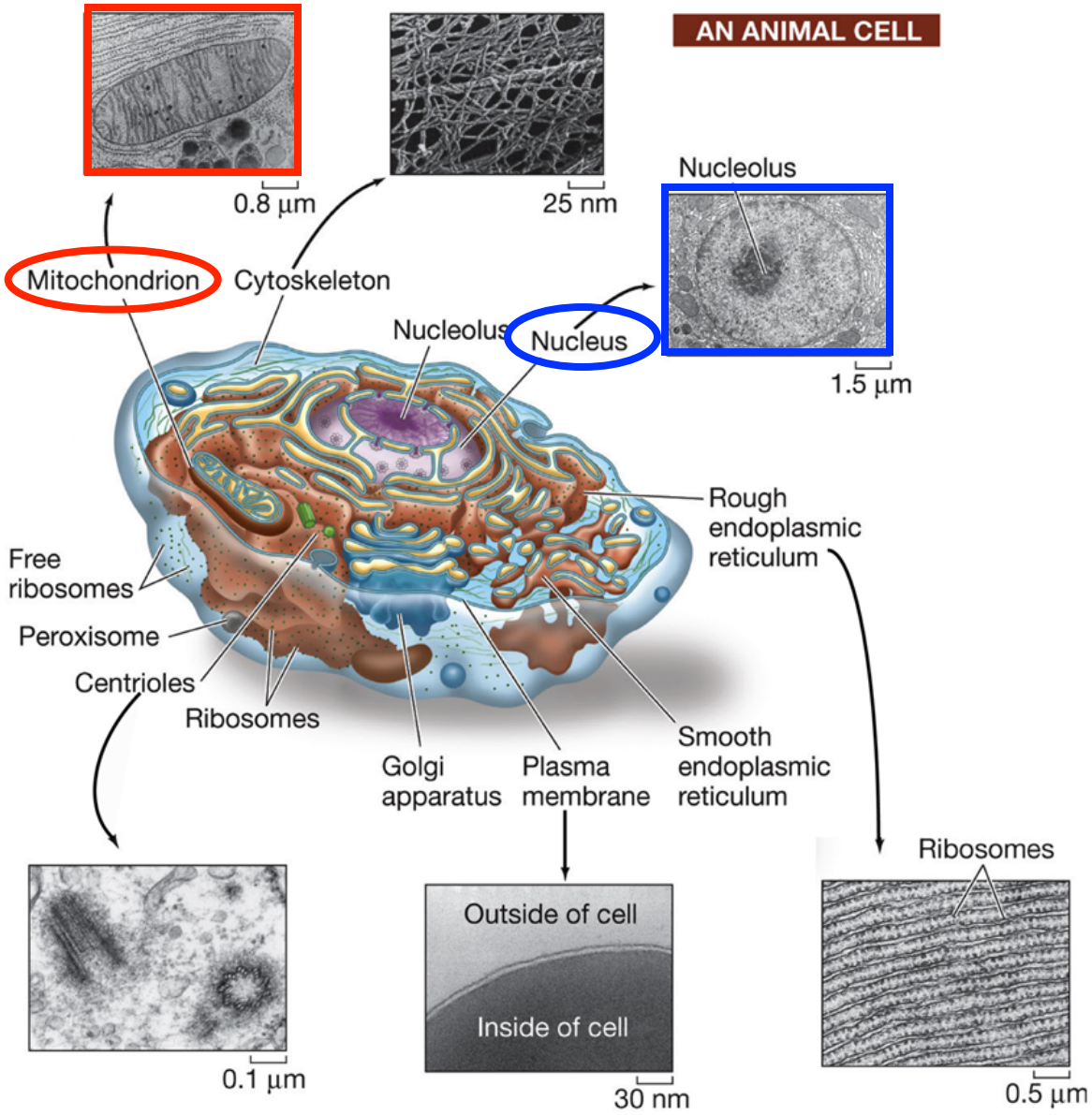
Lecture 7
Your Personal Genome &
Tracing Your Ancestry

UCLA

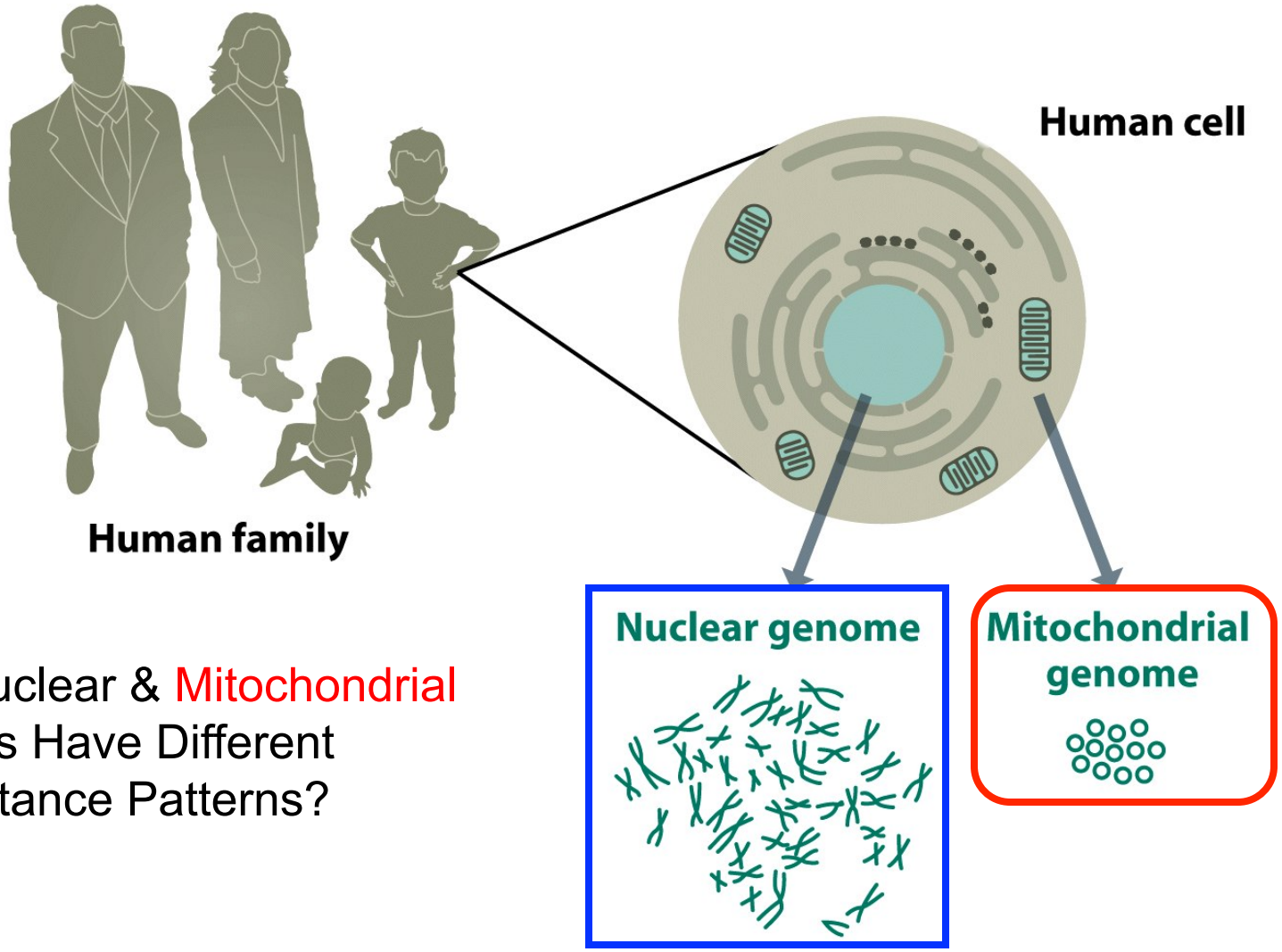
TUSKEGEE UNIVERSITY

UCDAVIS
UNIVERSITY OF CALIFORNIA

Human Cells Have Two Genomes



……One in the Nucleus and One in the Mitochondria



Do Nuclear & Mitochondrial Genes Have Different Inheritance Patterns?

Figure 1-1 Genomes 3 (© Garland Science 2007)

The Nuclear and Mitochondrial Genomes Differ in Size & Shape

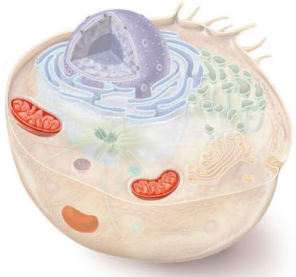
Nuclear	Mitochondrial
3.2 Mb	17 kb
25,000 Genes	30 Genes
24 Linear Pieces	1 Circle

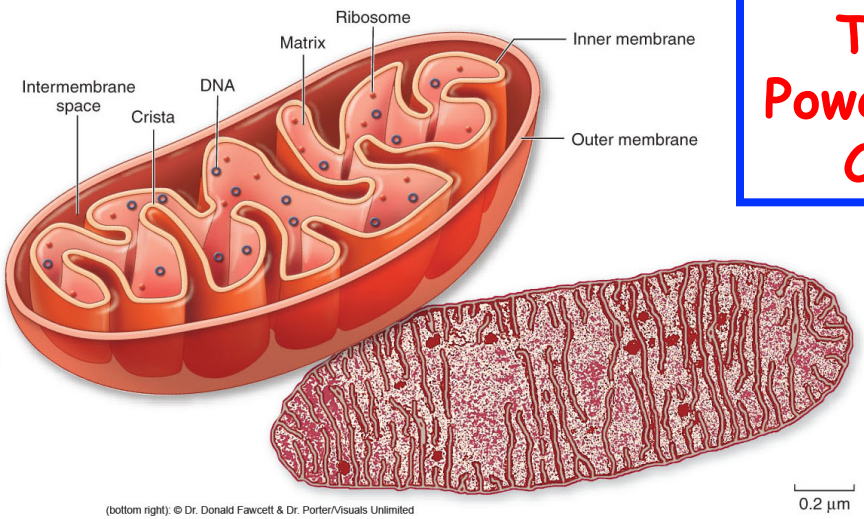
Table 9.1: The human nuclear and mitochondrial genomes

	Nuclear genome	Mitochondrial genome
Size	3200 Mb	16.6 kb
No. of different DNA molecules	23 (in XX cells) or 24 (in XY cells); all linear	One circular DNA molecule
Total no. of DNA molecules per cell	46 in diploid cells, but varies according to ploidy	Often several thousands (but variable – see *Box 9.1*)
Associated protein	Several classes of histone and nonhistone protein	Largely free of protein
No. of genes	~ 30 000–35 000	37
Gene density	~ 1/100 kb	1/0.45 kb
Repetitive DNA	Over 50% of genome, see *Figure 9.1*	Very little
Transcription	The great bulk of genes are transcribed individually (*monocistronic transcription units*)	Co-transcription of multiple genes from both the heavy and the light strands (*polycistronic transcription units*)
Introns	Found in most genes	Absent
% of coding DNA	~ 1.5%	~ 93%
Codon usage	See *Figure 1.22*	See *Figure 1.22*
Recombination	At least once for each pair of homologs at meiosis	Not evident
Inheritance	Mendelian for sequences on X and autosomes; paternal for sequences on Y	Exclusively maternal

Mitochondria Power Human Cells and Contain a Circular Genome

Each Cell Has Many Mitochondria





(bottom right): © Dr. Donald Fawcett & Dr. Porter/Visuals Unlimited

Makes ATP Energy That Powers All Cells!

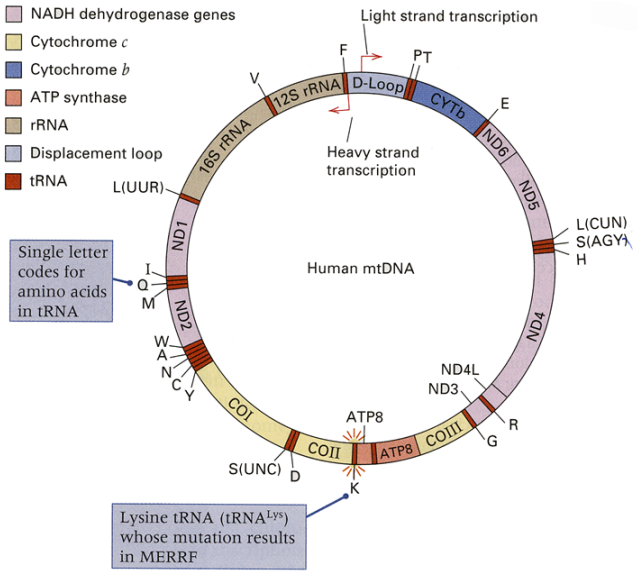


Figure 16.3 Genes in human mitochondrial DNA. The tRNA genes are indicated by the one-letter amino acid symbols; hence $tRNA^{Lys}$ is denoted K. The positions of these and other genes in the mitochondrial DNA are indicated by color according to the key at the upper left. The arrows indicate the promoters for transcription of the heavy and light strands. [Courtesy of N-G. Larsson and D. A. Clayton. With permission, from the *Annual Review of Genetics* 29: 151. Copyright 1995 by Annual Reviews, www.AnnualReviews.org.]

Semi-Autonomous Genome

DNA

Divides
Transcription
Translation

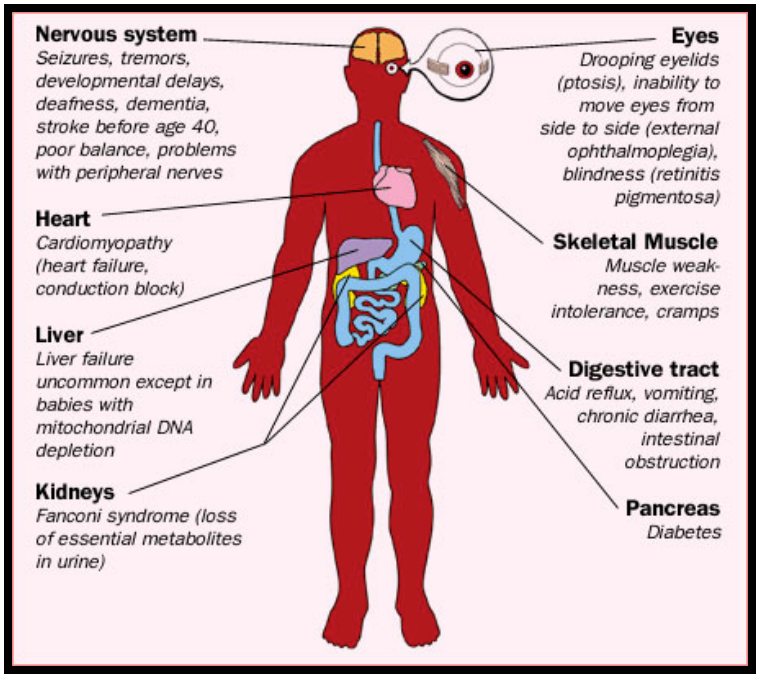
→ **Mitochondrial Proteins**

UNITED MITOCHONDRIAL DISEASE FOUNDATION.
HOPE. ENERGY. LIFE.

Mitochondrial DNA Diseases

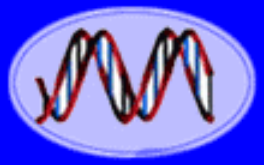
Affect 1/4000 People

- Alpers Disease
- Barth syndrome
- Beta-oxidation Defects
- Carnitine-Acyl-Carnitine Deficiency
- Carnitine Deficiency
- Creatine Deficiency Syndromes
- Co-Enzyme Q10 Deficiency
- Complex I Deficiency
- Complex II Deficiency
- Complex III Deficiency
- Complex IV Deficiency
- Complex V Deficiency
- COX Deficiency
- CPEO
- CPT I Deficiency
- CPT II Deficiency
- Glutaric Aciduria Type II
- KSS
- Lactic Acidosis
- LCAD
- LCHAD
- Leigh Disease or Syndrome
- LHON
- LIC (Lethal Infantile Cardiomyopathy)
- Luft Disease
- MAD
- MCAD
- MELAS
- MERRF
- MIRAS
- Mitochondrial Cytopathy
- Mitochondrial DNA Depletion
- Mitochondrial Encephalopathy
- Mitochondrial Myopathy
- MNGIE
- NARP
- Pearson Syndrome
- Pyruvate Carboxylase Deficiency
- Pyruvate Dehydrogenase Deficiency
- POLG Mutations
- Respiratory Chain
- SCAD
- SCHAD
- VLCAD



Treatment

At this time, there are no cures for these disorders.



DNA
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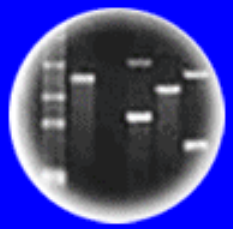
Entire Genetic Code of a Bacteria



DNA Fingerprinting

Cloning: Ethical Issues and Future Consequences

Plants of Tomorrow

MERRF: A Mitochondrial Disease Example

Myoclonic Epilepsy and Ragged-Red Fiber Syndrome

MERRF Is Rare – Affecting 1/400,000 People

MERRF

Long Name: Myoclonic Epilepsy and Ragged-Red Fiber Disease.

Symptoms: Myoclonus, epilepsy, progressive ataxia, muscle weakness and degeneration, deafness, and dementia.

Cause: Mitochondrial DNA point mutations: A8344G, T8356C **Serine tRNA**

MERRF is a progressive multi-system syndrome usually beginning in childhood, but onset may occur in adulthood. The rate of progression varies widely. Onset and extent of symptoms can differ among affected siblings.

The classic features of MERRF include:

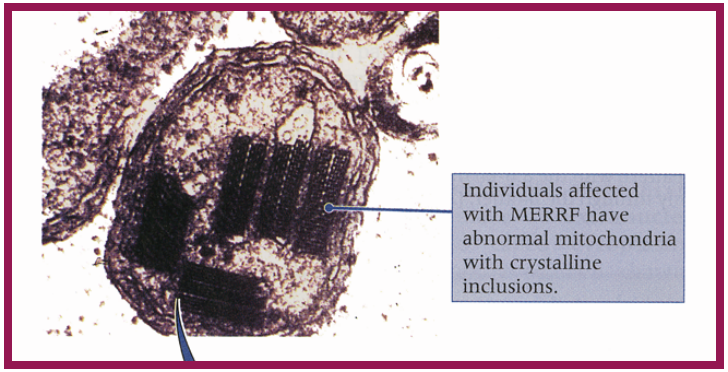
- Myoclonus (brief, sudden, twitching muscle spasms) – the most characteristic symptom
- Epileptic seizures
- Ataxia (impaired coordination)
- Ragged-red fibers (a characteristic microscopic abnormality observed in muscle biopsy of patients with MERRF and other mitochondrial disorders) Additional symptoms may include: hearing loss, lactic acidosis (elevated lactic acid level in the blood), short stature, exercise intolerance, dementia, cardiac defects, eye abnormalities, and speech impairment.

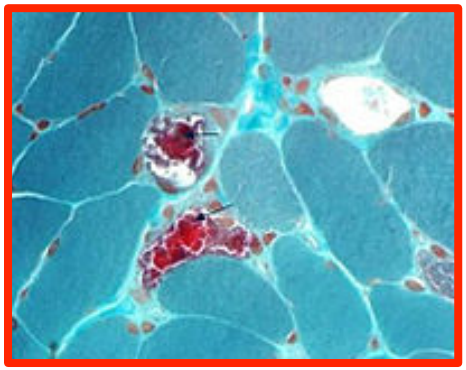
Although a few cases of MERRF are sporadic, most cases are maternally inherited due to a mutation within the mitochondria. The most common MERRF mutation is A8344G, which accounted for over 80% of the cases (GeneReview article). Four other mitochondrial DNA mutations have been reported to cause MERRF. While a mother will transmit her MERRF mutation to all of her offspring, some may never display symptoms.

As with all mitochondrial disorders, there is no cure for MERRF. Therapies may include coenzyme Q10, L-carnitine, and various vitamins, often in a "cocktail" combination. Management of seizures usually requires anticonvulsant drugs. Medications for control of other symptoms may also be necessary.

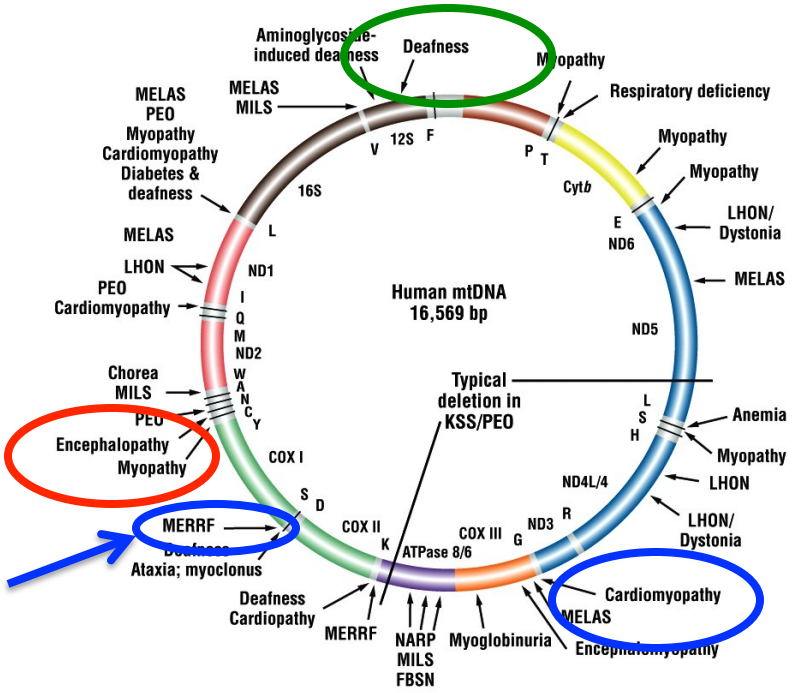
The prognosis for MERRF varies widely depending on age of onset, type and severity of symptoms, organs involved, and other factors.

Sources: Dr. Rolf Luft; The development of mitochondrial medicine. [Review] ; *Proceedings of the National Academy of Sciences of the United States of America* ; 1994 ; 91(19) ; 8731-8 & DiMauro





The Circular Mitochondrial Genome is Inherited Maternally

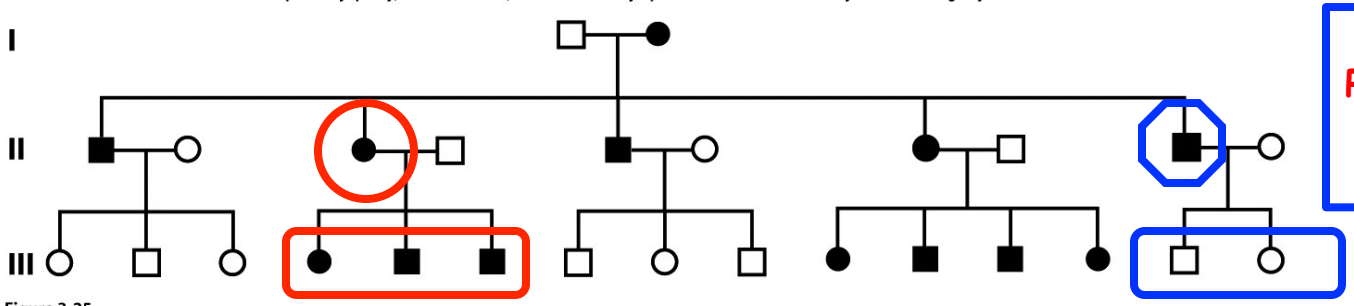


Disease Genes Present on the Mitochondrial Genome

Many Affect Muscles Because Mitochondria Produce Energy Needed For Muscle Activity

Diseases:

MERRF	Myoclonic epilepsy and ragged red fiber disease	MMC	Maternally inherited myopathy and cardiomyopathy
LHON	Leber hereditary optic neuropathy	PEO	Progressive external opthalmoplegia
NARP	Neurogenic muscle weakness, ataxia, and retinitis pigmentosum	KSS	Kearns–Sayre syndrome
MELAS	Mitochondrial encephalomyopathy, lactic acidosis, and strokelike symptoms	MILS	Maternally inherited Leigh syndrome



Note: Passed on From Mother to All Children

Figure 3-25
Introduction to Genetic Analysis, Ninth Edition

Provide a Hypothesis For the Variation in Disease Symptoms

NUCLEAR TRANSPLANTATION

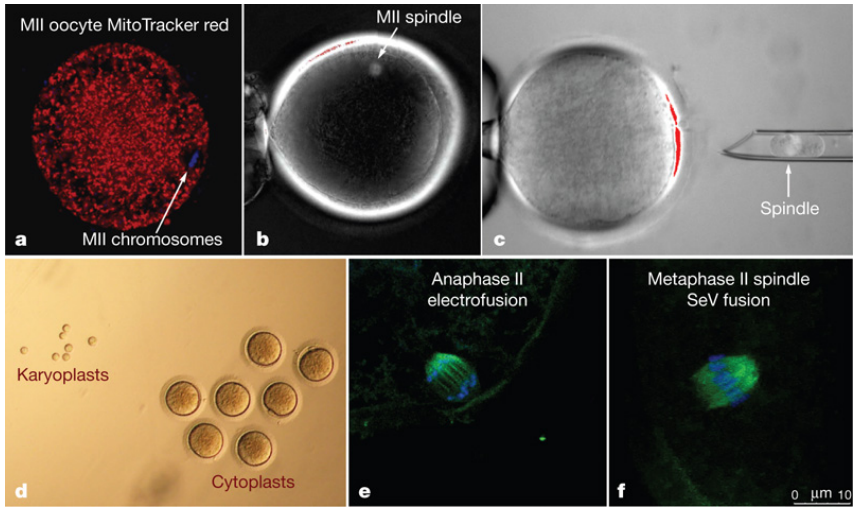
Researchers Prevent Inheritance of Faulty Mitochondria in Monkeys

Vol 461|17 September 2009|doi:10.1038/nature08368 nature

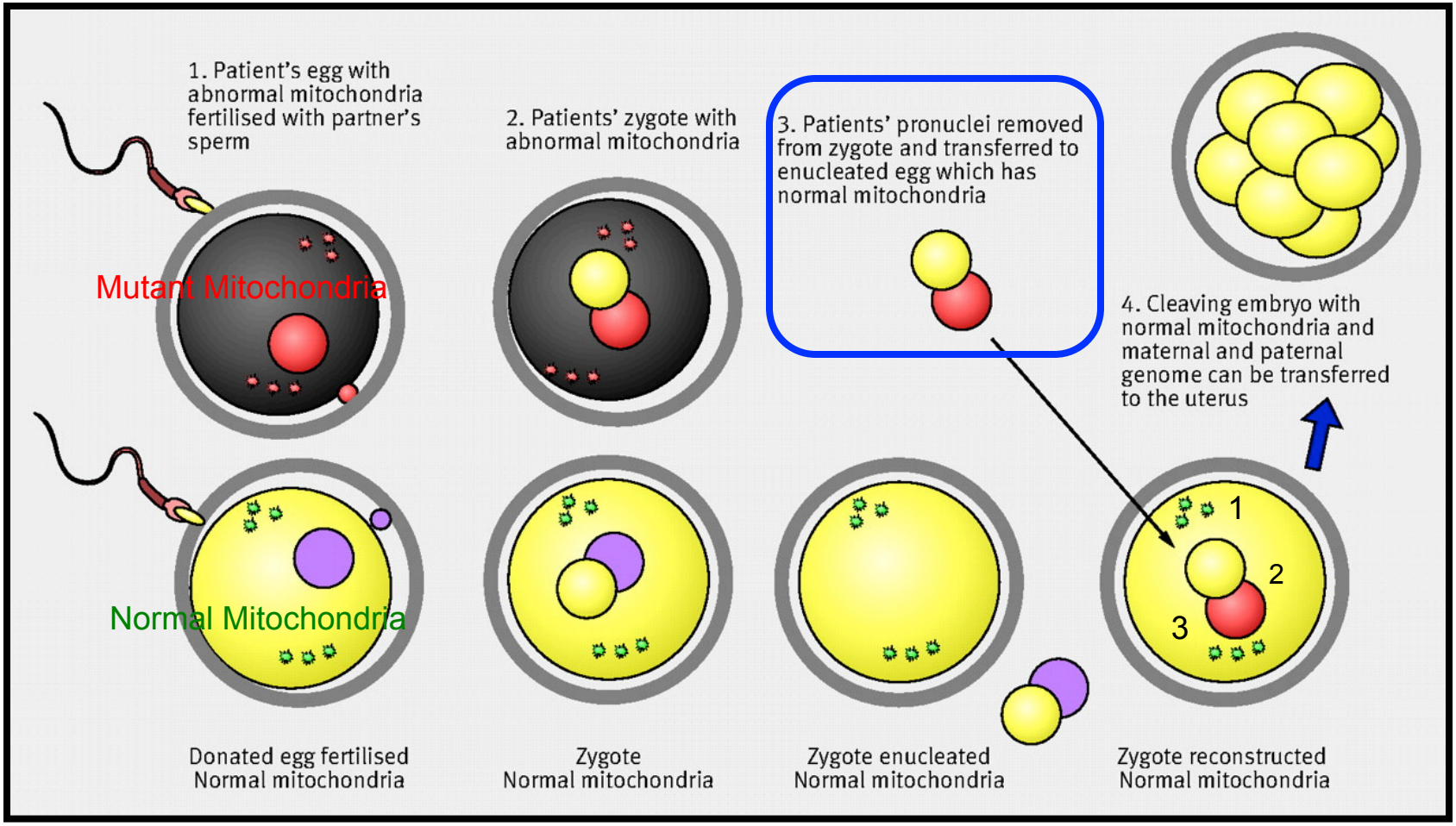
Nature 461, September 17, 2009

ARTICLES

Mitochondrial gene replacement in primate offspring and embryonic stem cells



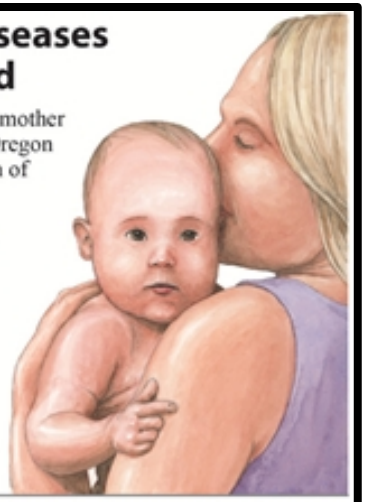
Future Mitochondrial Gene Replacement Therapy



***Note:* The Zygote Contains THREE Genomes --**
One from Mother, One From Father, and One From Donor Mitochondria

Gene therapy to prevent diseases passed from mother to child

More than 300 genetic diseases can be passed from mother to child because of mutated genes. Researchers at Oregon Health & Science University have developed a form of gene therapy to prevent these diseases.

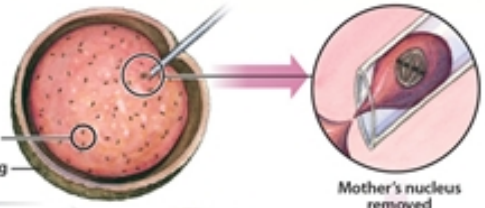


The mitochondria

Mitochondria are the powerstations of a cell, providing it with the energy to function. A mother's egg cell contains thousands of mitochondria, each containing its own DNA. If defective, the DNA in these cells can pass diseases from mother to child. Here's how researchers hope to use gene therapy to prevent these diseases:

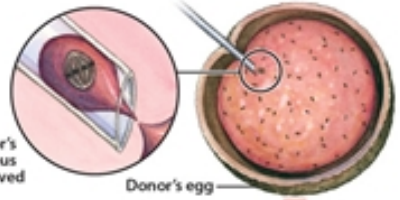
1 Removing mother's nucleus

The cell nucleus holds chromosomes, which contain more than 99 percent of a person's DNA. The nucleus is removed from the mother's egg cell.



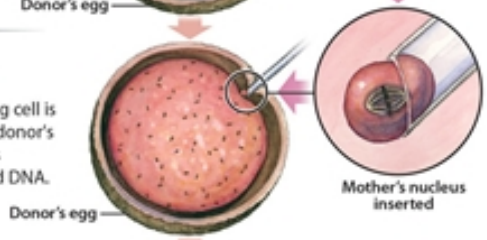
2 Removing nucleus from the donor's egg

The nucleus is also removed from an egg cell provided by a donor.



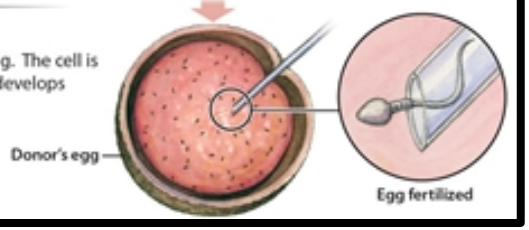
3 Inserting mother's nucleus in donor's egg

The nucleus removed from the mother's egg cell is inserted into the donor egg cell. Thus, the donor's normal mitochondria replaces the mother's defective mitochondria containing mutated DNA.



4 Fertilizing the egg

A sperm cell is injected to fertilize the egg. The cell is then re-implanted into the mother and develops into a healthy baby.



NATURE | NEWS

DNA-swap technology almost ready for fertility clinic

Mitochondrial transfer could reduce the risk of childhood disease.

David Cyranoski

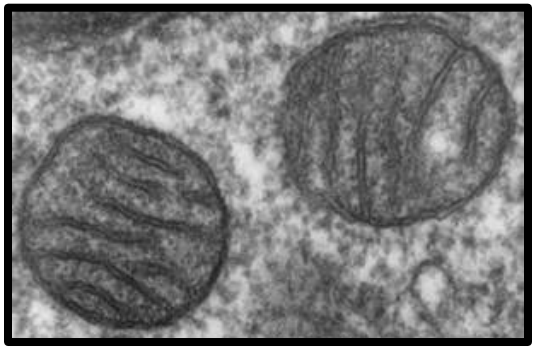
24 October 2012

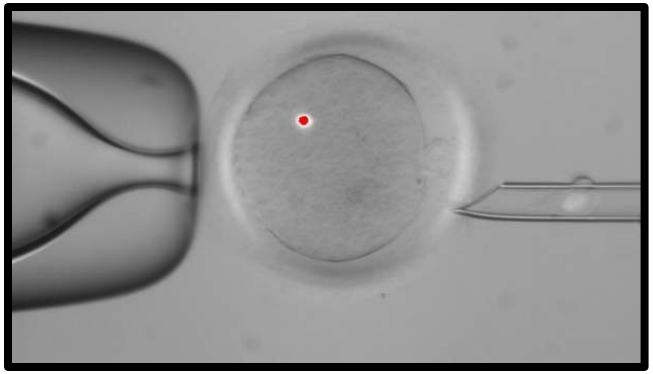
Geneticists Breach Ethical Taboo By Changing Genes Across Generations

NATURE NEWS BLOG

Bioethics board backs embryo alteration for mitochondrial disease

11 Jun 2012 | 23:01 BST | Posted by Ewen Callaway | Category: Biology & Biotechnology, Health and medicine

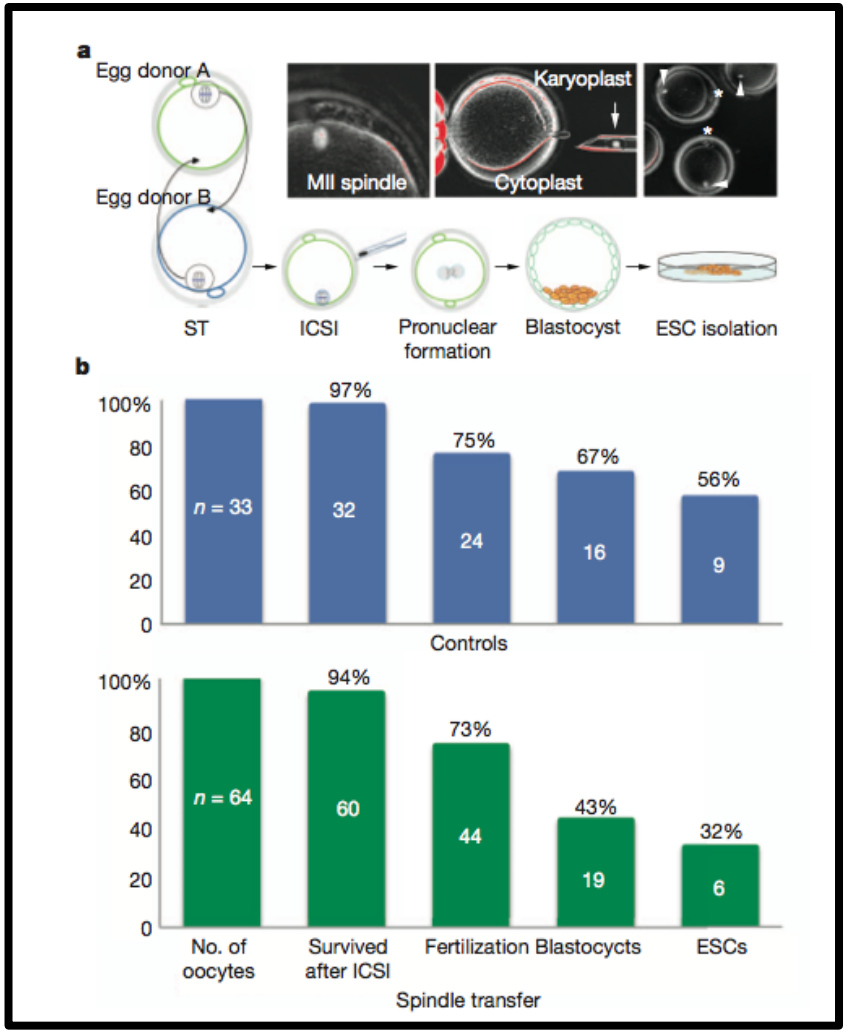




Towards germline gene therapy of inherited mitochondrial diseases

Nature, October, 2012

Using Human Eggs and Embryos



Pilot Study Only

Ethics of mitochondrial gene replacement: from bench to bedside

The prospect of using mitochondrial gene replacement to conceive children free of mitochondrial disease highlights the need for a sound ethical framework for reproductive genetic technology, say **Annelien Bredenoord** and **Peter Braude**

- How to Test Whether It Works?
- Testing on Live Human Embryos
- When To Test Its Effectiveness
- Safety & Long-Term Potential Problems
- Approved Research Protocols
- IRB (Institutional Review Board) Oversight
- Informed Consent of Parents

British Medical Journal, January 8, 2011,342, 87-89

RFLPs Can Be Used to Identify Individuals Using Mitochondrial DNAs

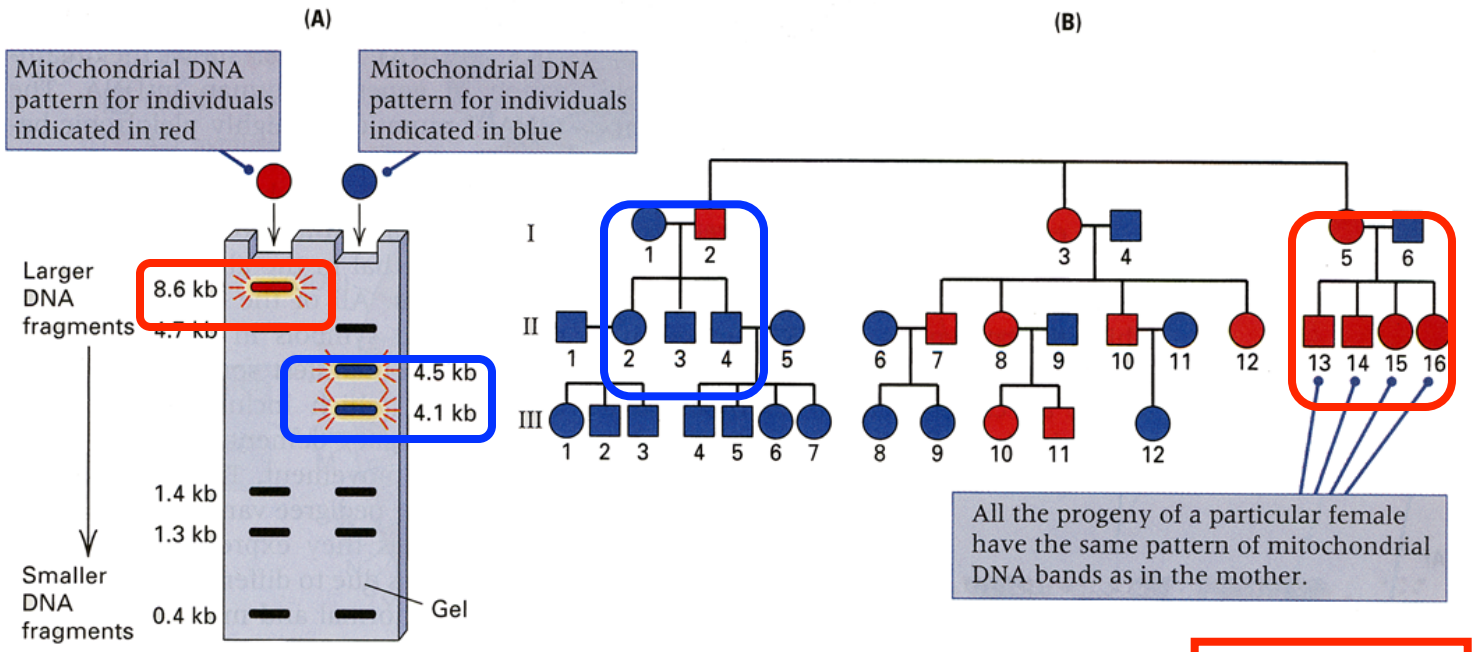
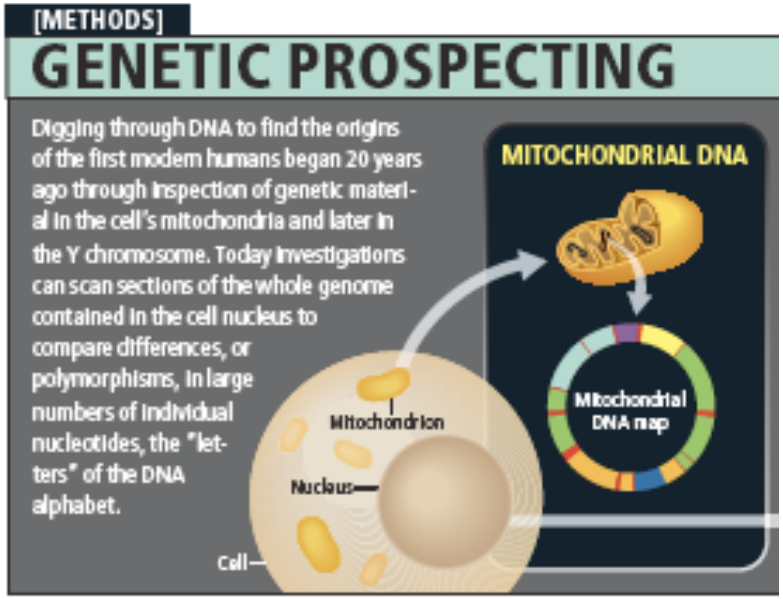


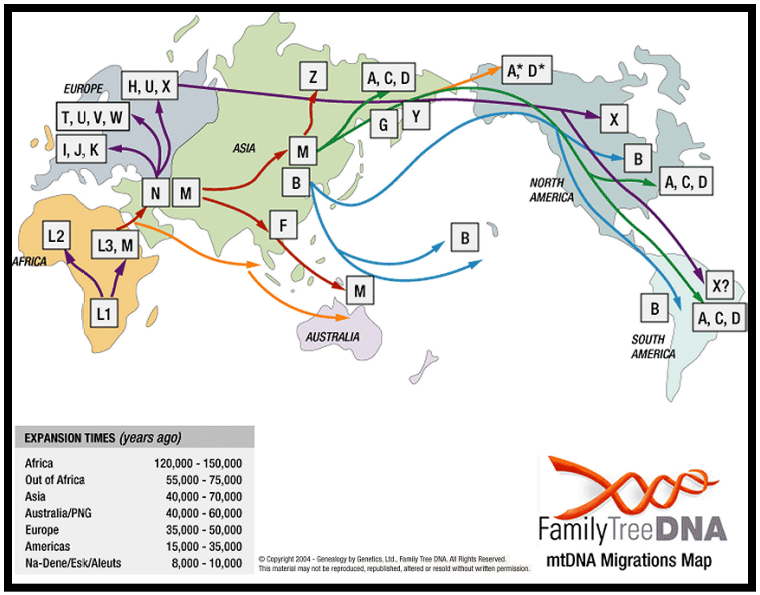
Figure 16.1 Maternal inheritance of human mitochondrial DNA. (A) Pattern of DNA fragments obtained when mitochondrial DNA is digested with the restriction enzyme *Hae*II. The DNA type at the left includes a fragment of 8.6 kb (red). The DNA type at the right contains a cleavage site for *Hae*II within the 8.6-kb fragment, which results in smaller fragments of 4.5 kb and 4.1 kb (blue). (B) Pedigree showing maternal inheritance of the DNA pattern with the 8.6-kb fragment (red symbols). The mitochondrial DNA type is transmitted only through the mother. [After D. C. Wallace. 1989. *Trends in Genetics* 5: 9.]

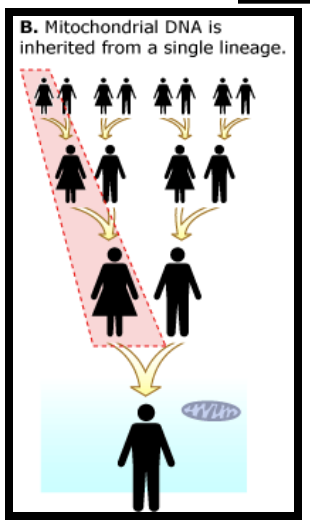
100% of Children Have 8.6 kb DNA Fragment From Mother

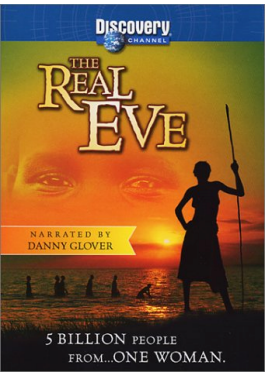
Note How Mitochondrial RFLP Markers Are Inherited !!

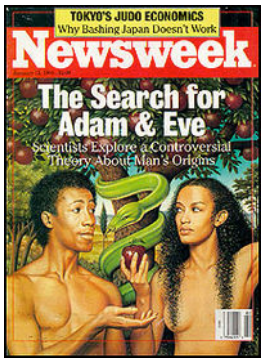
Tracing Human Populations Using Mitochondrial DNA Polymorphisms - Back to Eve!











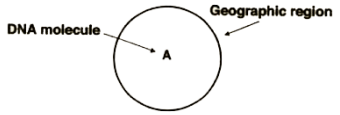
Oldest Populations Contain the Most Diversity

Analysis of human mtDNA led to the Mitochondrial Eve Hypothesis

In the 1980s, Allan Wilson pioneered the use of mtDNA to study human evolution.

In two papers published in 1987 and 1991, he and his colleagues at Cal proposed that we all come from a population of humans that lived in Africa approximately 200,000 years ago.

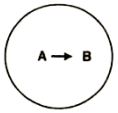
Here's the logic behind the hypothesis.



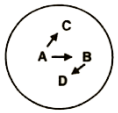
Start with A.

Time

Detected By Using Specific Markers (RFLPs or SNPS)



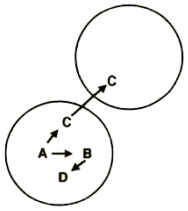
Mutation generates B from A;
now have individuals with both A and B DNAs in population.



Additional mutations generate diversity;
now have individuals with both A, B, C and D DNAs.

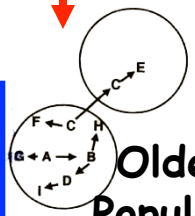
Newest Population

Subset of "Old" Variants + New Variants



C migrates to form separate population.

Lots of "Old" Variants



Oldest Population

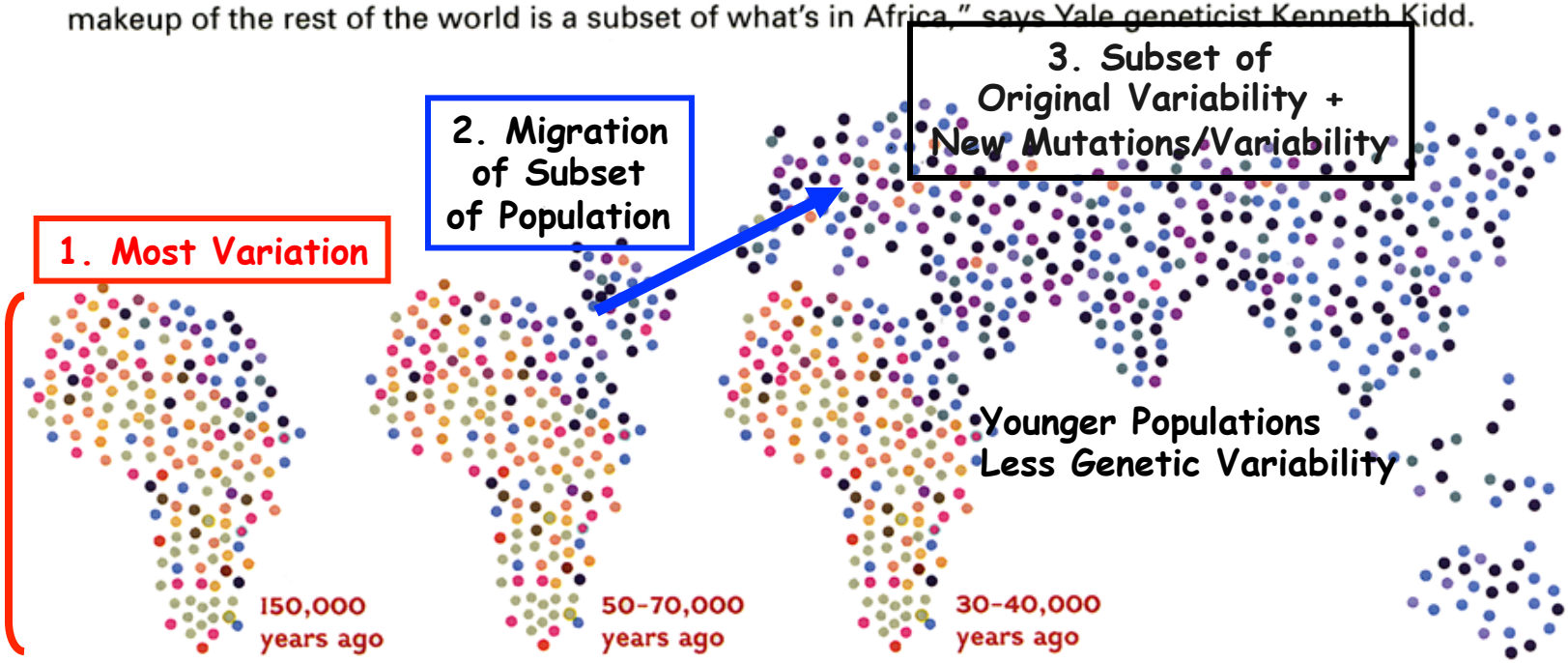
Additional mutations diversify DNAs in populations:
original population more diverse (A, B, C, D, F, G, H, I) than newer population (C, E).

Old Variants Trace Ancient Lineage. New Variants Mark New Populations SPECIFICALLY

Most Genetic Diversity Originated in the Founder Populations to Modern Humans!

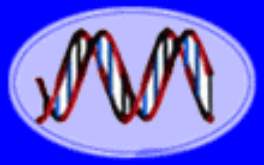
Diverse From the Start

The diversity of genetic markers is greatest in Africa (multicolored dots in map), indicating it was the earliest home of modern humans. Only a handful of people, carrying a few of the markers, walked out of Africa (center) and, over tens of thousands of years, seeded other lands (right). "The genetic makeup of the rest of the world is a subset of what's in Africa," says Yale geneticist Kenneth Kidd.



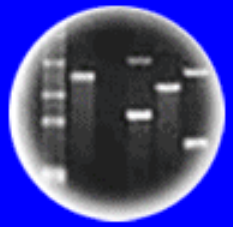
Genetic Variation Proportional to Population Age

Markers From Original Population + New Markers For "New" Population



DNA
Genetic Code of Life

Entire Genetic Code
of a Bacteria

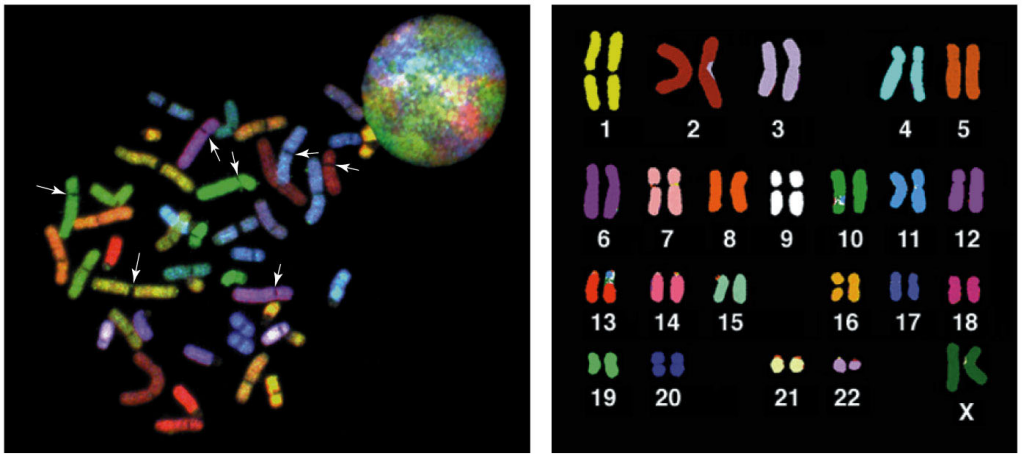


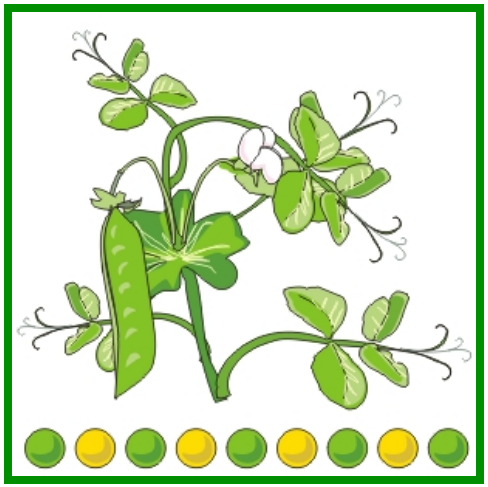
DNA Fingerprinting

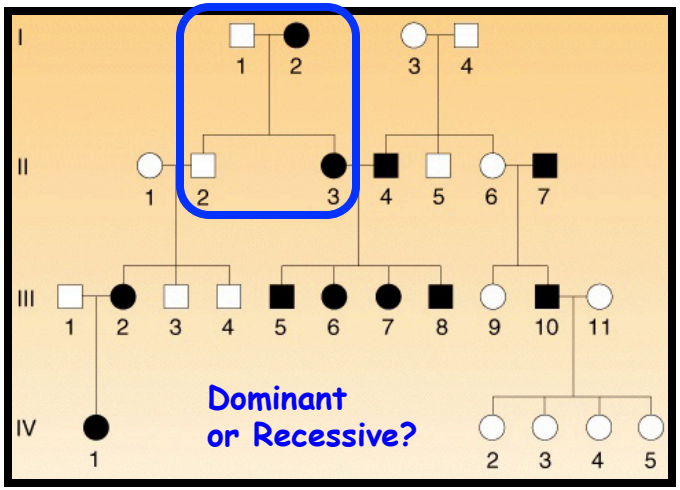
Cloning: Ethical Issues
and Future Consequences

Plants of Tomorrow

The Nuclear Genome

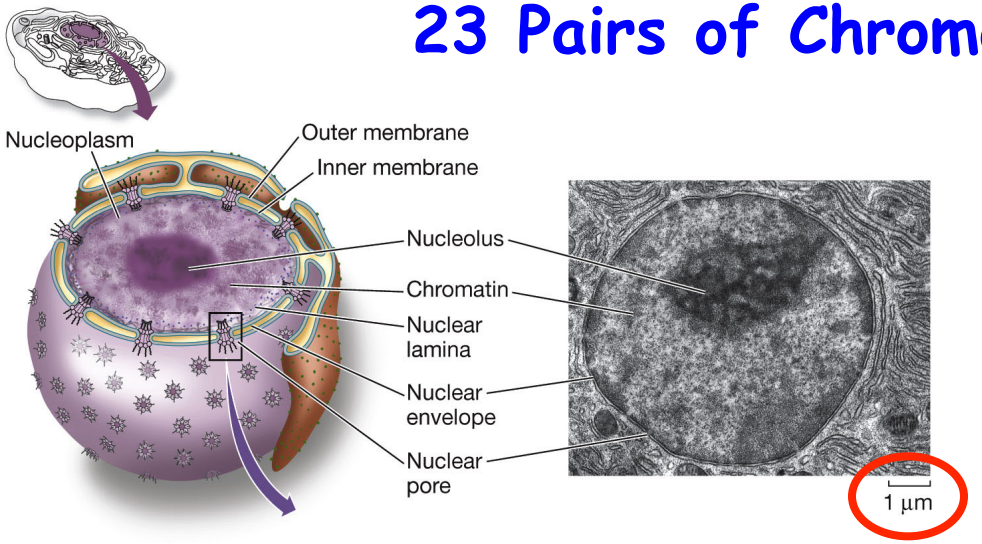


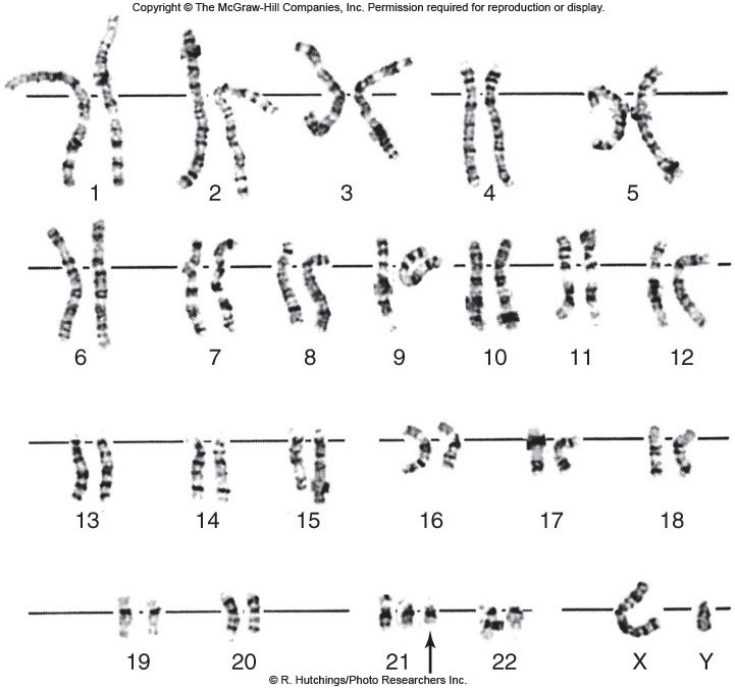




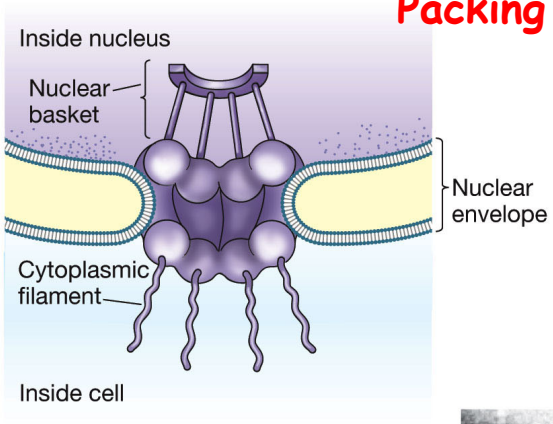
Note: Gene is Inherited in a Mendelian Pattern

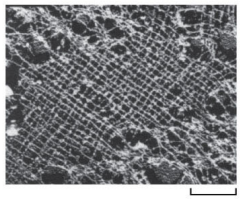
The Nucleus Is A Complex Organelle With 23 Pairs of Chromosomes (Humans)



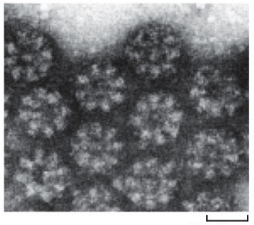


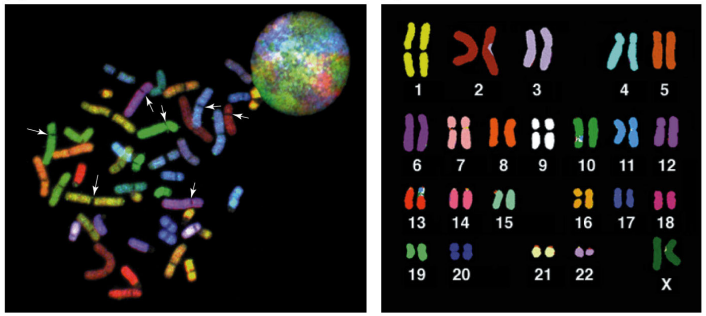
Packing Problem?





RNA & Protein Transport





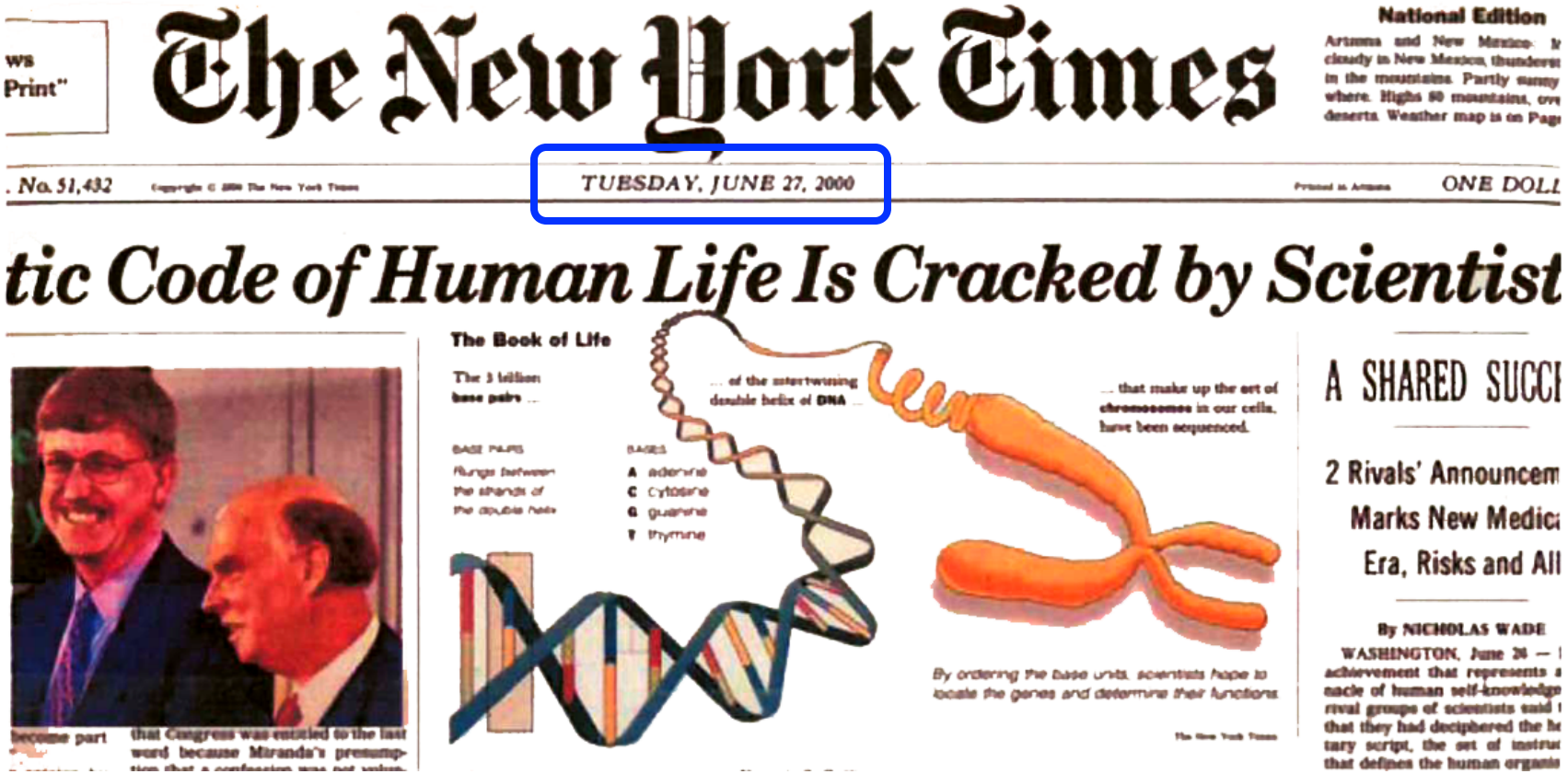
The Human Genome End to End is 1.1 Meters in Length!!!!!!

Note: Chromosome Sizes & Bands = Markers

LIFE 8e, Figure 4.8 (Part 2)

The Human Genome Was Sequenced Ten Years Ago!

The Human Genome Project



The New York Times

National Edition

TUESDAY, JUNE 27, 2000

ONE DOLL

tic Code of Human Life Is Cracked by Scientist

The Book of Life

A SHARED SUCCI

2 Rivals' Announcem

Marks New Medic

Era, Risks and All

By NICHOLAS WADE

WASHINGTON, June 26 —

Public & Private Effort Using Different Strategies - A Race!

3 Billion Dollars & Took 15 Years

PERSPECTIVE

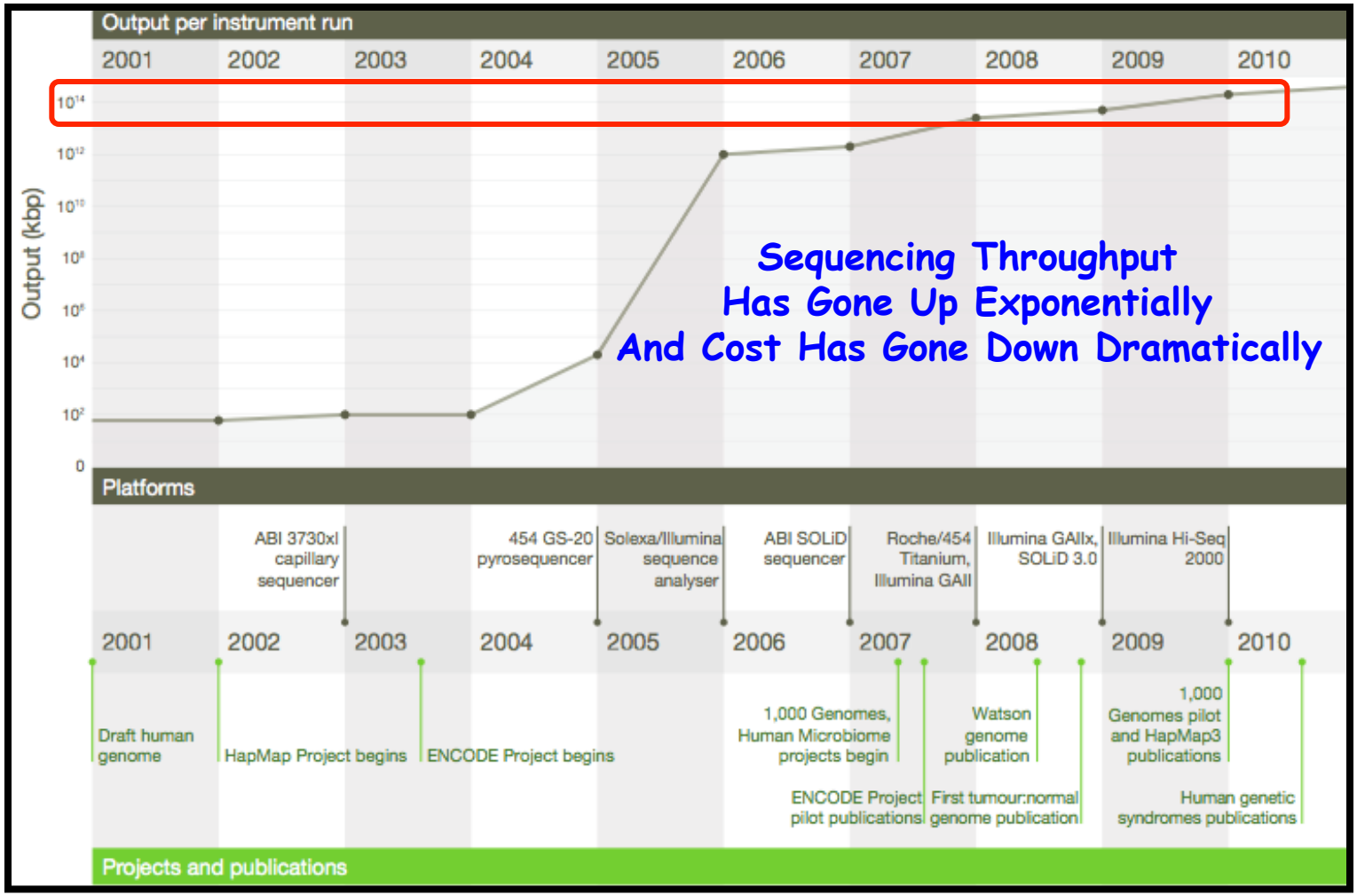
doi:10.1038/nature09796

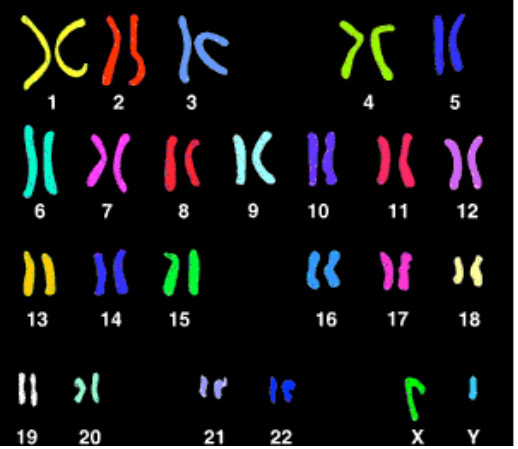
A decade's perspective on DNA sequencing technology

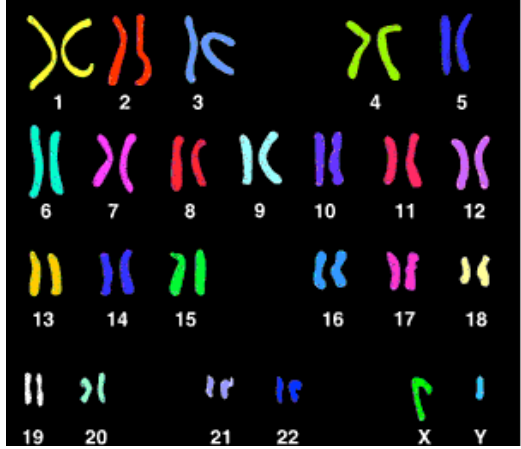
Nature, February 10, 2011

Elaine R. Mardis[1]

10^{14} kbp





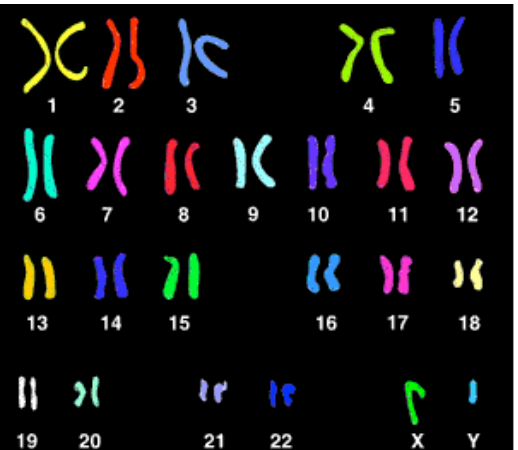


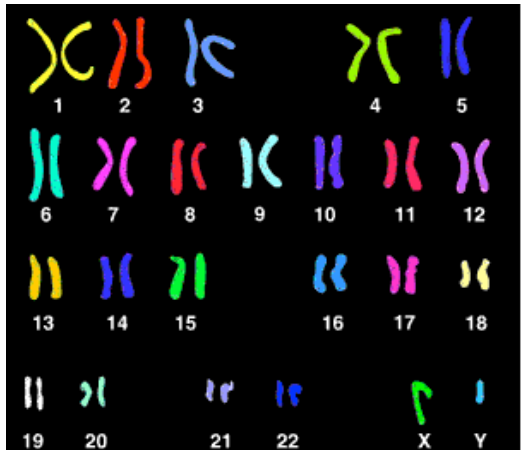
The Human Genome

Large

Small

Chromosome	Including gaps	Sequenced	Gaps
1	247,249,719	224,999,719	22,250,000
2	242,951,149	237,712,649	5,238,500
3	199,501,827	194,704,827	4,797,000
4	191,273,063	187,297,063	3,976,000
5	180,857,866	177,702,766	3,155,100
6	170,899,992	167,273,992	3,626,000
7	158,821,424	154,952,424	3,869,000
8	146,274,826	142,612,826	3,662,000
9	140,273,252	120,143,252	20,130,000
10	135,374,737	131,624,737	3,750,000
11	134,452,384	131,130,853	3,321,531
12	132,349,534	130,303,534	2,046,000
13	114,142,980	95,559,980	18,583,000
14	106,368,585	88,290,585	18,078,000
15	100,338,915	81,341,915	18,997,000
16	88,827,254	78,884,754	9,942,500
17	78,774,742	77,800,220	974,522
18	76,117,153	74,656,155	1,460,998
19	63,811,651	55,785,651	8,026,000
20	62,435,964	59,505,253	2,930,711
21	46,944,323	34,171,998	12,772,325
22	49,691,432	34,851,332	14,840,100
X	154,913,754	151,058,754	3,855,000
Y	57,772,954	25,652,954	32,120,000
M	16,571	16,571	0
Total genome	**3,080,436,051**	**2,858,034,764**	**222,401,287**

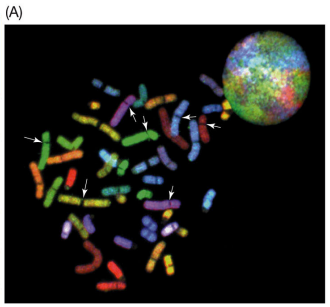




Only A Small Fraction of the Human Genome Encodes Proteins

TABLE 18.1 Classes of DNA Sequences Found in the Human Genome

Class	Frequency (%)	Description
Protein-encoding genes	1.5	Translated portions of the 25,000 genes scattered about the chromosomes
Introns	24	Noncoding DNA that constitutes the great majority of each human gene
Segmental duplications	5	Regions of the genome that have been duplicated
Pseudogenes (inactive genes)	2	Sequence that has characteristics of a gene but is not a functional gene
Structural DNA	20	Constitutive heterochromatin, localized near centromeres and telomeres
Simple sequence repeats	3	Stuttering repeats of a few nucleotides such as CGG, repeated thousands of times
Transposable elements	45	21%: Long interspersed elements (LINEs), which are active transposons 13%: Short interspersed elements (SINEs), which are active transposons 8%: Retrotransposons, which contain long terminal repeats (LTRs) at each end 3%: DNA transposon fossils



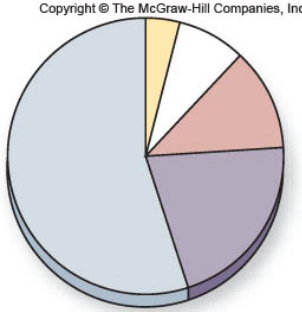
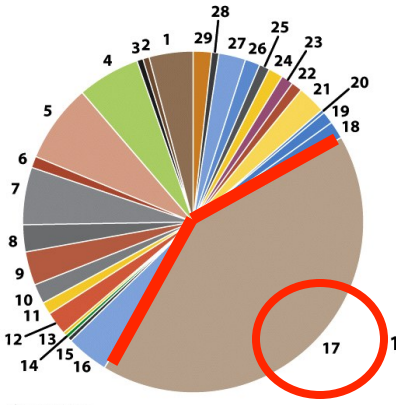


Table 20.6 Average characteristics of genes in the human genome

Characteristic	Average
Number of exons	8.8
Size of internal exon	145 bp
Size of intron	3,365 bp
Size of 5′ untranslated region	300 bp
Size of 3′ untranslated region	770 bp
Size of coding region	1,340 bp
Total length of gene	27,000 bp

Table 20-6

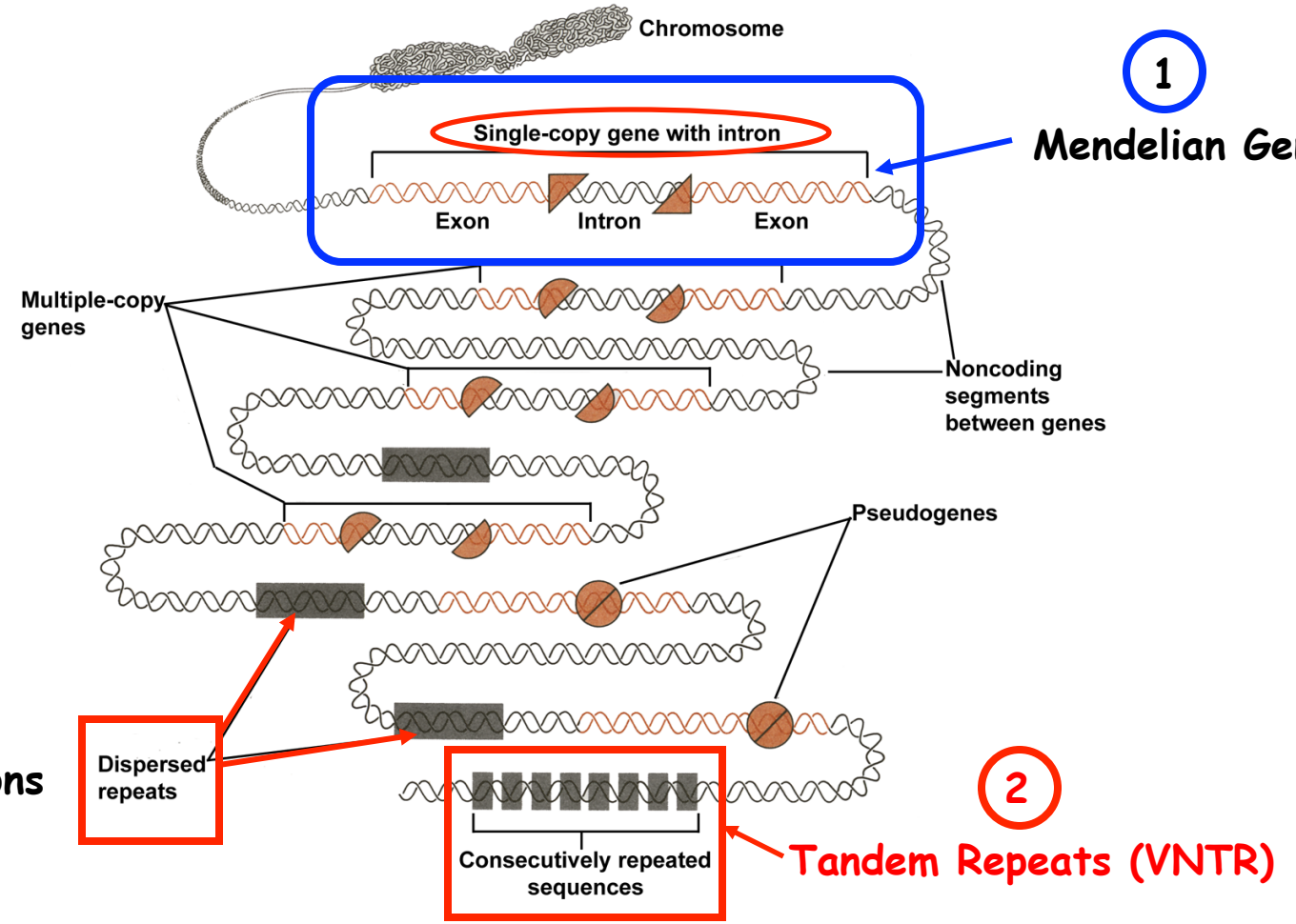
The Human Genome Has DNA Sequences Present Once As Well as Repeated Many Times



1. Miscellaneous
2. Viral protein
3. Transfer or carrier protein
4. Transcription factor
5. Nucleic acid enzyme
6. Signaling molecule
7. Receptor
8. Kinase
9. Select regulatory molecule
10. Transferase
11. Synthase and synthetase
12. Oxidoreductase
13. Lyase
14. Ligase
15. Isomerase
16. Hydrolase
17. Molecular function unknown
18. Transporter
19. Intracellular transporter
20. Select calcium-binding protein
21. Protooncogene
22. Structural protein of muscle
23. Motor
24. Ion channel
25. Immunoglobulin
26. Extracellular matrix
27. Cytoskeletal structural protein
28. Chaperone
29. Cell adhesion

Human Genes are Large but Contain Mostly Introns

The Human Genome Landscape

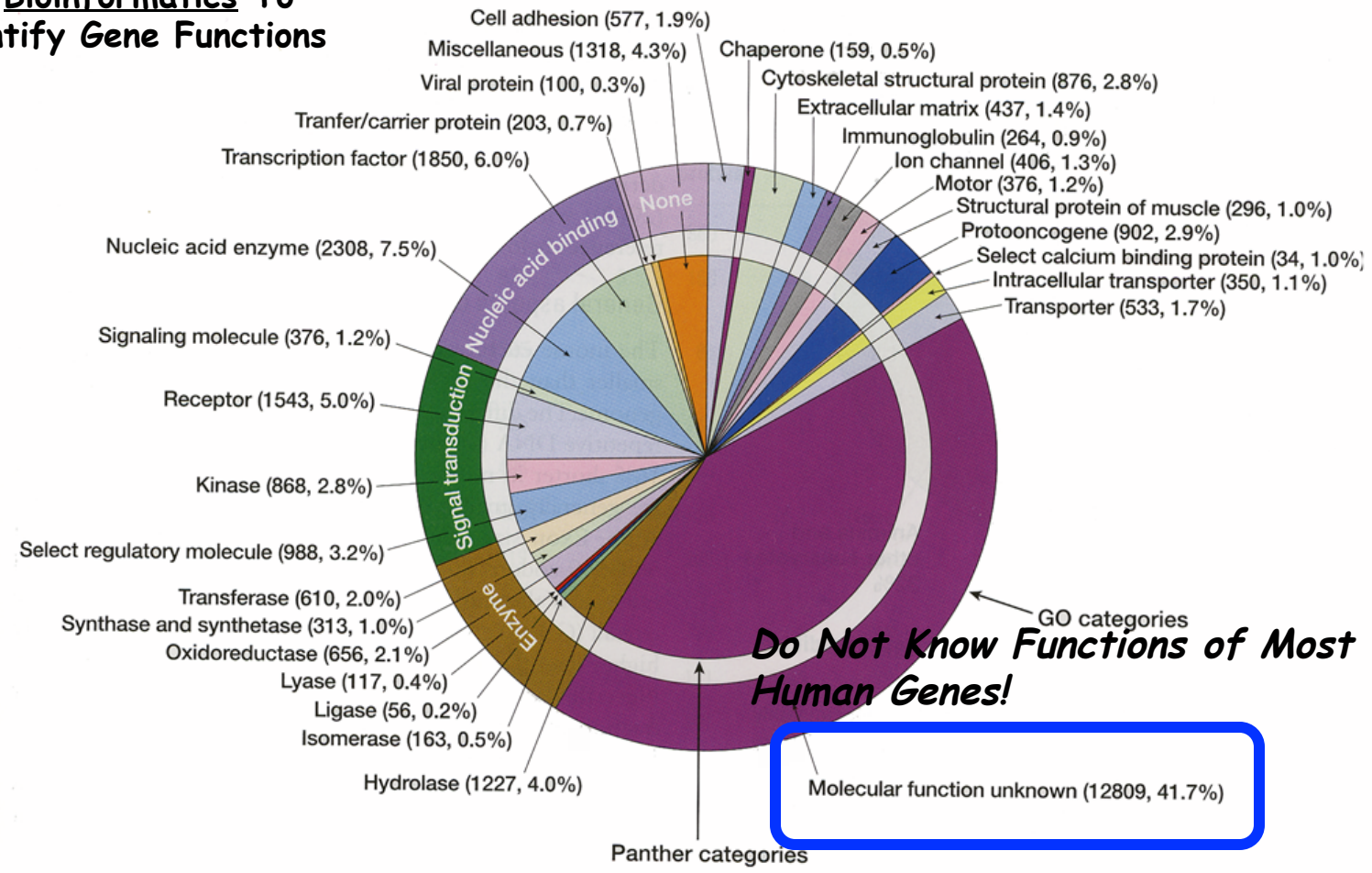


Tandem Repeats or VNTRs are Useful for DNA Fingerprinting Studies!

e.g., DIS80 Locus For Class DNA Fingerprint on Chromosome 4 Core = 16bp

The Human Genome Contains ~25,000 Different Genes

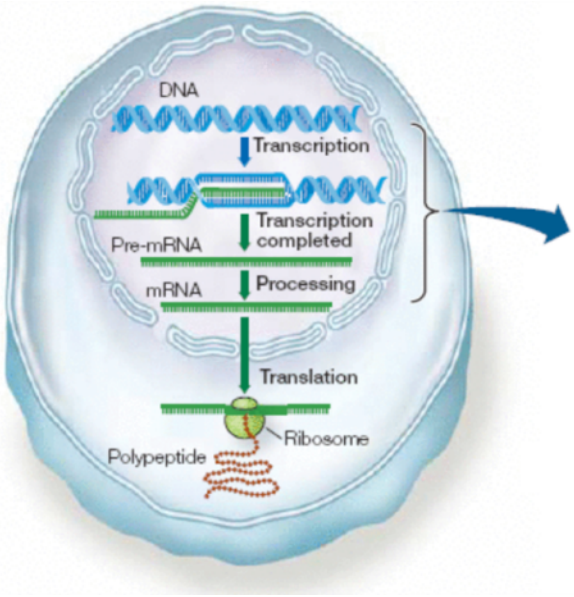
Use Bioinformatics To Identify Gene Functions



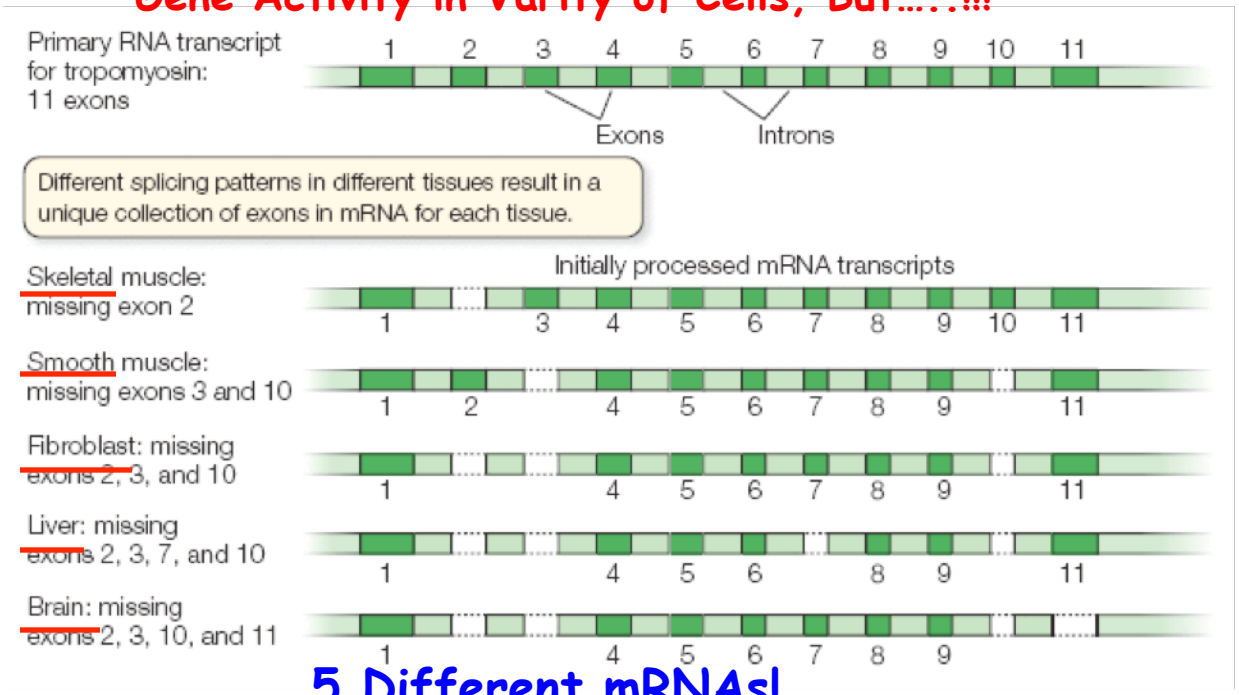
Do Not Know Functions of Most Human Genes!

How Many Encoded Proteins? Alternative Splicing?

Alternative Splicing- One Gene → Several mRNAs & Proteins



Gene Activity in Varity of Cells, But…..!!!



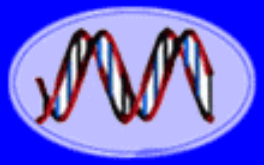
5 Different mRNAs!

Different mRNA = Different Proteins = Different Functions!

Implication- Human Genome Has Only 25,000 Genes But Can Give Rise to Many More Proteins which Are Responsible For Producing the Phenotype

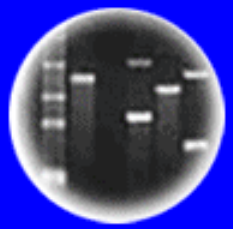
Reason Why Human Genome Can Contain Same Number of Genes as Fly and Plant Genomes!!

Implications for Genetic Engineering? Use Specific cDNA!



DNA
Genetic Code of Life

Entire Genetic Code of a Bacteria

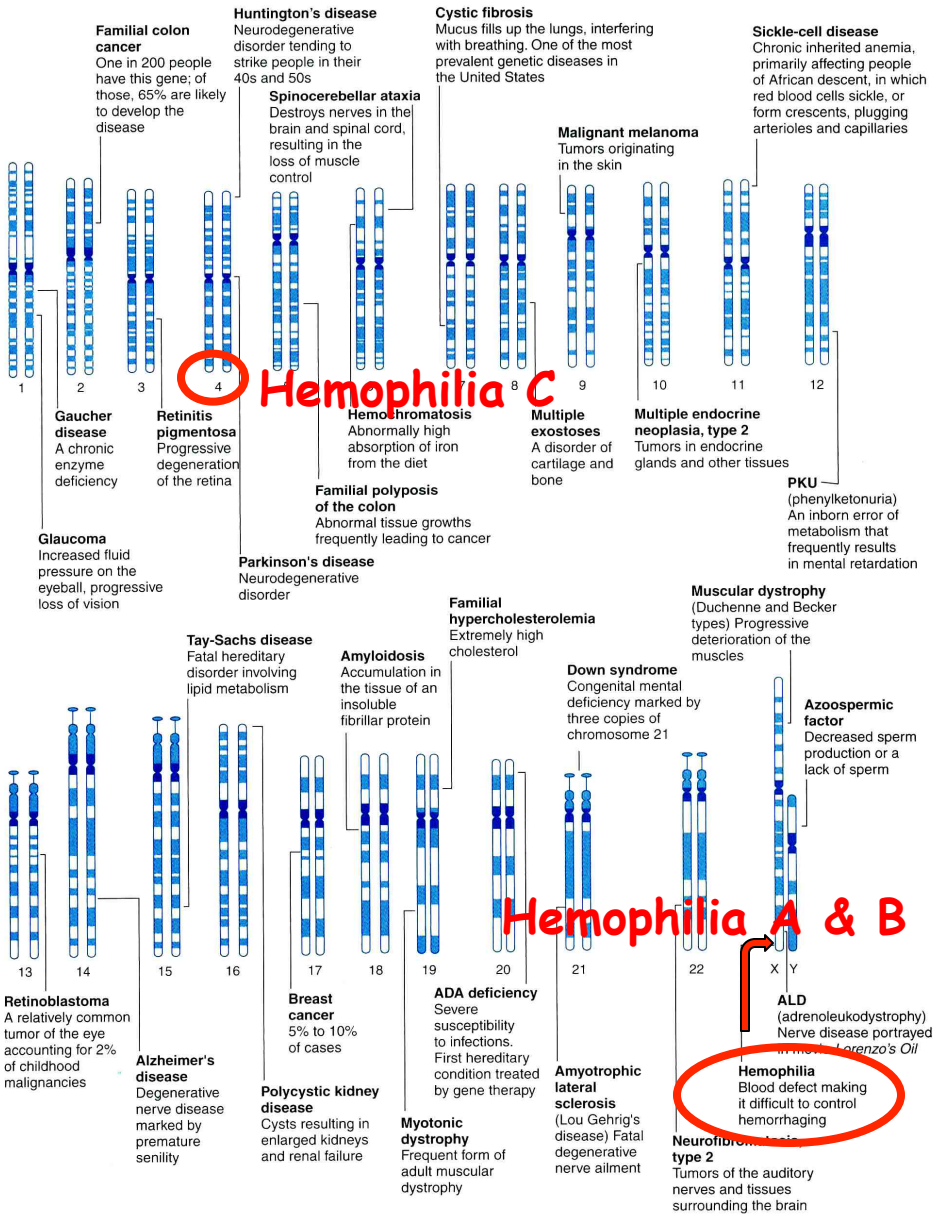


DNA Fingerprinting

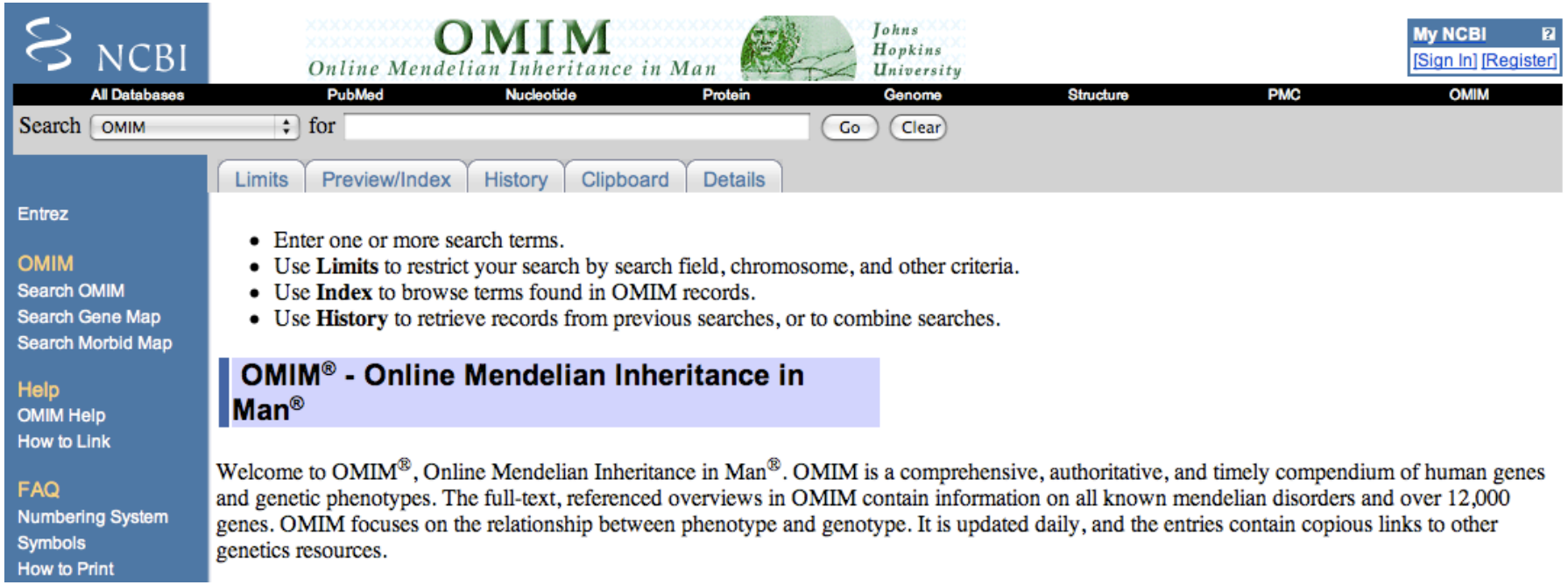
Cloning: Ethical Issues and Future Consequences

Plants of Tomorrow

Human Disease Genes Are Present on All Chromosomes



How Many Human Disease Genes Have Been Identified?



There are ~25,000 Genes in The Human Genome

1. ~3,413 Genes Correlate With a Disease Phenotype
2. The Molecular Basis of These Genetic Diseases Are Known (e.g., Sickle Cell Anemia, Hemophilia A, Tay-Sachs, Cystic Fibrosis, Duchene Muscular Dystrophy, Huntington Disease, etc,)

Genetic Tests Exist For These Disease Genes

OMIM, February 19, 2013

Structure, function and diversity of the healthy human microbiome

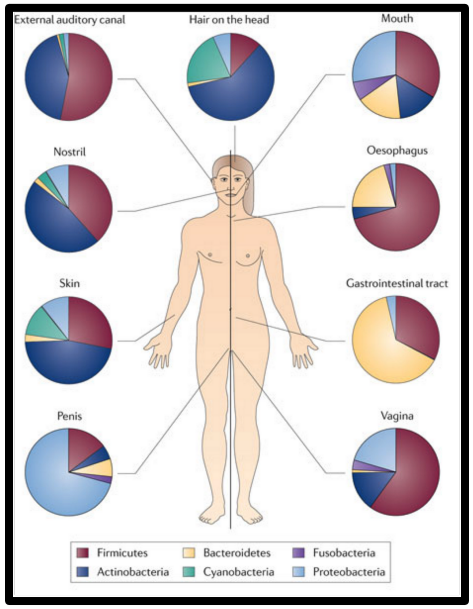
Microbe census maps out human body's bacteria, viruses, other bugs

It gives scientists a reference point of what the microbial community looks like in healthy people, and they plan to use it to study how changes in a person's microbiome can lead to illness.

By Rosie Mestel, Los Angeles Times

5:20 PM PDT, June 13, 2012

The Human Microbiome Project



Now that they have a picture of what a healthy microbiome looks like, scientists say they can use it as a reference point to compare with the microscopic life inside those who are sick, and probe whether changes in their microbial communities could be contributing to their illnesses.

Already, studies have linked microbial conditions to forms of inflammatory bowel disease such as ulcerative colitis and Crohn's disease. But there are suggestions that our flora may be involved in many more disorders, such as diabetes, psoriasis, asthma, heart disease, rheumatoid arthritis, obesity and colorectal cancer.

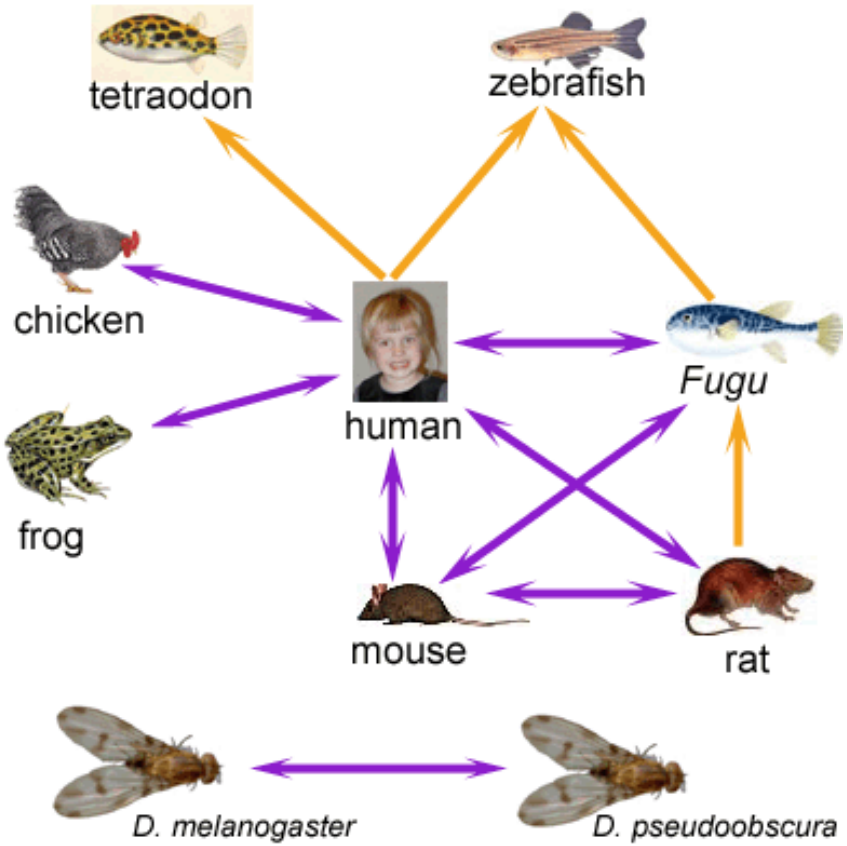
In time, researchers hope to develop therapies to put a perturbed or just plain broken microbiome back to rights. They might feed a person corrective bacteria, for example, or the type of food that would encourage the right microbes to grow.

In one small but dramatic example of what might one day be routine, Finnish researchers reported in March that patients with recurring *Clostridium difficile* infections recovered after fresh fecal material from healthy donors was transplanted into their guts.

Despite the current preoccupation with probiotics as cure-alls, scientists say they have a long way to go before they truly know how to design such therapies.

The emerging appreciation for bacteria raises important questions about whether overuse of antibiotics is contributing to disease, said Dr. David A. Relman, a microbiologist and infectious-disease clinician at the Stanford University School of Medicine, who wrote a commentary that accompanies the Nature papers. For instance, *C. difficile* infections can occur when antibiotic treatments kill off normal gut flora and permit the dangerous bacteria to flourish.

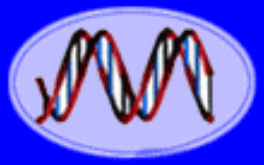
The Genomes of Many Organisms Have Been Sequenced Providing New Knowledge About Our Origins and Cellular Functions



The Future is Unlimited!

183 Eukaryotic &
3,950 Prokaryotic
Genomes Have Been
Sequenced as of 2013
&
17,500 Genome Projects
Ongoing!
http://www.genomesonline.org/cgi-bin/GOLD/bin/gold.cgi

Providing Thousands of New Genes and Proteins To Be Engineered For Practical Applications (e.g., cellulases in termite gut bacteria for biofuel production)



DNA
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Entire Genetic Code
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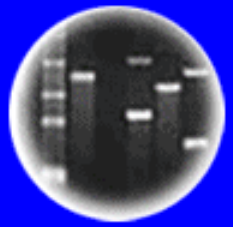

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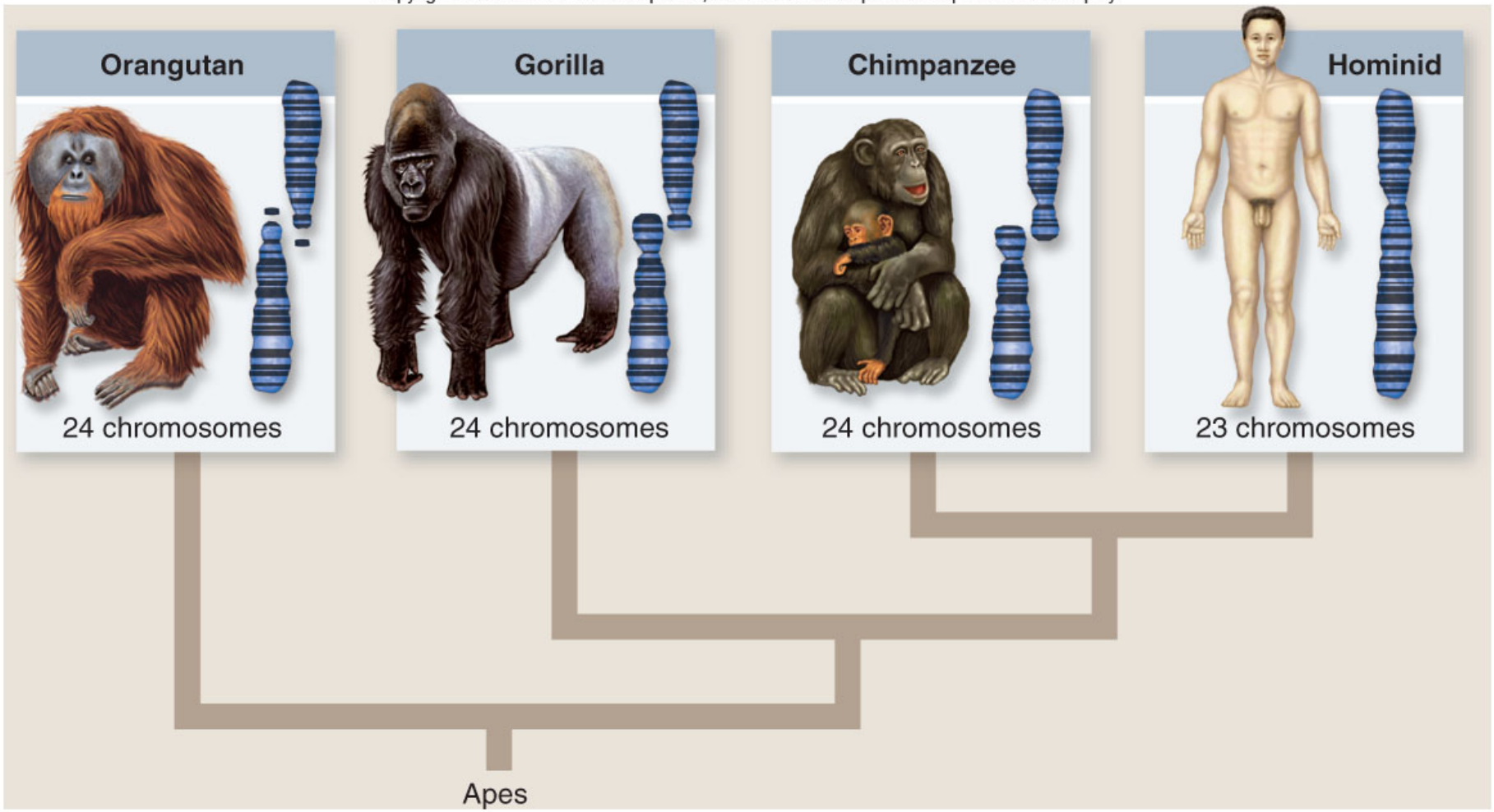
Plants of Tomorrow

A New Comparative Genomics Field Has Emerged Allowing the Comparison of Entire Genomes!

Comparison of Mammalian Genomes Attempts To Determine "What Makes a Man, a Man and a Mouse a Mouse"

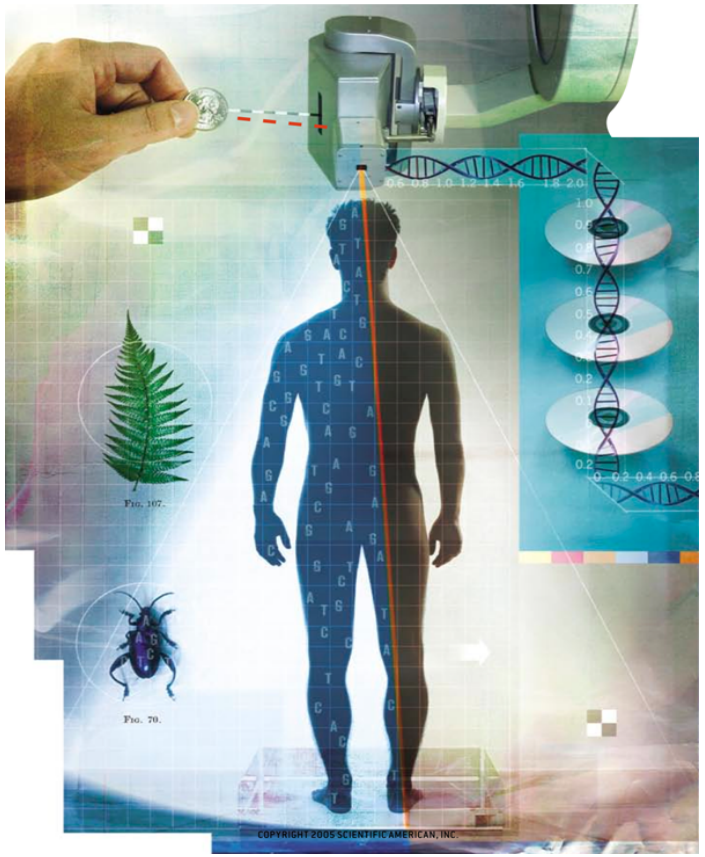


There is <1% Difference Between Human & Chimpanzee DNAs!

The Ultimate Measure of Individuality Personal Genome Sequence & Comparing Individual Human Genomes

Genomes for ALL

Next-generation technologies that make reading DNA fast, cheap and widely accessible are coming in less than a decade. Their potential to revolutionize research and bring about the era of truly personalized medicine means the time to start preparing is now

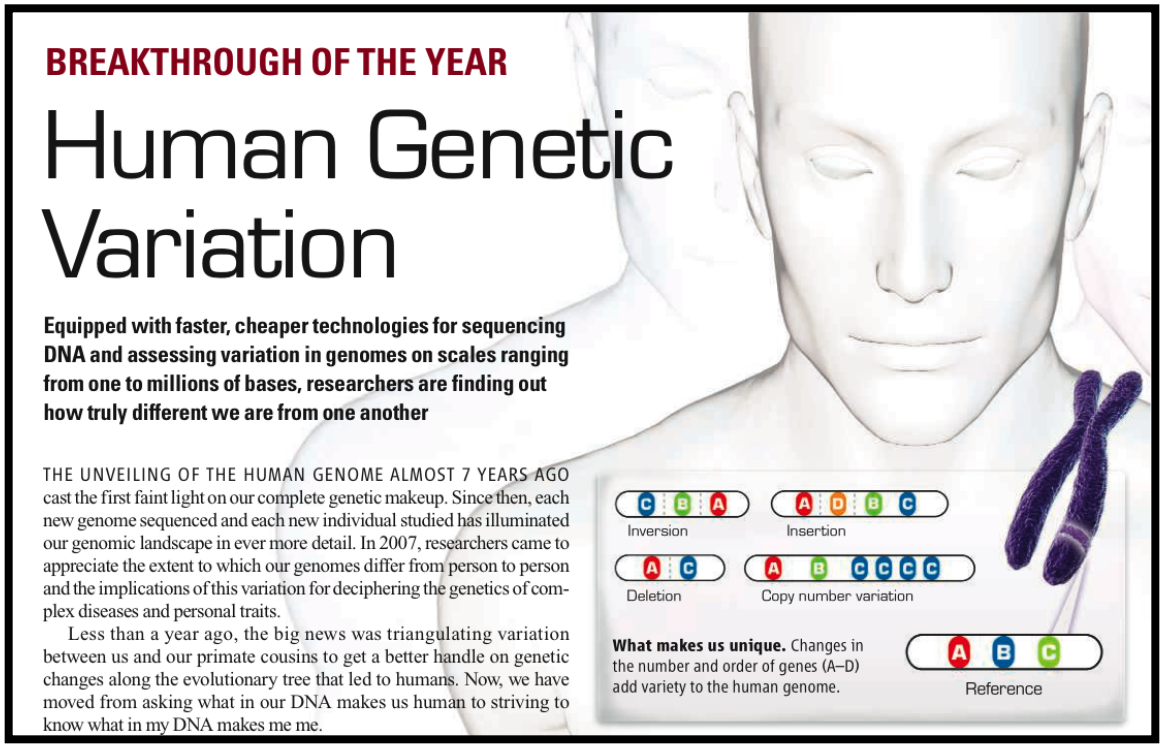


Find DNA Variability in <u>All</u> Genes & Associate with Specific Traits!

Ultimately-You <u>Are</u> What Is In Your Genome

Identifying DNA Variations Between Individuals Many Uses

1. Marking and Identifying Disease Genes
2. Paternity, Individual Identification, Forensics
3. Human Population History and Origins



BREAKTHROUGH OF THE YEAR

Human Genetic Variation

Equipped with faster, cheaper technologies for sequencing DNA and assessing variation in genomes on scales ranging from one to millions of bases, researchers are finding out how truly different we are from one another

THE UNVEILING OF THE HUMAN GENOME ALMOST 7 YEARS AGO cast the first faint light on our complete genetic makeup. Since then, each new genome sequenced and each new individual studied has illuminated our genomic landscape in ever more detail. In 2007, researchers came to appreciate the extent to which our genomes differ from person to person and the implications of this variation for deciphering the genetics of complex diseases and personal traits.

Less than a year ago, the big news was triangulating variation between us and our primate cousins to get a better handle on genetic changes along the evolutionary tree that led to humans. Now, we have moved from asking what in our DNA makes us human to striving to know what in my DNA makes me me.

What makes us unique. Changes in the number and order of genes (A–D) add variety to the human genome.

Your Complete Genome Can Now Be Decoded and Sequenced Very Inexpensively ($1,000)!!

Genome of DNA Pioneer Is Deciphered

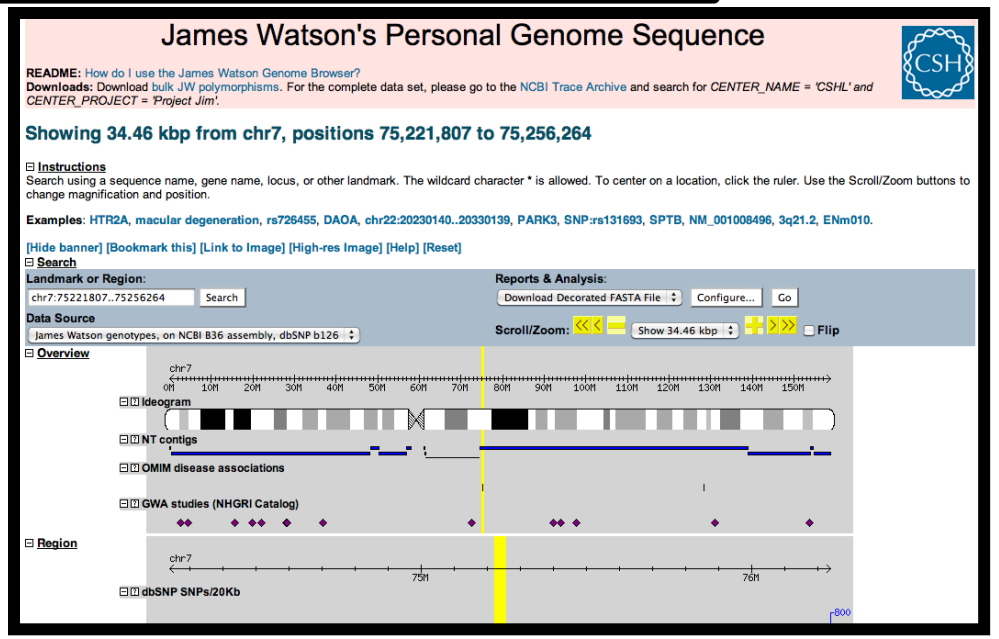
By NICHOLAS WADE
Published: May 31, 2007

A map of human genome variation from population-scale sequencing

~200 Individual Genomes

The 1000 Genomes Project Consortium*

Nature, October 28, 2010



The Era of Personalized Genomes is Here!

PRENATAL DIAGNOSIS

Maternal Plasma DNA Sequencing Reveals the Genome-Wide Genetic and Mutational Profile of the Fetus

Non-Invasive Advantage of Sequencing Fetal Genome

February 18, 2013

DNA Test for Rare Disorders Becomes More Routine

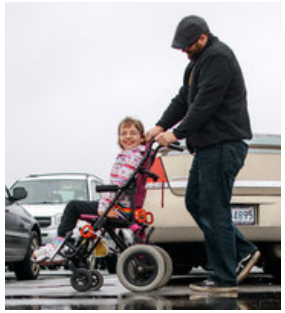
By GINA KOLATA

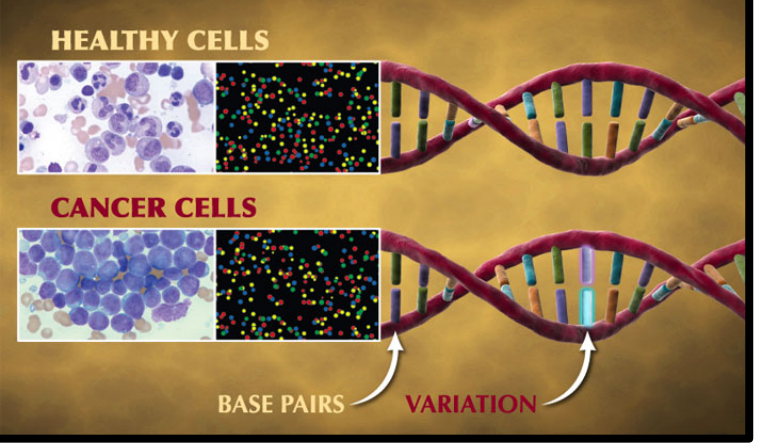
Advantages of Sequencing Genome

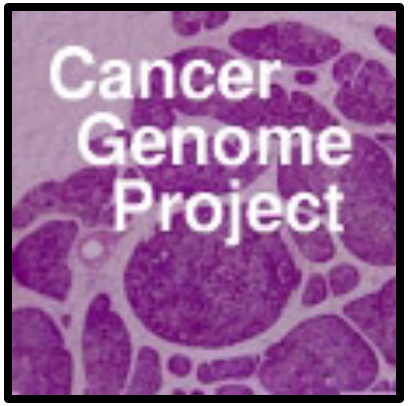
- Determine If a Genetic Basis of Disease
- 25% Detection of Genetic Cause
- 3% Better Care & 1% Actual Treatment
- Eligible For Insurance & Special Care
- Certainty in Knowing Something is Wrong
- Treatment Possibilities

GeneDx DNA DIAGNOSTIC EXPERTS

CASK Gene Defect
10 Cases in World
CASK Gene ~450,000b in Length & Encodes a Protein Important For Neuron Interactions







Mapping Cancer Genes

The 1,000 Genomes Project Will Provide Novel Insight in Human Genomes, Ancestry, & Disease Genes

Only Possible Using New Sequencing Methods

1,000 Genomes

Gene-sequencing projects keep getting bigger.
Tuesday, January 22, 2008
By Emily Singer

In a testament to the steady plummet in sequencing costs, today the National Human Genome Research Institute (NHGRI) announced a massive international collaboration to sequence the genomes of 1,000 people from around the world.

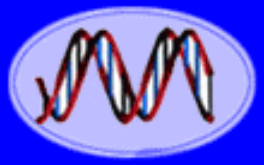
According to the NHGRI statement,

> "The 1000 Genomes Project will examine the human genome at a level of detail that no one has done before," said Richard Durbin, Ph.D., of the Wellcome Trust Sanger Institute, who is co-chair of the consortium. "Such a project would have been unthinkable only two years ago. Today, thanks to amazing strides in sequencing technology, bioinformatics and population genomics, it is now within our grasp. So we are moving forward to build a tool that will greatly expand and further accelerate efforts to find more of the genetic factors involved in human health and disease."
>
> During its two-year production phase, the 1000 Genomes Project will deliver sequence data at an average rate of about 8.2 billion bases per day, the equivalent of more than two human genomes every 24 hours. The volume of data--and the interpretation of those data--will pose a major challenge for leading experts in the fields of bioinformatics and statistical genetics.

2 Human Genomes Every 24 hrs !

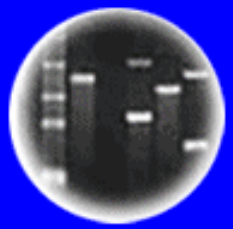
The 1,000 volunteers will be selected from those who participated in the HapMap project, a map of common genetic variation (see "A New Map for Health"), and will include:

Yoruba in Ibadan, Nigeria; Japanese in Tokyo; Chinese in Beijing; Utah residents with ancestry from northern and western Europe; Luhya in Webuye, Kenya; Maasai in Kinyawa, Kenya; Toscani in Italy; Gujarati Indians in Houston; Chinese in metropolitan Denver; people of Mexican ancestry in Los Angeles; and people of African ancestry in the southwestern United States.



DNA
Genetic Code of Life

Entire Genetic Code of a Bacteria



DNA Fingerprinting

Cloning: Ethical Issues and Future Consequences

Plants of Tomorrow

ARTICLE

Nature, October 28, 2010

doi:10.1038/nature09534

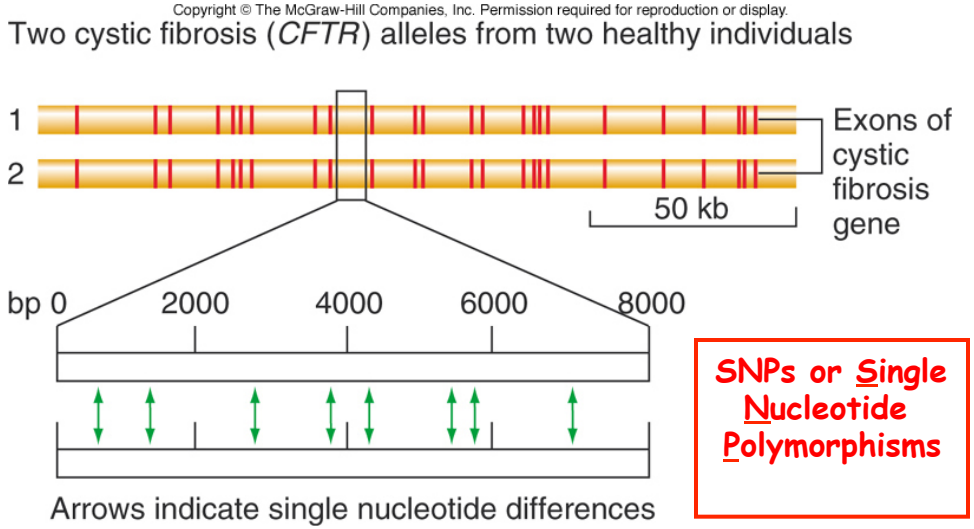
A map of human genome variation from population-scale sequencing

The 1000 Genomes Project Consortium*

The 1000 Genomes Project aims to provide a deep characterization of human genome sequence variation as a foundation for investigating the relationship between genotype and phenotype. Here we present results of the pilot phase of the project, designed to develop and compare different strategies for genome-wide sequencing with high-throughput platforms. We undertook three projects: low-coverage whole-genome sequencing of 179 individuals from four populations; high-coverage sequencing of two mother–father–child trios; and exon-targeted sequencing of 697 individuals from seven populations. We describe the location, allele frequency and local haplotype structure of approximately 15 million single nucleotide polymorphisms, 1 million short insertions and deletions, and 20,000 structural variants, most of which were previously undescribed. We show that, because we have catalogued the vast majority of common variation, over 95% of the currently accessible variants found in any individual are present in this data set. On average, each person is found to carry approximately 250 to 300 loss-of-function variants in annotated genes and 50 to 100 variants previously implicated in inherited disorders. We demonstrate how these results can be used to inform association and functional studies. From the two trios, we directly estimate the rate of *de novo* germline base substitution mutations to be approximately 10^{-8} per base pair per generation. We explore the data with regard to signatures of natural selection, and identify a marked reduction of genetic variation in the neighbourhood of genes, due to selection at linked sites. These methods and public data will support the next phase of human genetic research.

- Sequenced Genomes of ~900 individuals
- From Seven Different Global Populations
- Identified 15,000,000 SNPs
- 50-100 Variants in Disease Genes Per Person
- 10^{-8} Mutations Per bp Per Generation (~30 per Genome)
- 3,000,000 Unique SNPs Per Person
- 750,000 Unique Indels Per Person

Most DNA Variations Between Individuals Occur Because of Base-Pair Changes in Non-Coding Regions of the Genome



SNPs or Single Nucleotide Polymorphisms

To Be on the safe side, suppose you assume that only 80% (0.8) of the 3 billion base pairs in the genome are noncoding, and on average only 1 base pair in 700 is polymorphic. With these assumptions, you can determine the frequency of polymorphism within a single individual by multiplying 3 billion by 0.8 and then multiplying that amount by 1/700:

(3x109) x 0.8 = 2.4 x 109, (2.4 x 109) x 1/700 = 3.4 million.

The result of 3.4 million is astonishing: It means that there are millions of differences between any two haploid sets of human chromosomes. Combined with differences in coding and regulatory sequences (which occur much less frequently), the millions of polymorphisms at anonymous loci contribute to an enormous pool of potential DNA markers.

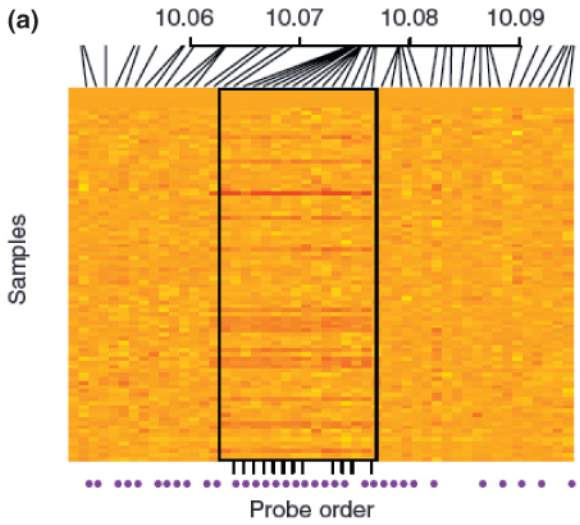
Types of DNA Polymorphisms

TABLE 11.1 Classes of DNA Polymorphisms

Class	Size of Locus	Number of Alleles	Number of Loci in Population	Rate of Mutation	Use	Method of Detection
SNP	Single base pair	2	100 million	10^{-9}	Linkage and association mapping	PCR followed by ASO hybridization or primer extension
Microsatellite	30–300 bp	2–10	200,000	10^{-3}	Linkage and association mapping	PCR and gel electrophoresis
Multilocus minisatellite	1–20 kb	2–10	30,000	10^{-3}	DNA fingerprinting	Southern blot and hybridization
Indels (deletions and duplications)	1–100 bp	2	N/A	$<10^{-9}$	Linkage and association mapping	PCR and gel electrophoresis

This is What Makes Us Unique Individuals!

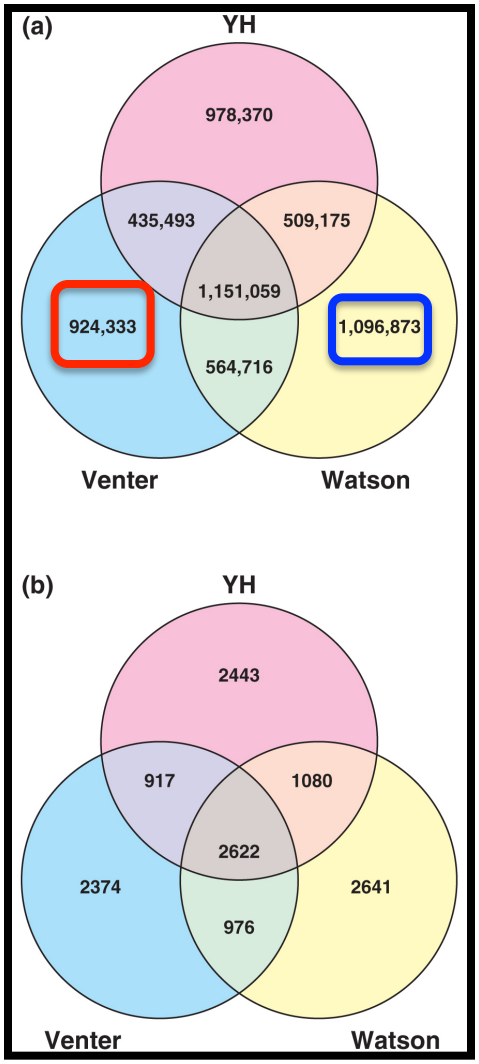
There is ~1bp Change per 700bp in Human Genomes or ~3.4 Million bp Differences Between Individuals ~0.1% of Genome



Copy Number Variants Also Occur in the Human Genome and Can Vary From Individual to Individual

And Can Be Correlated With Diseases (Cause or Effect?)

Comparison of Watson's and Ventner's Genomes Indicates That Individuals Have Unique SNPs!



YH= Anonymous Chinese Man

(a)

Allele	Genome	Single-Strand Notation
1	AGCTCTGATAC TCGAGACTATG	AGCTCTGATAC
2	AGCTCCGATAC TCGAGGCTATG	AGCTCCGATAC

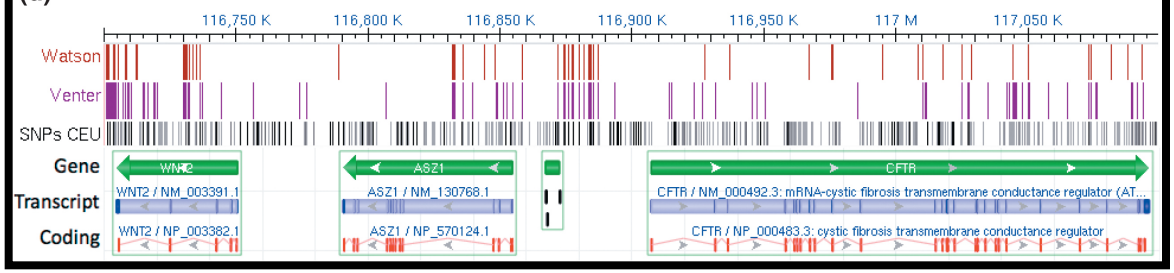
(b)

Genotype	Notation
Homozygous T	TT
Heterozygous T	TC
Homozygous C	CC

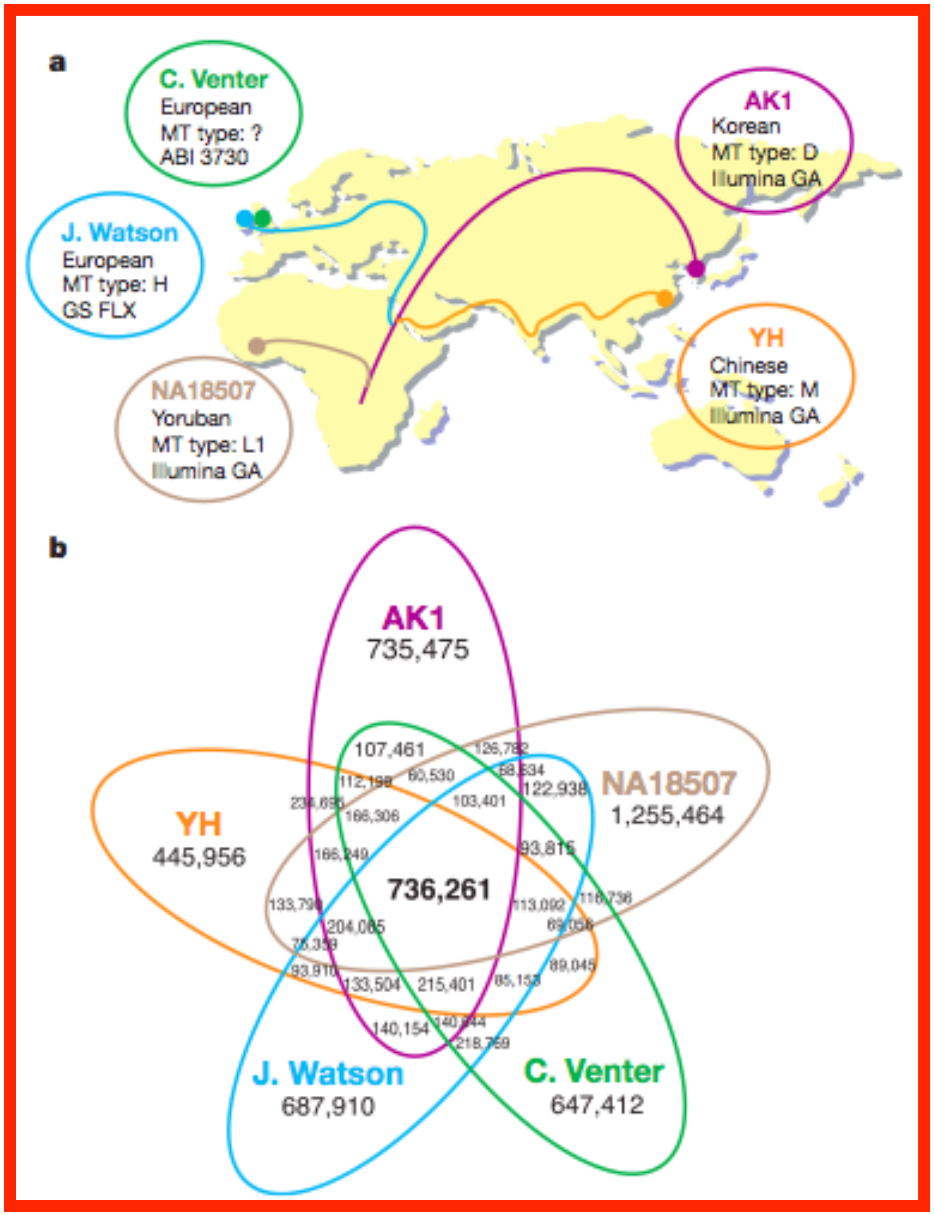
(c)

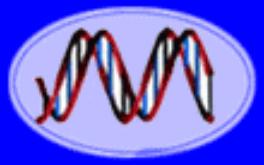
Human 1 TTGACGTATAAATGATCTTTATATTTTCAGAAGTC
Human 2 TTGACGTATAAATGATCTTTATATCTTCAGAAGTC
Chimp TTGACATATAAATGATCTTTATATCTTCAGAAGTC

(d)



In Fact, Everyone Has a Large Number of Unique SNPs!





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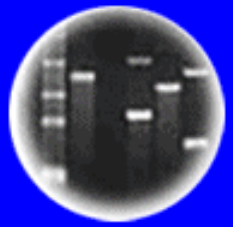

DNA Fingerprinting

Cloning: Ethical Issues
and Future Consequences

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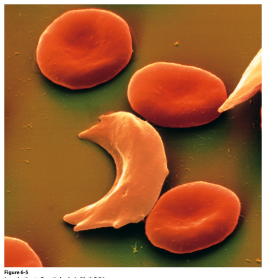
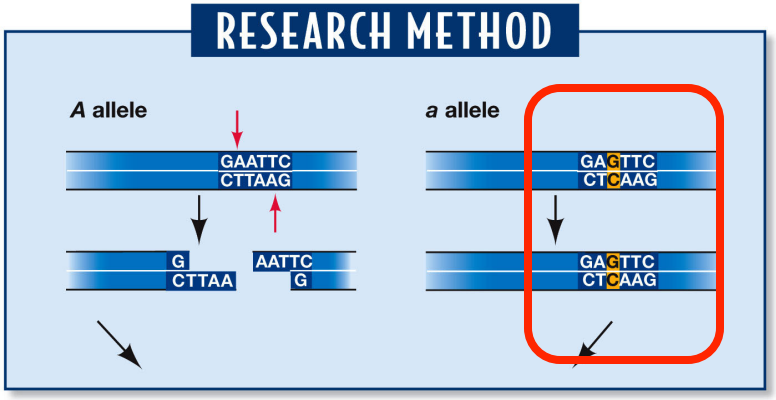
Using SNPs or DNA Sequence Variation As Markers For Disease Genes

Remember: Only a Small Fraction of Human Genes Are Known To Cause Diseases

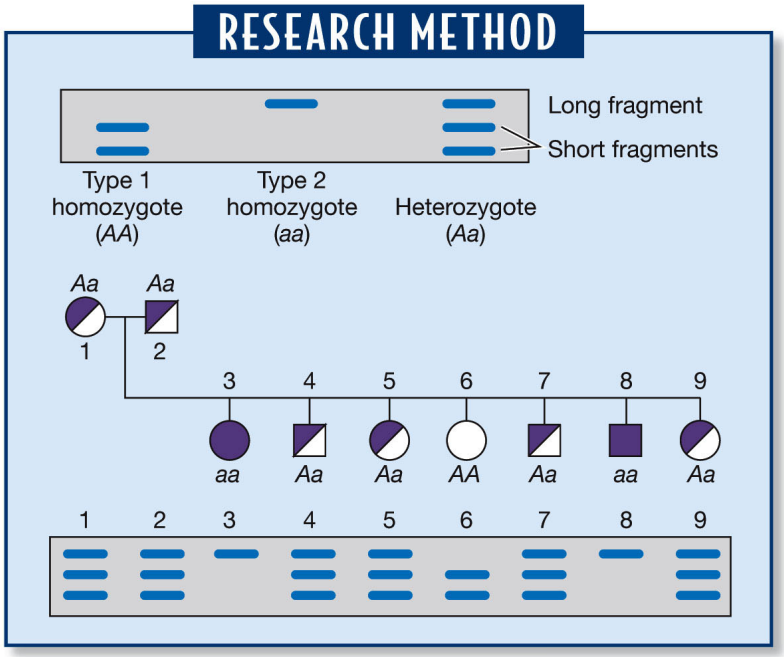


Using RFLPs + Markers to Identify the Sickle Cell Allele (Single Gene Test)



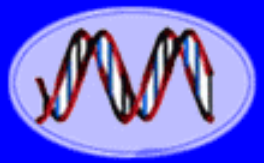
Loss of Restriction Site in a Allele (in gene)

Detected By Blots Or PCR



SNP Leads to RFLP!!!

LIFE 8e, Figure 17.8 (Part 2)



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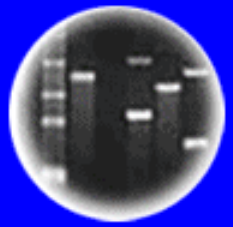

DNA Fingerprinting

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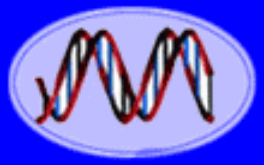
Plants of Tomorrow

Should DNA Testing Should Be Carried Out On Every Individual Born in the US?

a. Yes
b. No



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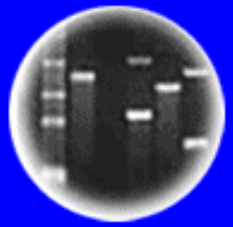


DNA Fingerprinting

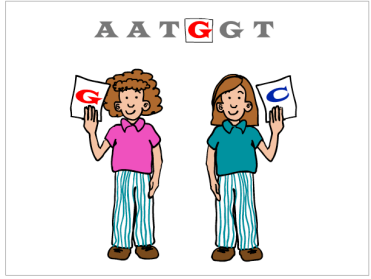
Cloning: Ethical Issues
and Future Consequences

Plants of Tomorrow

Are DNA Tests e Carried Out On Every New Baby Born in the US?

a. Yes
b. No

SNPs Can Be Associated/Linked With Specific Physical Traits



OCA2

From SNPedia

OCA2, the oculocutaneous albinism gene (also known as the human P protein gene, or, DN10), is a gene associated with albinism and certain pigmentation effects in general such as eye color, skin color, and hair color.

A large (>3,000 individuals) study of Caucasians indicates that the following **OCA2** variants, all located in the first intron of the gene, are preferentially linked to blue eye color inheritance; together, they form haplotypes that (in some cases at least) predict eye color with greater than 50:50 odds. [PMID 17236130; OMIM 203200.0013 (http://www.ncbi.nlm.nih.gov/entrez/dispomim.cgi?id=203200&a=203200_AllelicVariant0013)]

- rs7495174
- rs6497268
- rs11855019

The haplotypes are defined in order as listed above for these 3 SNPs, so, for example, the TGT haplotype refers to rs745174(T)-rs6497268(G)-rs11855019(T). The correspondence between diplotypes (the two haplotypes in one individual) and the % of individuals with blue/gray, green/hazel/ and brown eye color , respectively, was reported as follows for the most common diplotypes[PMID 17236130]:

- TGT/TGT: 62.5, 28.0, 9.5
- TGT/***TTC***: 47.1, 20.3, 32.6
- TGT/***CGT***: 28.6, 14.3, 57.1
- TGT/***TGC***: 27.9, 22.1, 50.0
- ***TGC***/***TTC***: 25.0, 8.3, 66.7
- ***TTT***/***TGC***: 20.7, 31.0, 48.3
- TGT/***TTT***: 17.6, 38.5, 44.0
- TGT/***CTC***: 7.9, 23.3, 68.8

The haplotypes shown in ***bold italics*** represent the ones reported by the authors of this study to be most associated with brown eye color. Furthermore, the haplotypes shown above are as published, and the associated SNPs - which have since changed # as well - are not in the orientation shown in dbSNP.

More recently, a study of a large Danish family led to associations with 2 SNPs in a different region of **OCA2** as linked to blue or brown eye color:

- rs12913832
- rs1129038

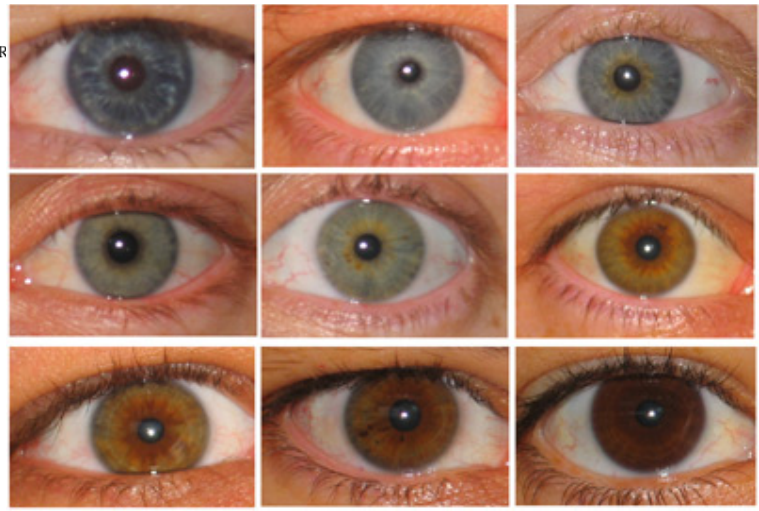
Earlier studies found different regions of the **OCA2** gene to also be predictive of eye color;

- **OCA2** SNP rs1800401 helps predict brown eye color. [PMID 12163334, PMID 15889046; OMIM 203200.0011 (http://www.ncbi.nlm.nih.gov/entrez/dispomim.cgi?id=203200&a=203200_AllelicVariant0011)]
- **OCA2** SNP rs1800407 may be associated with green/hazel eye color in some populations, but not others. [PMID 12163334, PMID 15889046; OMIM 203200.0012 (http://www.ncbi.nlm.nih.gov/entrez/dispomim.cgi?id=203200&a=203200_AllelicVariant0012)]

is a	gene
is	mentioned by
wikipedia	OCA2 (http://en.wikipedia.org/wiki/OCA2)
google	OCA2 (http://www.google.com/search?hl=en&q=OCA2)
gopubmed	OCA2 (http://www.gopubmed.org/search?q=OCA2)
23andMe	OCA2 (https://www.23andme.com/you/explorer/gene/?gene_name=OCA2)
GeneRIF	4948 (http://www.ncbi.nlm.nih.gov/sites/entrez?Db=gene&Cmd=ShowDetailView&TermToSearch=4948&ordinalpos=1&itool=EntrezSystem2.PEntrez.Gene.Gene_ResultsPanel.Gene_R
dbSNP	4948 (http://www.ncbi.nlm.nih.gov/SNP/snp_ref.cgi?locusId=4948&chooseRs=all)
PubMed	4948 (http://www.ncbi.nlm.nih.gov/sites/entrez?db=gene&cmd=Link&LinkName=gene_pubmed&from_uid=4948)
HugeNav	4948 (http://hugenavigator.net/HuGENavigator/huGEPedia.do?firstQuery=OCA2}&geneID=4948&typeSubmit=GO&check=y&typeOption=gene&which=2&pubOrderType=pubD)

	Chromosome position
Rs1129038	26,030,454
Rs11631797	26,175,874
Rs12593929	26,032,853
Rs1800401	25,933,648
Rs1800407	25,903,913
Rs2238289	26,126,810
Rs2240203	26,167,797
Rs28934272	25,903,842
Rs3935591	26,047,607
Rs3940272	26,142,318
Rs4778241	26,012,308
Rs7170852	26,101,581
Rs7183877	26,039,328
Rs7495174	26,017,833
Rs8028689	26,162,483
Rs916977	26,186,959

SNPs in Human P Protein (OCA2) Gene Lead To Different Eye Colors (Physical & Molecular Markers)



Human Eye Color

Constructing Portraits From DNA

Research & Discovery

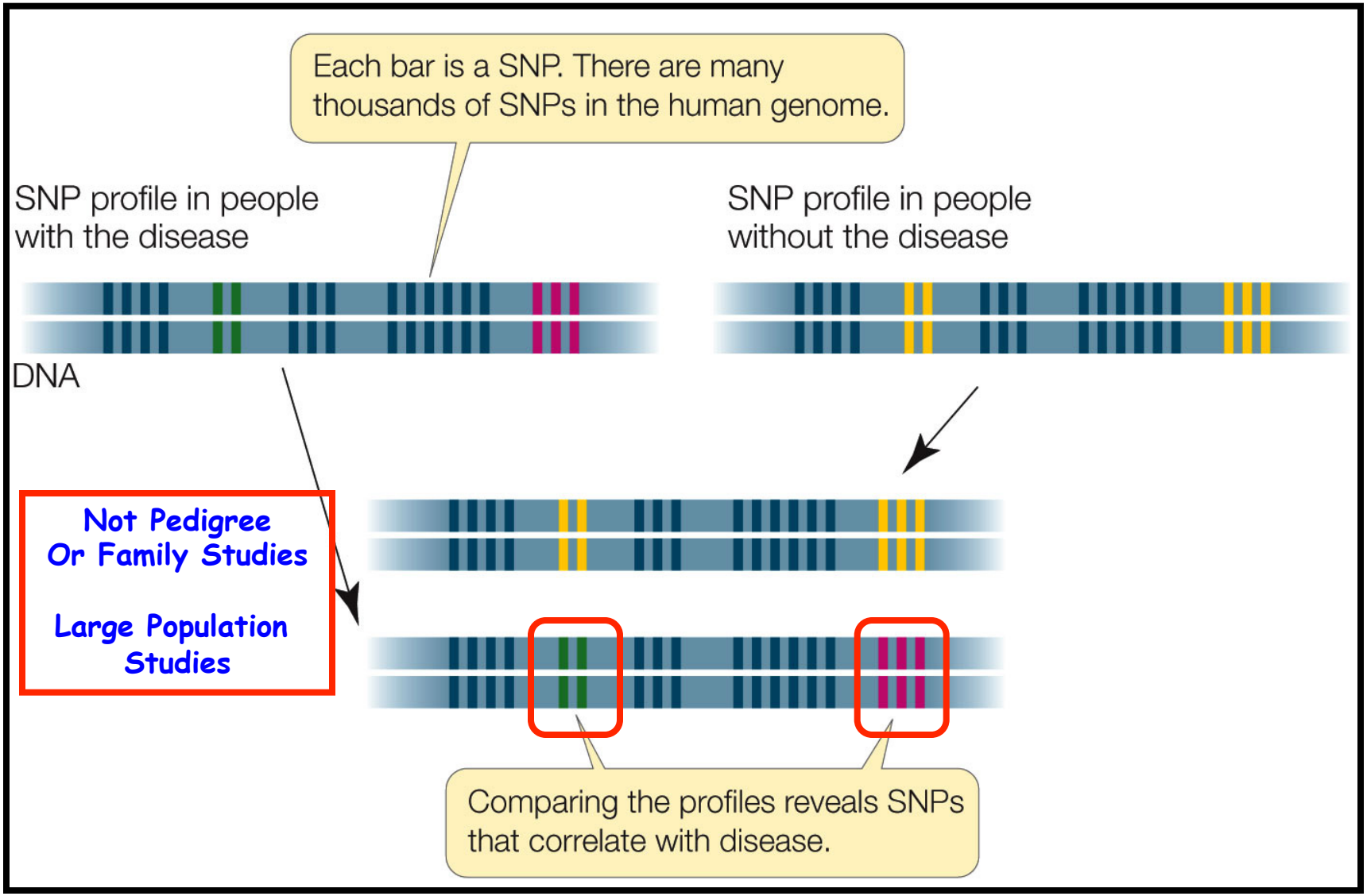
Portrait in DNA

Can forensic analysis yield police-style sketches of suspects? BY CHRISTINE SOARES

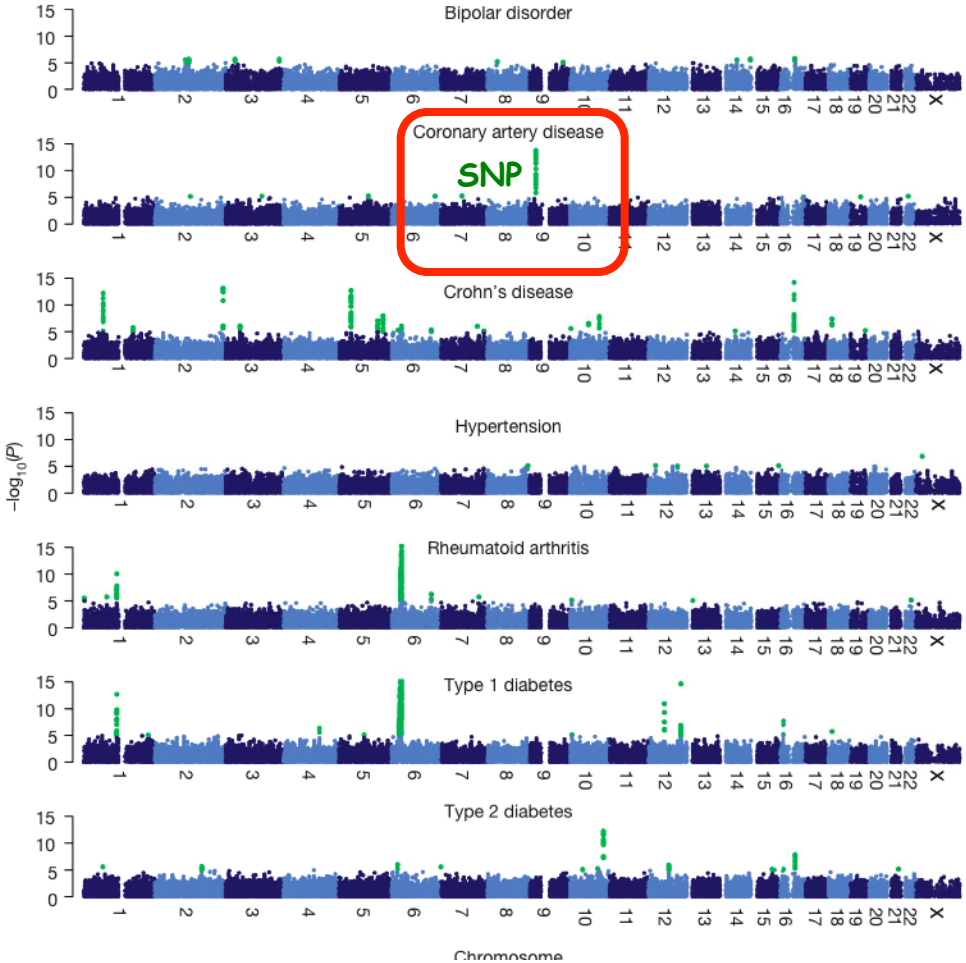
MALE, SHORT AND STOUT, WITH DARK SKIN, BROWN EYES, shovel-shaped teeth, type A+ blood and coarse, dark brown hair giving way to pattern baldness. He would have a high tolerance for alcohol and a higher-than-average risk of nicotine dependence—fortunately, he lived thousands of years before humans discovered smoking. The description of a Stone Age Greenland resident published in February paints an extraordinary portrait of a man who vanished more than 4,000 years ago, drawn almost solely from his DNA remains.

RECONSTRUCTED: Ancient DNA provided details about the looks of a man who lived in Greenland more than 4,000 years ago.

Using SNPs and Population Association Studies to Find Disease Markers and Genes



Correlating SNPs With Specific Diseases Using SNP Chips & Association Studies



Note: Probability

SNPs May Be Near Or In Relevant Genes

TABLE 17.5

SNP Human Genome Scans and Diseases

DISEASE	LOCATION OF SNP (CHROMOSOME NUMBER)	% INCREASED RISK	
		HETEROZYGOTES	HOMOZYGOTES
Breast cancer	8	20	63
Coronary heart disease	9	20	56
Heart attack	9	25	64
Obesity	16	32	67
Diabetes	10	65	277
Prostate cancer	8	26	58

Using Large Populations SNPs Can Be Used As Markers For Specific Genes/Traits

SNPedia (http://www.snpedia.com/)

- New model for prostate cancer based on 5 SNPs
- rs1815739 sprinters vs endurance athletes
- rs4420638 and rs429358 can raise the risk of Alzheimer's disease by more than 10x
- rs6152 can prevent baldness
- rs9939609 triggers obesity
- rs662799 prevents weight gain from high fat diets
- rs7495174 green eye color
- rs7903146 in 3% of the population greatly increases the risk of type-2 diabetes
- rs12255372 linked to type-2 diabetes and breast cancer
- rs2395029 asymptomatic HIV viral load set point
- rs324650 influences intelligence and alcohol dependence
- rs1799971 makes alcohol cravings stronger
- rs17822931 determines earwax

Caution

How Will You Use the Information?
How Good Are The Correlations?
What To Do With The Information?
Privacy Issues?
Group Differences? Discrimination?

- rs53576 in the oxytocin receptor influences social behavior and personality
- rs1815739 muscle performance
- rs7412 and rs429358 can raise the risk of Alzheimer's disease by more than 10x
- rs6152 can influence baldness
- rs333 resistance to HIV
- rs1800497 in a dopamine receptor may influence the sense of pleasure
- rs1805007 determines red hair and sensitivity to anesthetics
- rs9939609 triggers obesity and type-2 diabetes
- rs662799 prevents weight gain from high fat diets
- rs7495174 green eye color and rs12913832 for blue eye color
- rs7903146 in 3% of the population greatly increases the risk of type-2 diabetes
- rs12255372 linked to type-2 diabetes and breast cancer
- rs1799971 makes alcohol cravings stronger
- rs17822931 determines earwax
- rs4680 varied cognitive effects
- rs1333049 coronary heart disease
- rs1801133 folate metabolism and several cancers
- rs1051730 and rs3750344 nicotine dependence
- rs4988235 lactose intolerance

Examples of SNPs in SNPedia Database

Examples of Whole Genomes in SNPedia Database

(http://www.snpedia.com/)

These are the 105 public genomes. They are from real people who've chosen to share their data to help all of us learn more about our genomes. but be sure to check the report header to understand how up to date each is.

	Platform	Raw data available	Summary
Aaron Vollrath	23andMe v2		Male on 23andMe
Almelina	23andMe v2	true	Female with cancer 2x
Bgreshake	23andMe v3		German Male 23andMe v3
Blainebettinger	23andMe v2 FTDNA Family Finder		23andMe v. FTDNA Family Finder data
Corpas aunt	23andMe v3		Visualized family snps; whole family 23andMe genotypes
Corpas dad	23andMe v3		Visualized family snps; whole family 23andMe genotypes
Corpas mom	23andMe v3		Visualized family snps; whole family 23andMe genotypes
Corpas sister	23andMe v3		Visualized family snps; whole family 23andMe genotypes
Daniel MacArthur	23andMe v3 23andMe v2 Lumigenix		1st Lumigenix, GNZ, 23andMe v2+3, blogger
David Ewing Duncan	Complete Genomics 23andMe v2 DeCODEme Navigenics		Full genome from Complete Genomics, but also microarrays from 23a
DeCODEme	DeCODEme		Sample deCODEme male
Denisova	Full Sequencing		a 41k year old member of the genus Homo
Dichro	23andMe v2 23andMe v1	true	23andMe male (v1 + v2)

DNA Can Be Used To Test For Hundreds of Disease Genes and Human Traits and Generate Personalized Gene Profiles

What Are the Problems & Laws That Govern Direct To Consumer DNA Tests?

And Before Birth!!!

23andMe

DNA Testing Into the Home - Fast & Inexpensive DNA Testing Kits!

Paternity

Ancestry

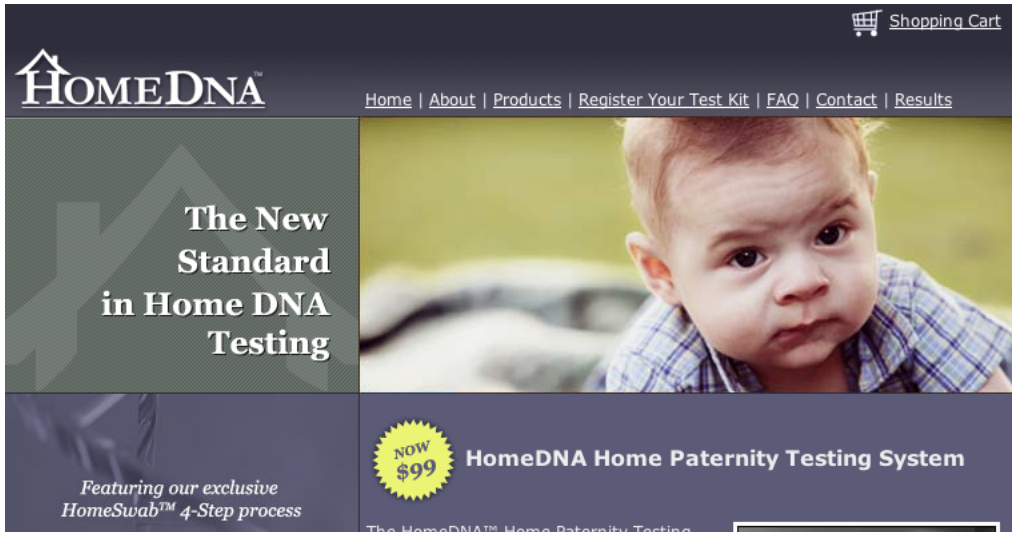
23andMe

DNA TRIBES

Navigenics

IDENTIGENE

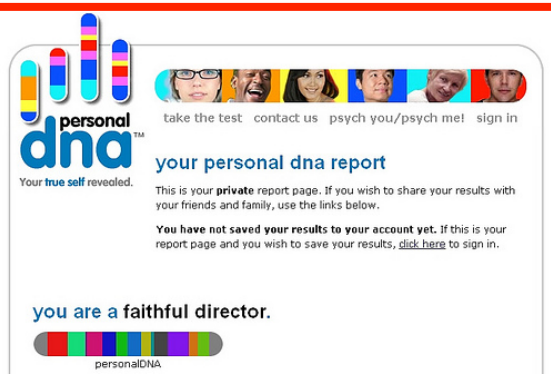
HOMEDNA

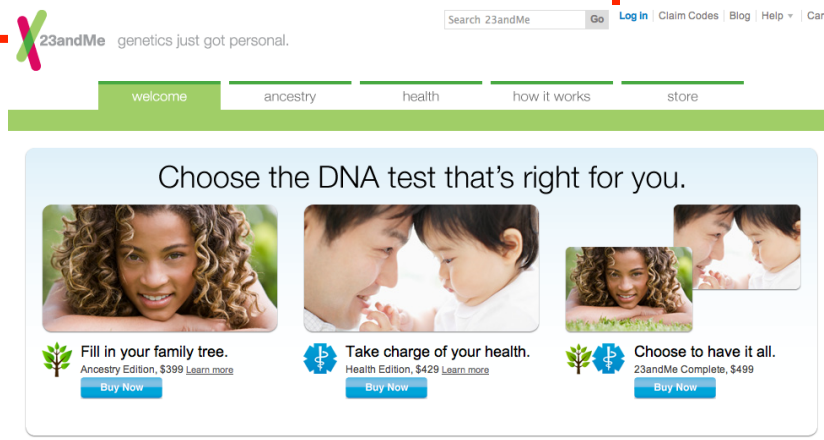


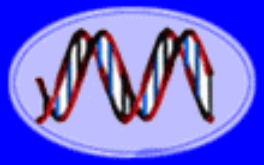
Immigration

The Problems With Human Genome Testing Companies Are?

a. Reliability of Results?
b. Validity of Association Studies
c. Privacy?
d. What To Do With Information Obtained?
e. FDA Regulatory Oversight?
f. Deceptive Practices
g. All of Above?







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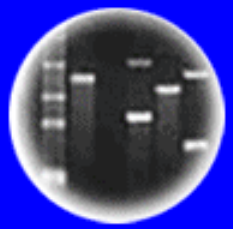

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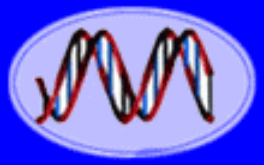
Problem: Different Companies-Different Predictions-No Oversight!

TABLE 1: PREDICTIONS FOR DISEASE RELATIVE RISKS FOR FIVE INDIVIDUALS

Disease	Female A	Female B	Female C	Male D	Male E
Breast cancer	↑↑	↑↑	↓↓		
Coeliac disease	↓↓	↓↓	↓↓	↓↓	↓↓
Colon cancer	==	==	=↓	↑↑	=↓
Crohn's disease	↓↑	↓↑	↓↓	↓↓	↓=
Heart attack	↓↓	=↓	=↓	=↓	↑↑
Lupus	↑↓	↓↓	↓↓	↑=	↑=
Macular degeneration	↓↓	↓↓	↑=	↓↓	↓↓
Multiple sclerosis	↑↑		↓↓	↓↓	↓↓
Prostate cancer				↑↑	↓↑
Psoriasis	↓↑		↑↓	↑↑	↓↓
Restless legs syndrome	=↓	↑↑	↓=	↓↑	↑↑
Rheumatoid arthritis	↑↑	↑↑	↓↓	↓↓	↑↑
Type 2 diabetes	↓↓	=↓	↓↓	↑↓	=↓

↑ increased risk (RR > 1.05), ↓ decreased risk (relative risk (RR) < 0.95), = average risk (0.95 ≤ RR ≤ 1.05). First prediction is from 23andMe; second prediction is from Navigenics. Different predictions are highlighted in beige.



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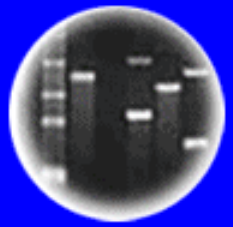

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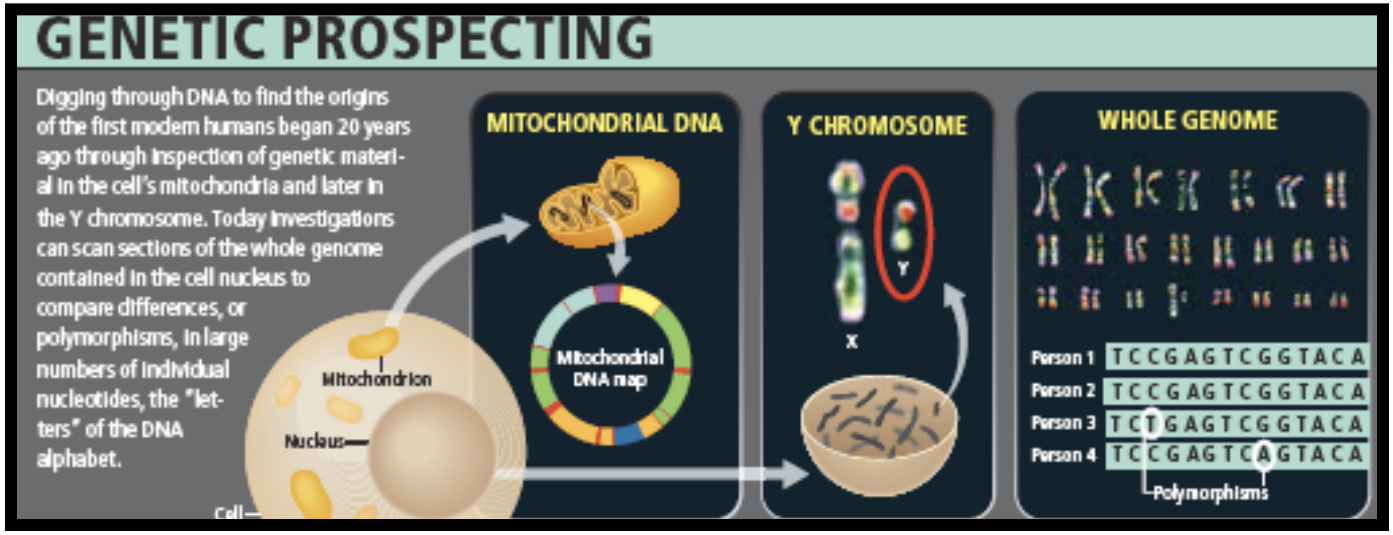
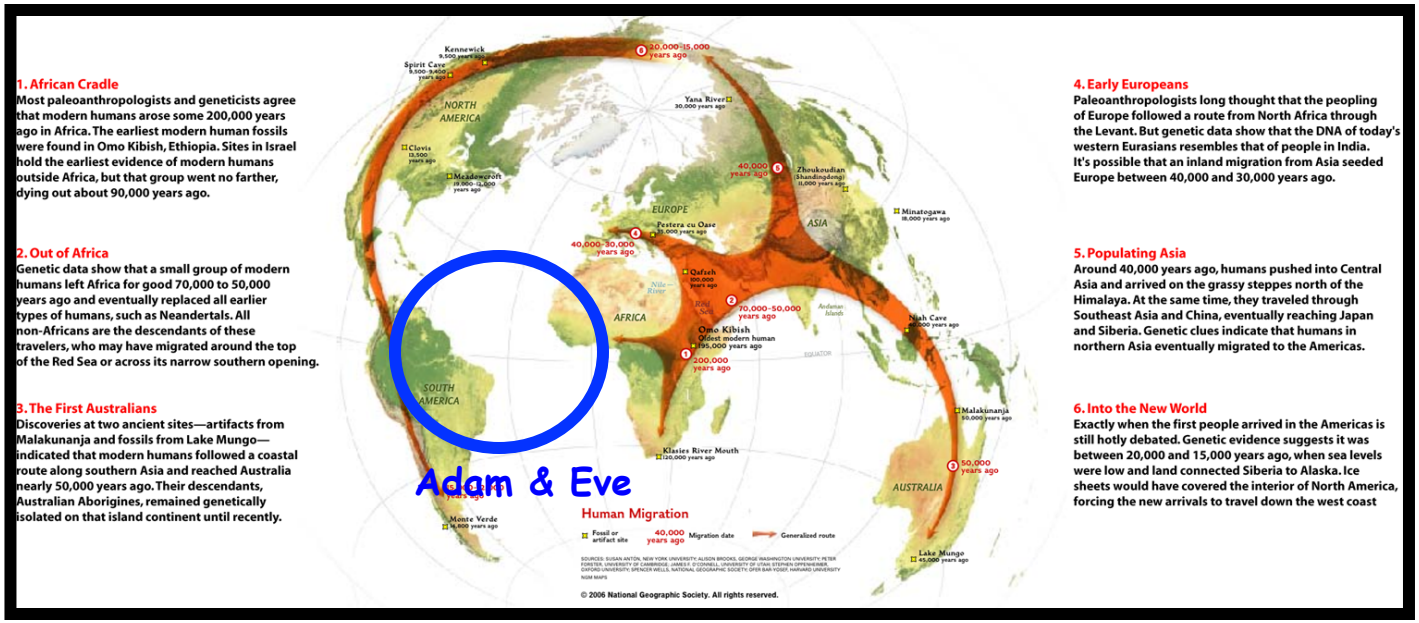
SNPS Can Be Used To Trace Human Populations & Origins





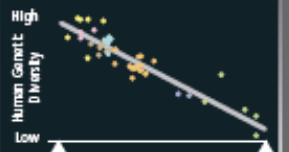
Human Population Relationships and Origins Using Whole-Genome Comparisons

[WHOLE-GENOME RESULTS]

LOOKING FAR AND WIDE

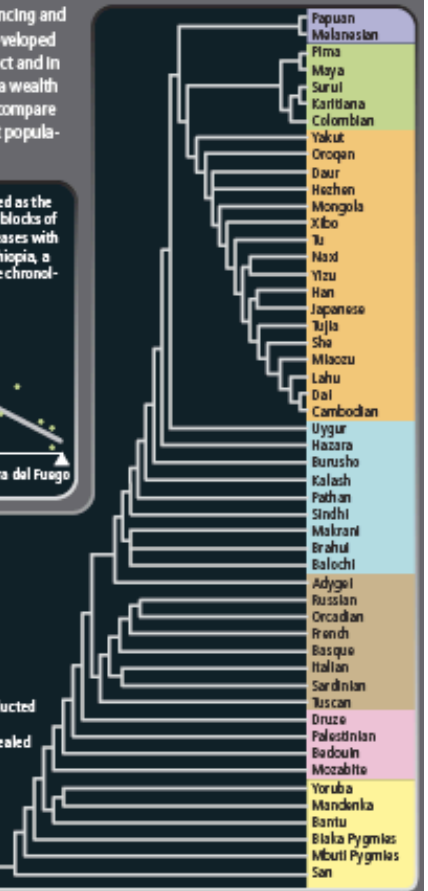
High-powered genetic sequencing and computational techniques developed for the Human Genome Project and in its aftermath have furnished a wealth of data that lets researchers compare genomes drawn from distinct populations around the globe.

The diversity of DNA—measured as the variation of nucleotides within blocks of DNA called haplotypes—decreases with distance from Addis Ababa, Ethiopia, a pattern that corresponds to the chronology of human migrations.

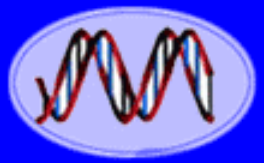


Geographic Region
- Oceania
- Americas
- East Asia
- Central and South Asia
- Europe
- Middle East
- Africa

Whole-genome analysis conducted by researchers at Stanford University and elsewhere revealed many of the populations that form the branches of a genetic tree beginning in Africa and expanding out to the rest of the world.



A genomic map of the world, crafted by researchers at the University of Michigan at Ann Arbor, shows that genetic diversity decreases outside of Africa. Each colored tile represents a common haplotype. Africa has more tiles than found on other continents and ones that correspond to haplotypes found nowhere else.



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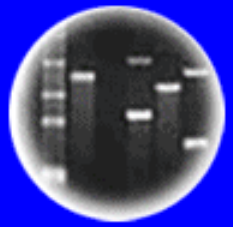

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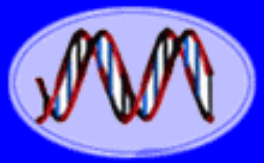
HUMAN DIVERSITY

RICHARD LEWONTIN

Scientific American Library
1982 ISBN 07167-14698



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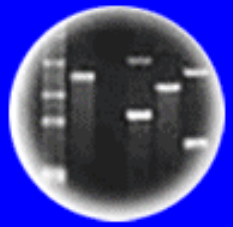

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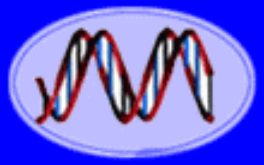
What Genes Are Responsible For Human Adaptations and Phenotypic Differences Between Major Human Groups?



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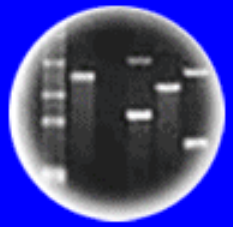

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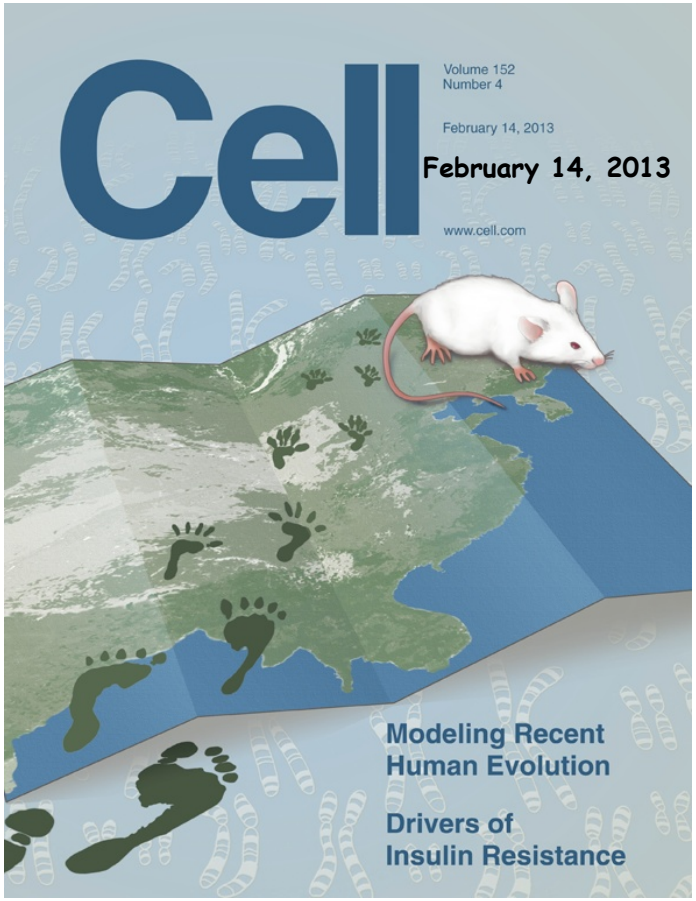
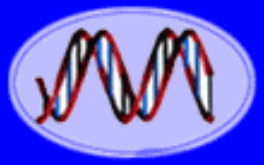
Identifying Recent Adaptations in Large-Scale Genomic Data



February 14, 2013

A map of human genome variation from population-scale sequencing

The 1000 Genomes Project Consortium*



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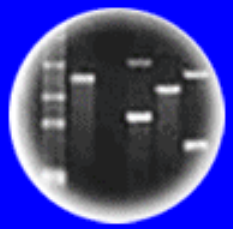

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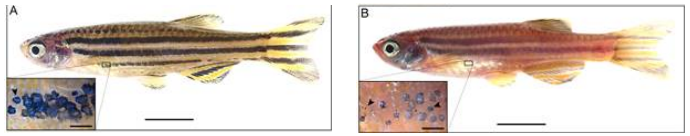
Human Loci Associated With Adaptive Traits

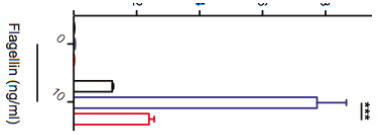
SLC24A5 – Solute Carrier Family 24 Member 5

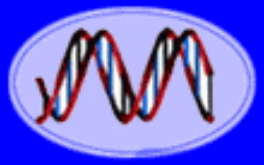
- One SNP changes 111th amino acid from alanine to threonine.
- Threonine is present in 98.5-100% of European populations, while alanine is present in 93%-100% of African populations.
- Largest degree of selection in human populations of European descent, because of greater sunlight requirement for Vitamin D synthesis makes lighter skin color more adaptive.
- And same amino acid change observed in "dark" and "golden" zebrafish!



TRL5 – Toll-like Receptor 5

- One SNP changes a leucine to phenylalanine amino acid
- Affects immunological clearance of bacterial pathogens and response to diseases, such as Legionnaire's Disease
- Variant may confer resistance to pathogens, and is found in 10% of European populations.





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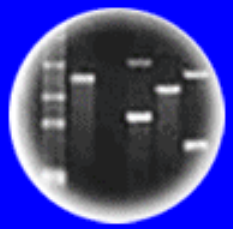

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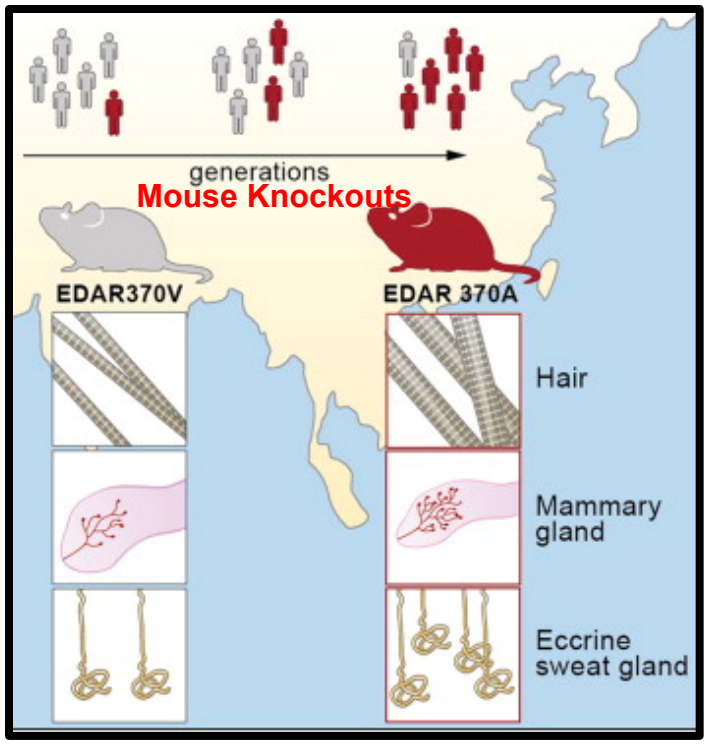
East Asian Physical Traits Linked to 35,000-Year-Old Mutation

By NICHOLAS WADE

What Is the Adaptive Significance?

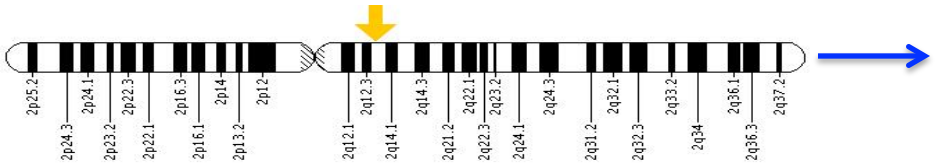


EDAR370 SNP in East Asians & Mouse Knock Out

- Thicker Hair Shafts
- More Sweat Glands
- Smaller Breasts
- Characteristic Teeth

Han Chinese	93%
Japanese	70%
Thai	70%
American Indians	80%

Ectodysplasin A Receptor Gene (EDAR)



The *EDAR* gene is located on the long (q) arm of chromosome 2 at position 13.

More precisely, the *EDAR* gene is located from base pair 109,510,926 to base pair 109,605,827 on chromosome 2.

Hair and Teeth Formation During Embryo Development

There is More Genetic Diversity Within Populations than Between Populations!! So Much for the Concept of Racial "Purity"!!!!

Proportion of genetic diversity accounted for within and between populations and races

Gene	Total $H_{species}$	Proportion		
		Within Populations	Within Races between Populations	Between Races
Hp	.994	.893	.051	.056
Ag	.994	.834	—	—
Lp	.639	.939	—	—
Xm	.869	.997	—	—
Ap	.989	.927	.062	.011
6PGD	.327	.875	.058	.067
PGM	.758	.942	.033	.025
Ak	.184	.848	.021	.131
Kidd	.977	.741	.211	.048
Duffy	.938	.636	.105	.259
Lewis	.994	.966	.032	.002
Kell	.189	.901	.073	.026
Lutheran	.153	.694	.214	.092
P	1.000	.949	.029	.022
MNS	1.746	.911	.041	.048
Rh	1.900	.674	.073	.253
ABO	1.241	.907	.063	.030
Mean		.854	.083	.063

Source: R. C. Lewontin, *Genetic Basis of Evolutionary Change* (Columbia University Press, 1974).

More Genetic Diversity Within Any Population Than Between Polulations

1. 85% of Human Genetic Variations Occurs Within Populations & Between Individuals in that Populations!
2. Remaining 15% of Human Genetic Variation Split Between Different Populations of Same "race" (8%) & Between Different "races" (6%)
3. Only 6% of Human Genetic Variation are to Differences between races!!! Mostly Geographic. Note: THERE ARE GROUP DIFFERENCES! Most likely as a result of geographical isolation and adaptive significance in that population.

Within Population Differences Account For 95% of Human Genetic Variation

Genetic Structure of Human Populations

Noah A. Rosenberg,[1]* Jonathan K. Pritchard,[2] James L. Weber,[3] Howard M. Cann,[4] Kenneth K. Kidd,[5] Lev A. Zhivotovsky,[6] Marcus W. Feldman[7]

We studied human population structure using genotypes at 377 autosomal microsatellite loci in 1056 individuals from 52 populations. Within-population differences among individuals account for 93 to 95% of genetic variation; differences among major groups constitute only 3 to 5%. Nevertheless, without using prior information about the origins of individuals, we identified six main genetic clusters, five of which correspond to major geographic regions, and subclusters that often correspond to individual populations. General agreement of genetic and predefined populations suggests that self-reported ancestry can facilitate assessments of epidemiological risks but does not obviate the need to use genetic information in genetic association studies.

Table 1. Analysis of molecular variance (AMOVA). Eurasia, which encompasses Europe, the Middle East, and Central/South Asia, is treated as one region in the five-region AMOVA but is subdivided in the seven-region design. The World-B97 sample mimics a previous study (*6*).

Sample	Number of regions	Number of populations	Variance components and 95% confidence intervals (%)		
			Within populations	Among populations within regions	Among regions
World	1	52	94.6 (94.3, 94.8)	5.4 (5.2, 5.7)	
World	5	52	93.2 (92.9, 93.5)	2.5 (2.4, 2.6)	4.3 (4.0, 4.7)
World	7	52	94.1 (93.8, 94.3)	2.4 (2.3, 2.5)	3.6 (3.3, 3.9)
World-B97	5	14	89.8 (89.3, 90.2)	5.0 (4.8, 5.3)	5.2 (4.7, 5.7)
Africa	1	6	96.9 (96.7, 97.1)	3.1 (2.9, 3.3)	
Eurasia	1	21	98.5 (98.4, 98.6)	1.5 (1.4, 1.6)	
Eurasia	3	21	98.3 (98.2, 98.4)	1.2 (1.1, 1.3)	0.5 (0.4, 0.6)
Europe	1	8	99.3 (99.1, 99.4)	0.7 (0.6, 0.9)	
Middle East	1	4	98.7 (98.6, 98.8)	1.3 (1.2, 1.4)	
Central/South Asia	1	9	98.6 (98.5, 98.8)	1.4 (1.2, 1.5)	
East Asia	1	18	98.7 (98.6, 98.9)	1.3 (1.1, 1.4)	
Oceania	1	2	93.6 (92.8, 94.3)	6.4 (5.7, 7.2)	
America	1	5	88.4 (87.7, 89.0)	11.6 (11.0, 12.3)	

But - There Are Differences! But…They Fall Into Geographical Groups -- Groups Divided Originally by Geographic Barriers (Ocean, Desert, Mountains). The 5% Difference Allows Us to Mark and Trace Ancestry!

Conclusions

1. If 85% of Human Genetic Variation Occurs Between Different People Within Any Given Population (localized)
2. If only 7% of Human Genetic Variation Occurs Between "Races" (novel alleles specific to "races") e.g. F_{yB}^{ES} , EDAR
3. Then Losing all "Races" Except One Retains 93% of all Human Genetic Variation!

[85% + (15%-7%)]= 93%

Variation That Occurs in Ancestral Population

85% Within Population genetic variability

8% Between Populations of Same "Race"

7% Between "Race" Genetic Variability

4. ∴ Humans Are Highly Heterozygous or Hybrids- & If Above Not True- Most of Us Would Not Be Here- Need Genetic Variation to Survive!

So What is a "Race"?

1. Primarily a sociological concept- but could be a localized or "inbred population" that has a higher frequency of alleles at a *very small number of loci*. Affects few physical features.
2. High frequency alleles in one "race" are present at lower frequencies in other "races". All humans have same genes- differ in form mostly within populations!
3. Heterozygosity (variation) high in human populations- all populations. None homozygous at all loci!
4. No such thing as a "pure" race - would have little variation
5. Genes affecting physical features not representation of genes across genome — "selected" traits with adaptive significance (e.g., vitamin D synthesis, sexual selection, pathogen susceptibility, etc.

Geographical Ancestry is relevant-many "racial" groups now have multiple ancestries because of admixture and migration

Knowledge or Certainty: The Ascent of Man Series

Jacob Bronowski, 1973