

# Genome Sequencing: Applications and Newborn Screening

June 2, 2014

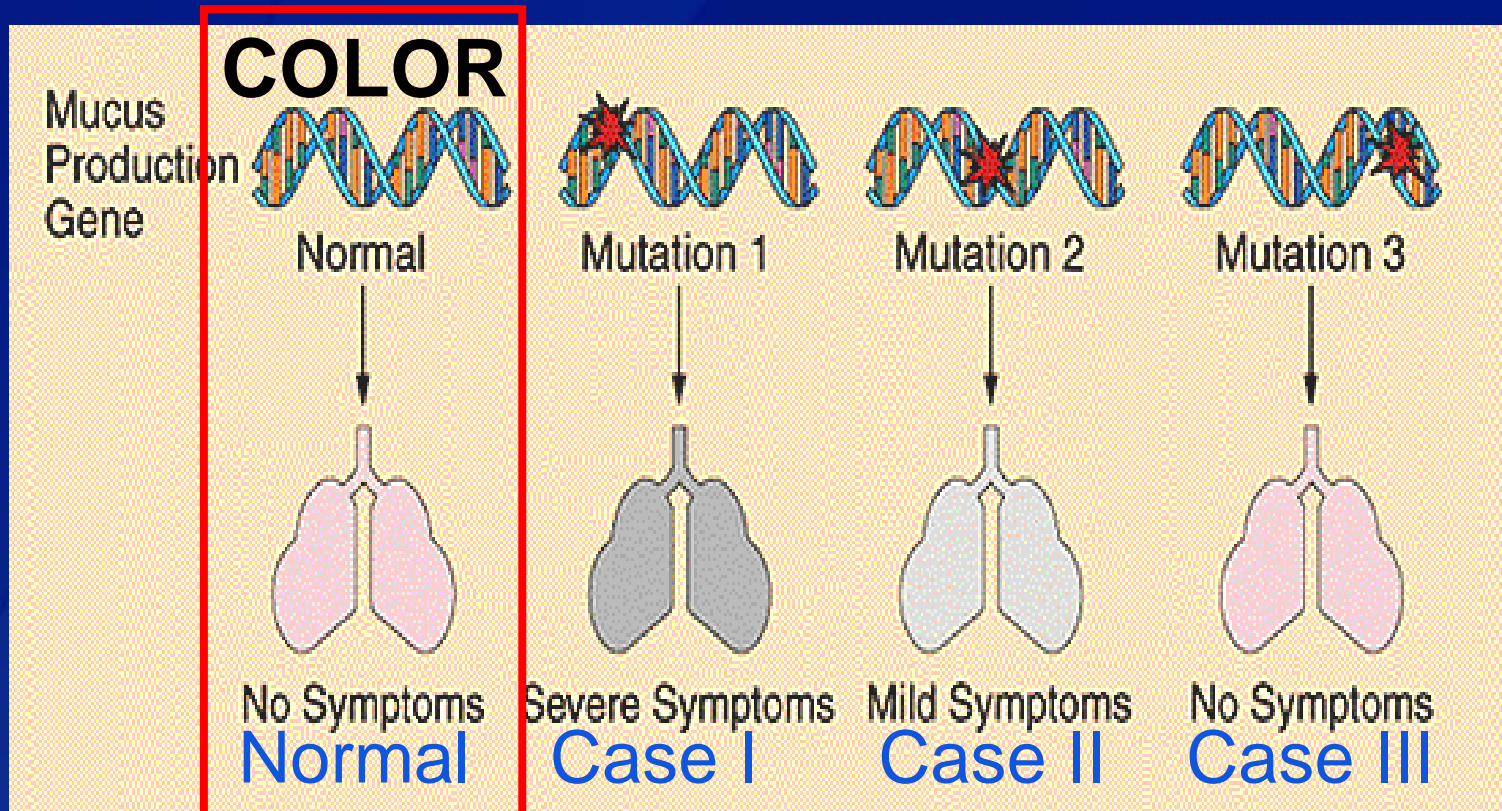
Suzanne Cordovado, PhD  
Molecular Quality Improvement Program  
Centers for Disease Control and Prevention

# When DNA is Replicated for Cell Division, Errors can Occur



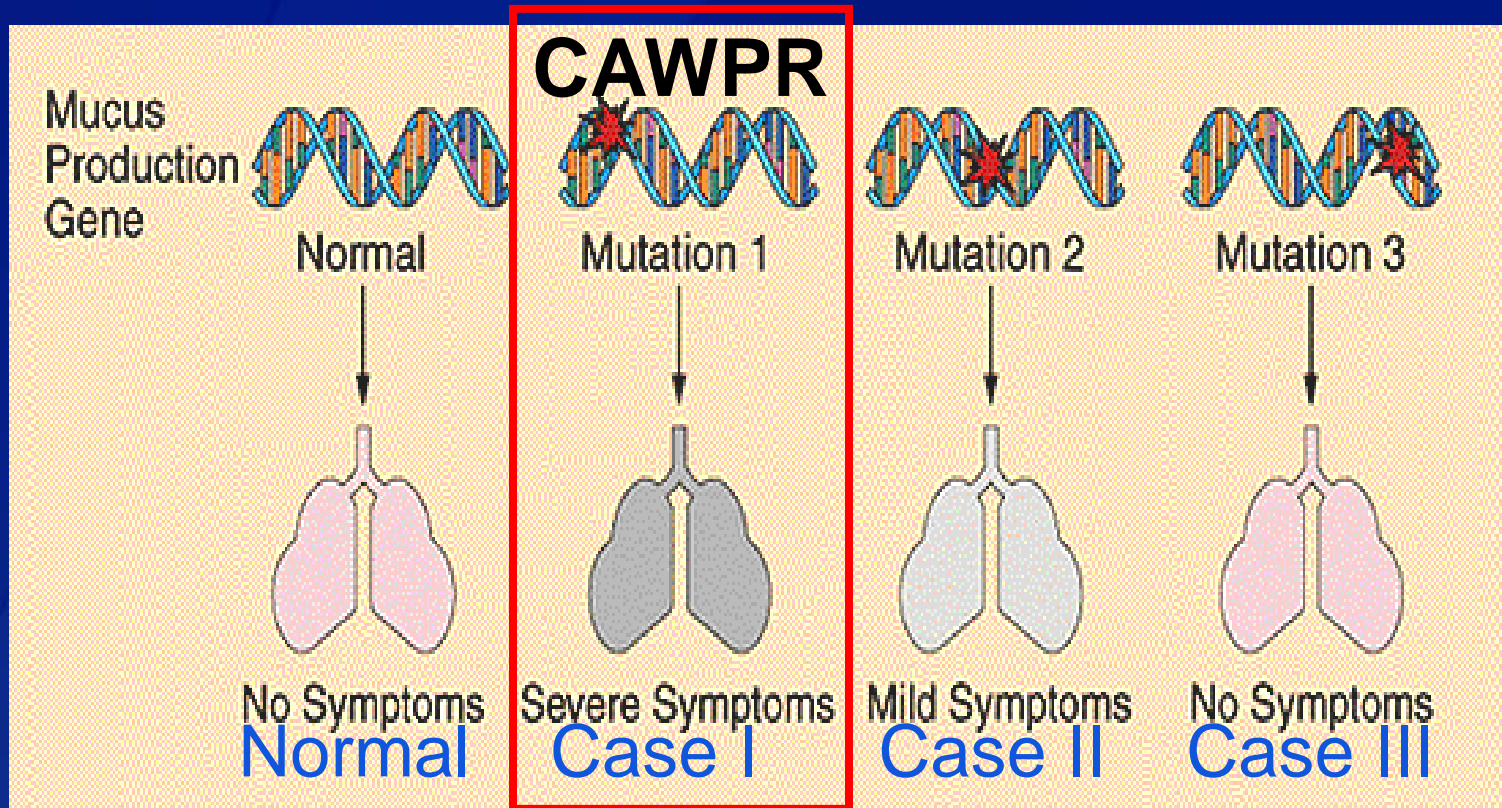
These errors can result in disease

# Mutations in the Cystic Fibrosis Gene



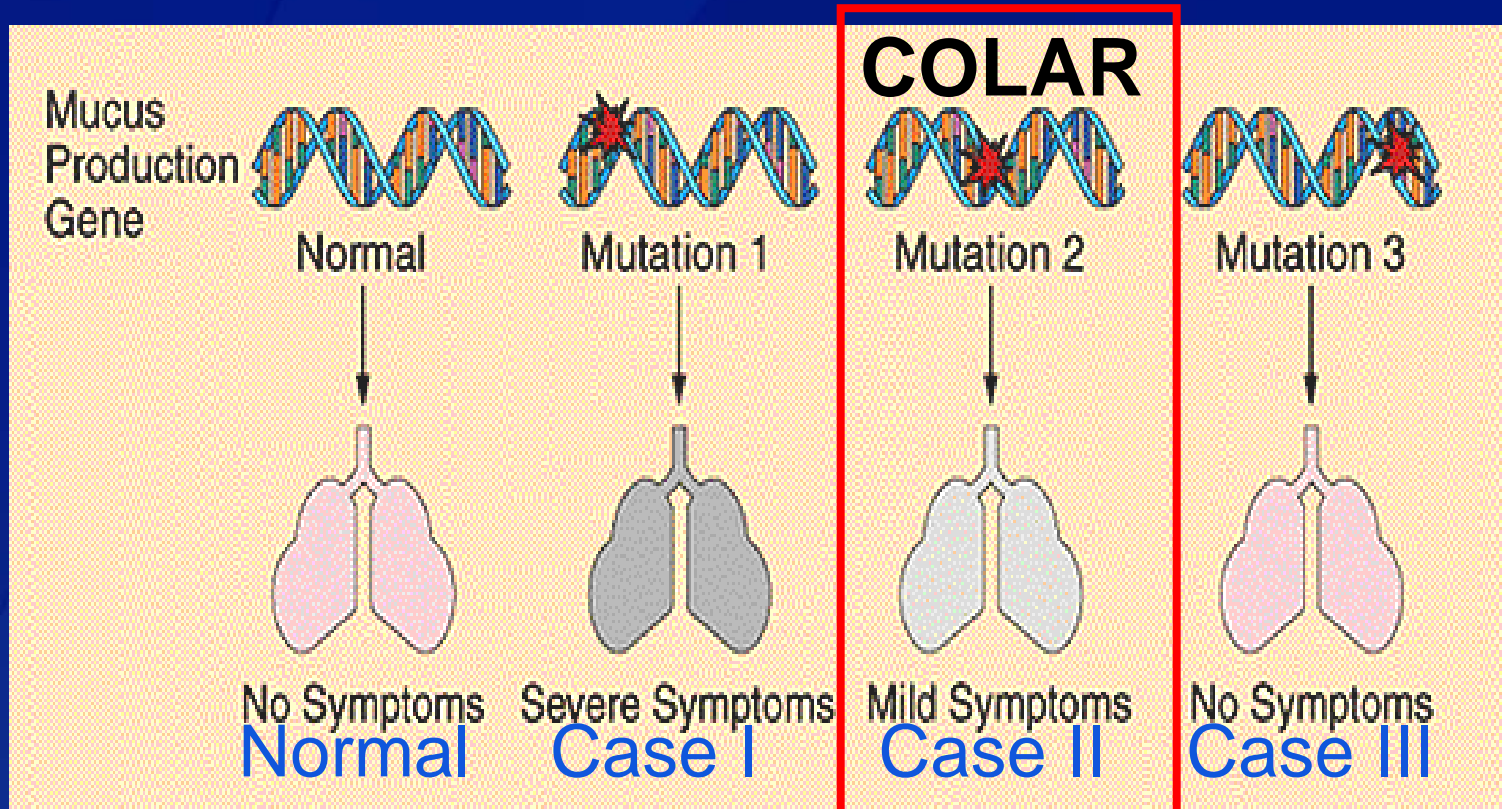
**Normal - no changes**

# Mutations in the Cystic Fibrosis Gene



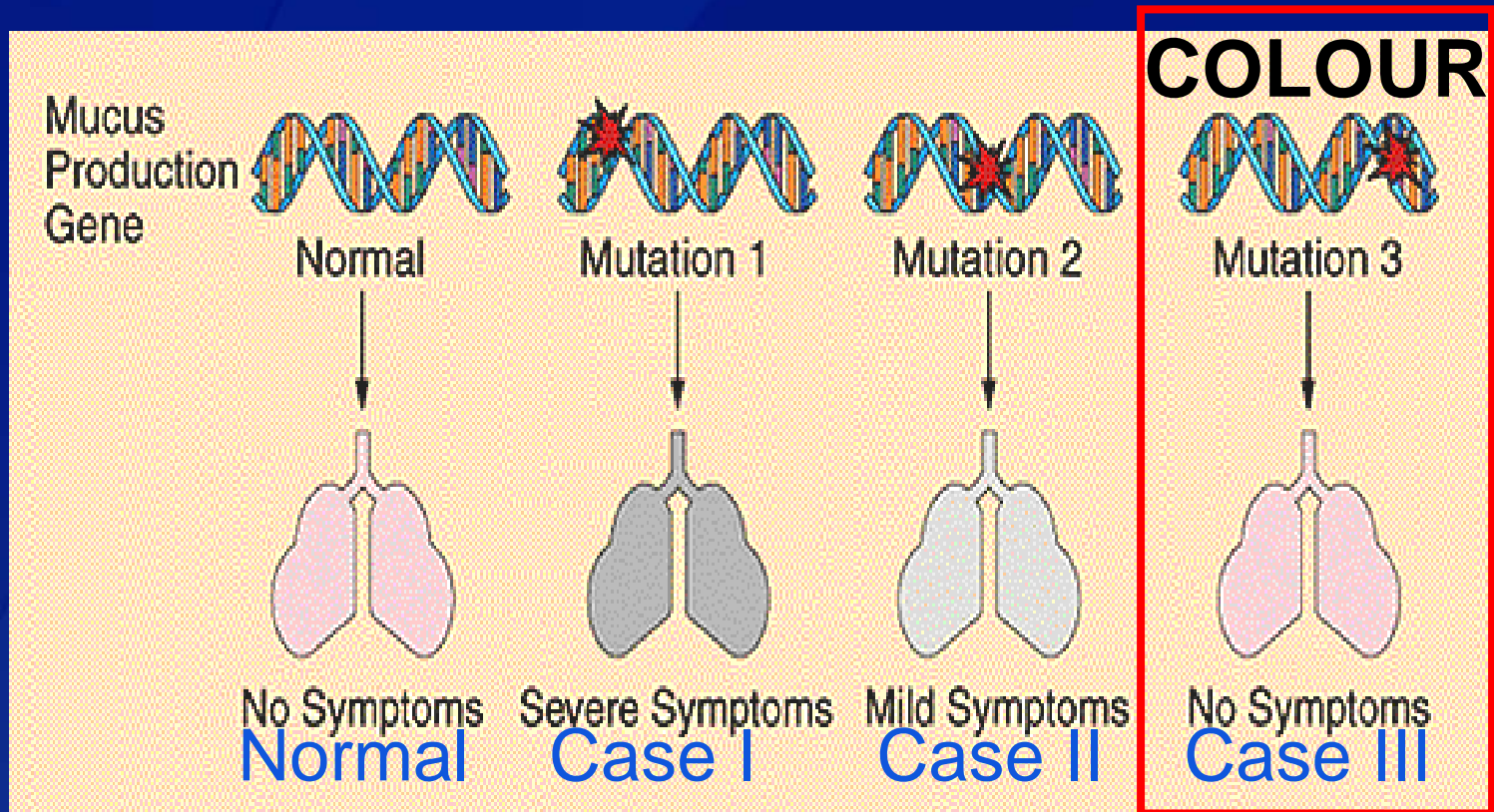
**Case I – unrecognizable**

# Mutations in the Cystic Fibrosis Gene



Case II – typo

# Mutations in the Cystic Fibrosis Gene

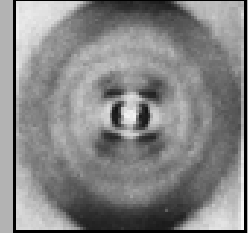


**Case III – American vs. British**

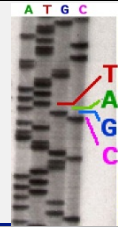
# Molecular Genetics Milestones



**1952:** Described DNA as a double helix (using x-ray diffraction)



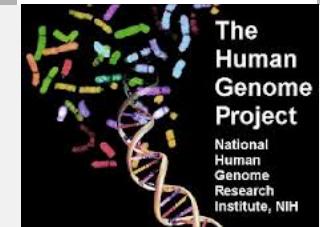
**1975:** Devised techniques for DNA sequencing



**1985:** Conducted first polymerase chain reaction (PCR) experiments to amplify specific gene regions



**2003:** Human Genome Sequencing Project is completed





# DNA Sequencing 1975 to 2014 and Beyond

## Next Generation Sequencing



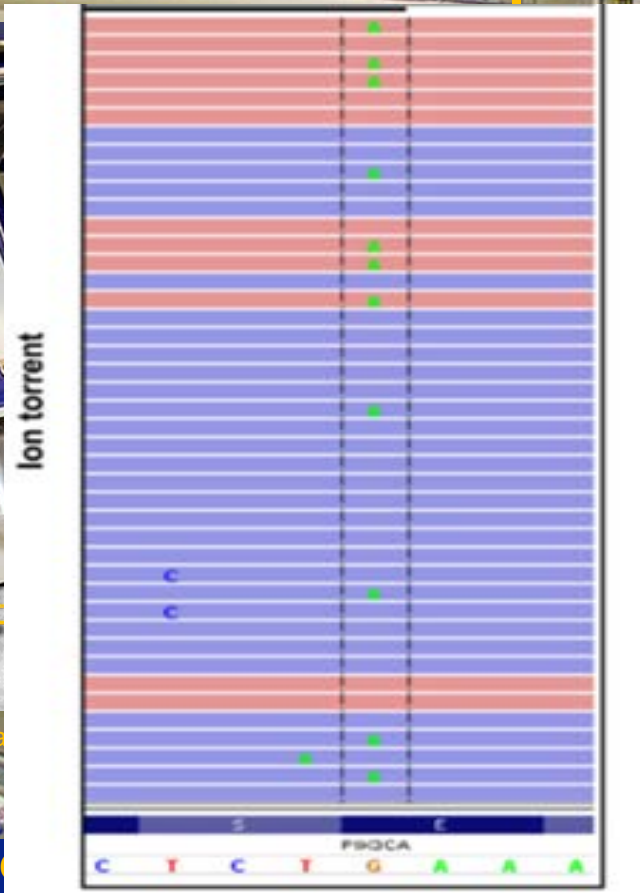
Life Technologies Ion Torrent



<http://molecularstar.com>



The Broad



Sanger DNA sequencing center



HiSeq 2500 Sequencer



<http://www.uvm.edu/~cgep/Education/Sequence.html>



large-scale

Singh et al. *Mol Diagn*, Vol 13(5), 601-2 (2013).



# Sequencing the Genome

- ❑ U.S. Human Genome Project began in 1989 and was completed by 23 collaborating laboratories in 13 years (cost ~\$2.7 billion)
- ❑ Latest DNA sequencers can sequence a human genome in a few days for less than \$5,000
- ❑ “2013 is likely to be the year where we see the \$1000 genome.” - Daniel Franklin, executive editor of *The Economist*



# Will Genome Sequencing be like a Healthcare Tsunami?



**Or Will We Ride  
the Wave?**

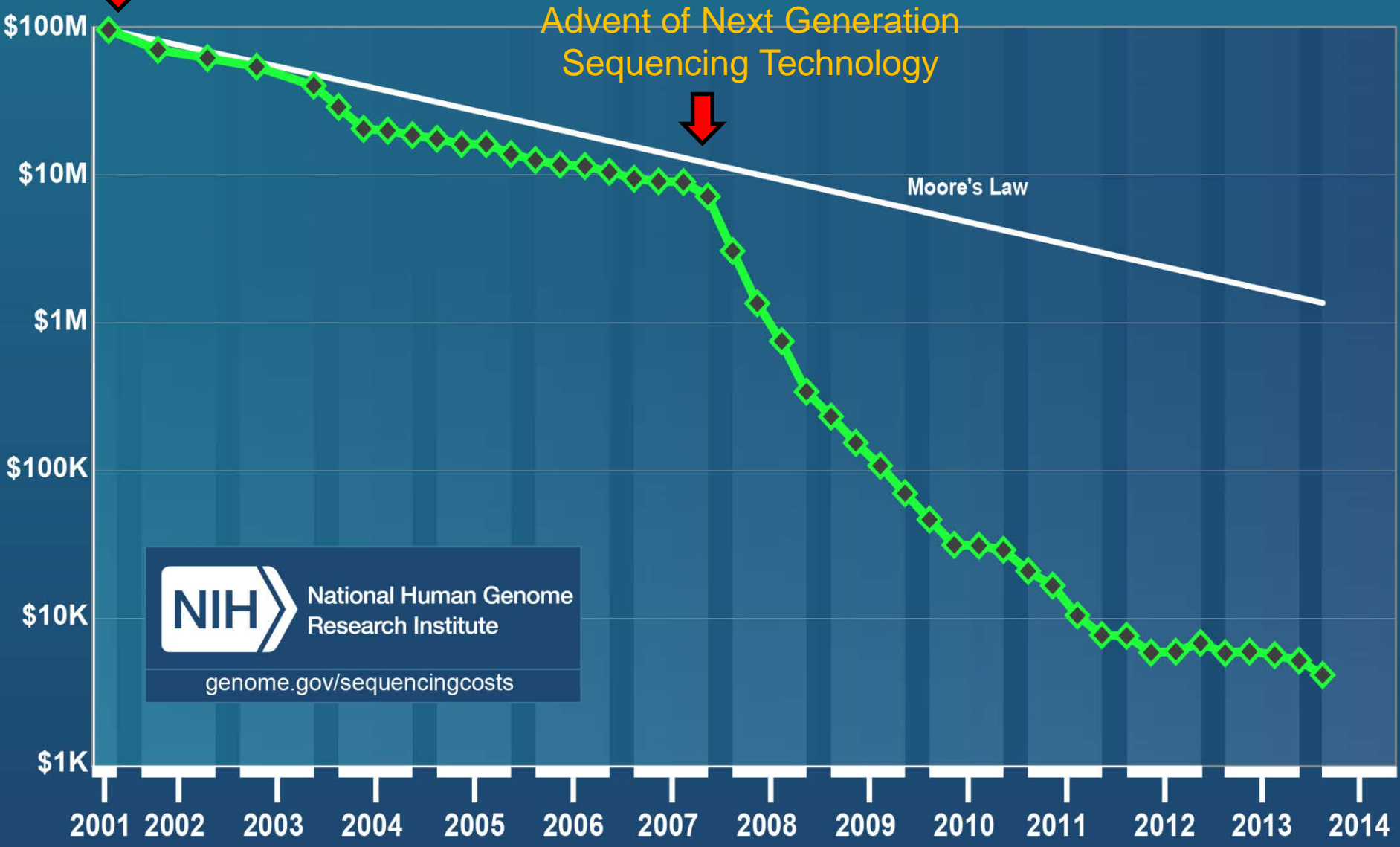
**Either way, we are going to get wet...**

**“...it may soon be easier and cheaper to sequence an entire genome than to test for a number of known mutations.”**

- Foundation for Genomics and Population Health

Sanger Sequencing  
Technology

# Cost per Genome



National Human Genome  
Research Institute

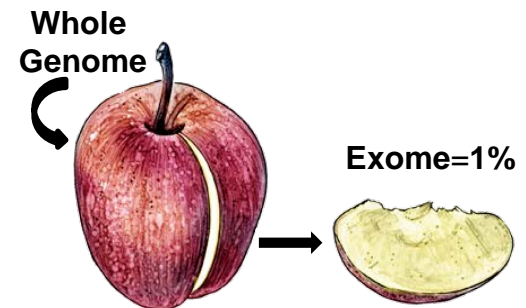
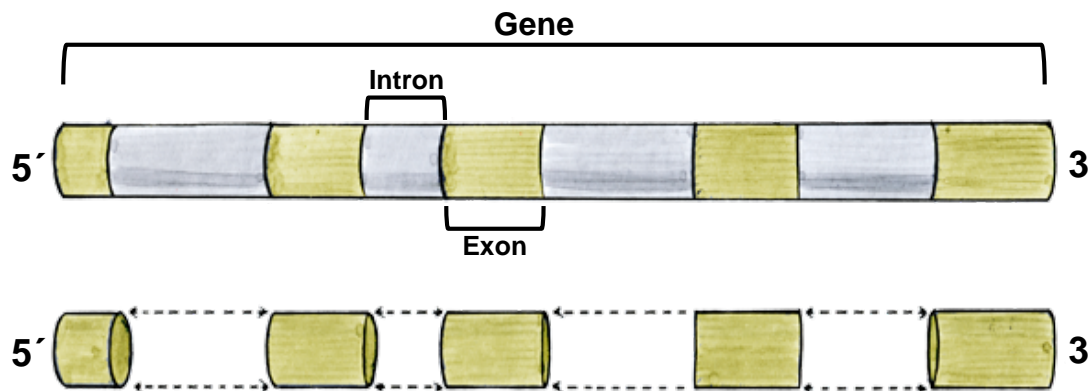
[genome.gov/sequencingcosts](http://genome.gov/sequencingcosts)



# Sequencing the Human Genome

- Genome is comprised of 3 billion bases
- Exome is approximately 1% of the genome
  - Includes DNA segments that contain genes
  - Genes hold the recipe for all the body's proteins

## Genome vs. Exome



# Genome Sequencing for Clinical Diagnosis

*The NEW ENGLAND JOURNAL of MEDICINE*

## Clinical Whole-Exome Sequencing for the Diagnosis of Mendelian Disorders

Yaping Yang, Ph.D., Donna M. Muzny, M.Sc., Jeffrey G. Reid, Ph.D.,  
Matthew N. Bainbridge, Ph.D., Alecia Willis, Ph.D., Patricia A. Ward, M.S.,  
Alicia Braxton, M.S., Joke Beuten, Ph.D., Fan Xia, Ph.D., Zhiyv Niu, Ph.D.,  
Matthew Hardison, Ph.D., Richard Person, Ph.D., Mir Reza Bekheirnia, M.D.,  
Magalie S. Leduc, Ph.D., Amelia Kirby, M.D., Peter Pham, M.Sc., Jennifer Scull, Ph.D.,  
Min Wang, Ph.D., Yan Ding, M.D., Sharon E. Plon, M.D., Ph.D.,  
James R. Lupski, M.D., Ph.D., Arthur L. Beaudet, M.D.,  
Richard A. Gibbs, Ph.D., and Christine M. Eng, M.D.



# Molecular Diagnosis using Genome Sequencing

- ❑ Exome sequencing to achieve a clinical diagnosis
- ❑ Recent NEJM study made a molecular diagnosis in 62 of 250 cases (25%)
- ❑ Marked improvement over testing single genes or gene panels currently used



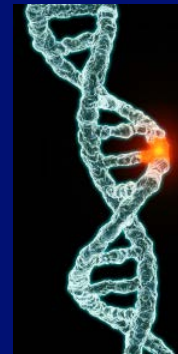
# Limitations of Sequencing

## No Method is Perfect

- ❑ Deletions removing large segments of DNA, rearrangements or copy number variations will not be detected
  - Examples of newborn diseases resulting from large deletions: Cystic fibrosis and Congenital Adrenal Hyperplasia
- ❑ Person to person DNA variation can give inaccurate results due to mis-priming
- ❑ Traditional sequencing has an error rate of 1/10,000 to 1/100,000 - Next Gen sequencing is considerably higher

# Challenges of Genome/Exome Sequencing

- ❑ **Major Challenge:** Determining whether any given variant is pathogenic
- ❑ **ACMG defined 5 categories to classify variants:**
  - Known pathogenic
  - Likely to be pathogenic
  - Unknown significance
  - Likely to be benign
  - Benign
- ❑ **Knowledge accruing daily, however the medical impact of most variants is unknown**



# Genome Sequencing Results

- ❑ What data should be returned to patients and physicians?
- ❑ Factors to consider
  - Patient autonomy
  - Patient privacy
  - Physician liability
  - Clinical laboratory guidelines for reporting



# Characteristics of Newborn Disorders Include

- Significant disease
- Prevention possible
- Not evident until harm is done
- Mass testing methods available
- Benefits justify costs



Slide Courtesy of Mike Glass  
Washington State Dept of Health

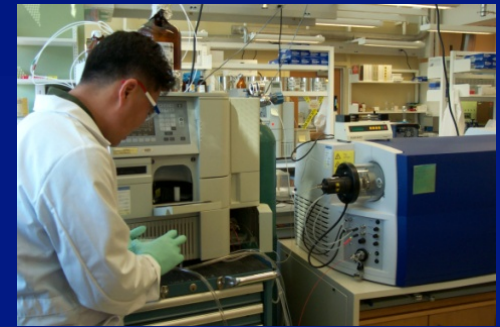
# Molecular Testing in Newborn Screening Laboratories

## ❑ Second tier molecular tests

- Increase sensitivity or specificity of primary assay
  - Cystic fibrosis
- Clarify an ambiguous result
  - Hemoglobinopathies
- Supplemental “Just in Time” assay
  - Galactosemia

## ❑ Primary molecular test

- When no other assay is available – Severe Combined Immunodeficiency (SCID)





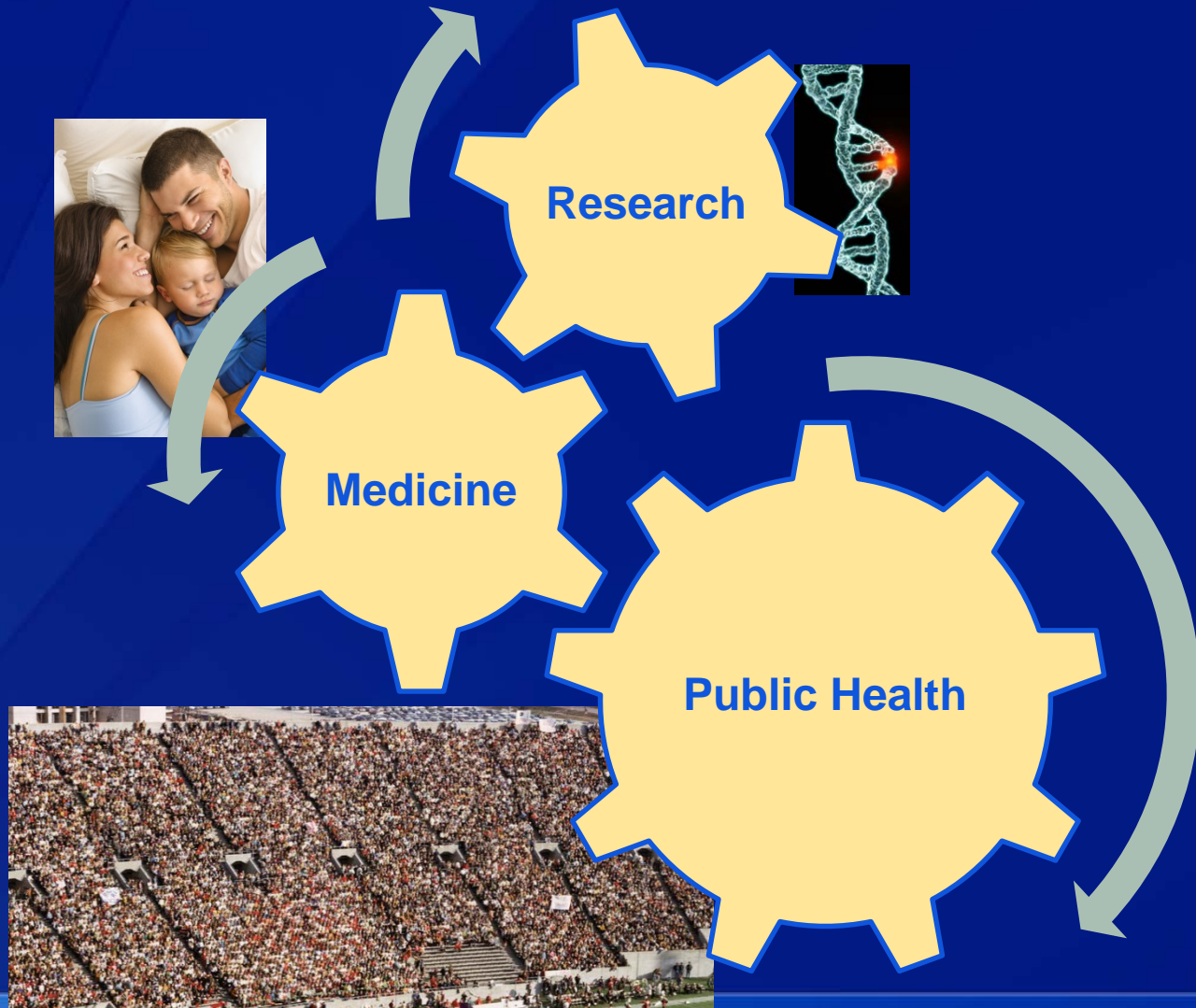


# Future of Sequencing in Newborn Screening...

- ❑ Targeted gene sequencing to identify mutations associated with diseases that have treatable or preventable outcomes
- ❑ Mutation specific drugs
  - Kalydeco – treats Cystic Fibrosis patients with specific mutations
    - G551D, G178R, S549N, S549R, G551S, G1244E, S1251N, S1255P & G1349D
- ❑ Exome and Genome sequencing will be explored over the next few years by NICHD grant recipients



# Translating Research to Medicine and Public Health



# Thank you!



## ***Newborn Screening***

***Saving Lives.***

***Promoting Healthier Babies.***

***Protecting our Future.***



**For more information please contact Centers for Disease Control and Prevention**

1600 Clifton Road NE, Atlanta, GA 30333

Telephone, 1-800-CDC-INFO (232-4636)/TTY: 1-888-232-6348

E-mail: [cdcinfo@cdc.gov](mailto:cdcinfo@cdc.gov) Web: [www.cdc.gov](http://www.cdc.gov)

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.

National Center for Environmental Health

Division of Laboratory Sciences

