

# Genetic Factors Governing Susceptibilities to Severe Infections

GSK-Chair of Infectious Diseases

Pr Jean-Paul MIRA

# **Sommes-nous tous égaux devant les infections graves?**

**Université catholique de Louvain**

**Ecole de médecine**

**18 Février 2005**

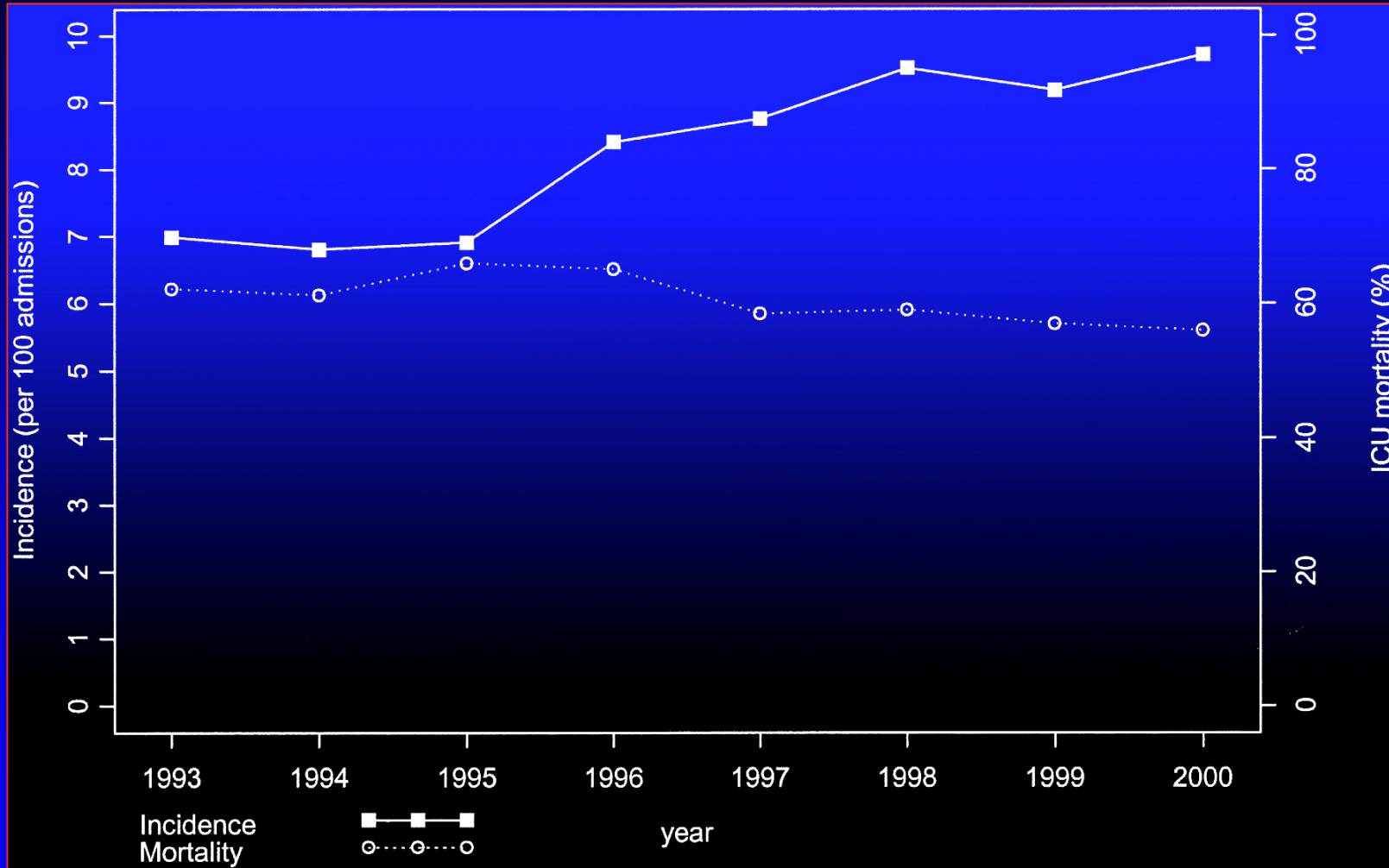
**Pr. Jean-Paul Mira**

**Réanimation Médicale et Département de Biologie Cellulaire  
Hôpital Cochin & Institut Cochin, Paris**

# SEPSIS

- Major Cause of Mortality
  - 1<sup>st</sup> cause of death in ICU
- 1,5 million of severe sepsis/year (Europe)
  - 9% of ICU admissions
  - Estimated cost : 17 milliards \$/year (USA)
  - Increased incidence over the years

# Septic Shock Epidemiology



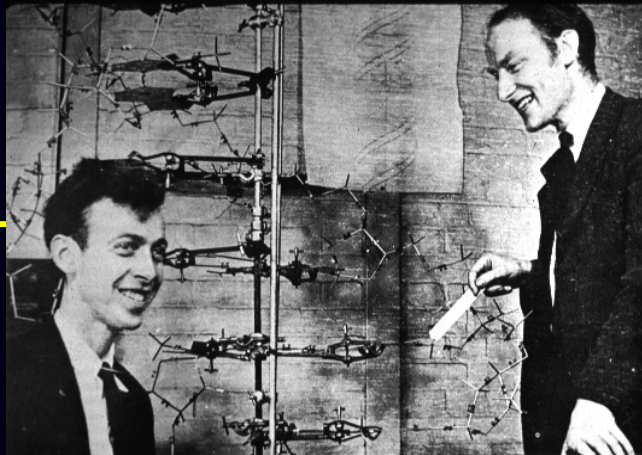




« If it were not for the great variability among individuals medicine might as well be a science and not an art »

*Sir William Osler, 1892*

-1953-



2001-2003 →



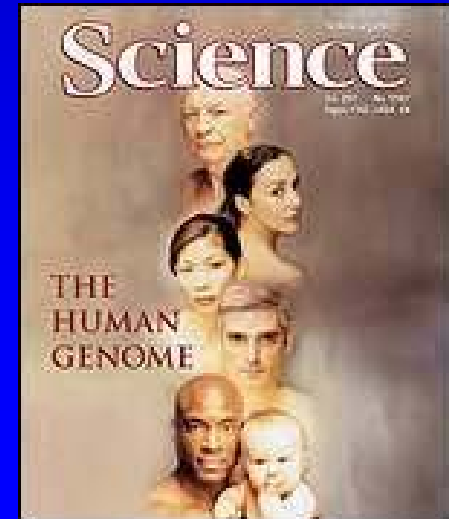
« Today we are learning the language in which God created life. It will revolutionize the diagnosis, prevention and treatment of most, if not all human diseases. »

*William J. Clinton, June 26, 2000*

# From Watson and Crick to Human Genome

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- 1953 Watson and Crick: double helical structure of DNA
- 1960s Role of RNA and Genetic Code
- 1970s Recombinant DNA technology
- 1977 Sanger and Gilbert: DNA sequencing
- 1983 Mapping of disorders by linkage (Huntington disease)
- 1986 Polymerase Chain Reaction
- 1990 Human Genome Project
- 1995 *Haemophilus influenzae* genome
- 2003 Mice and Human genome sequence  
Human SNP Map





# La Recherche



NOV 1990

## Génome humain

Les vrais enjeux d'un grand programme



Le génome humain: les enjeux de la recherche

Le génome humain: les enjeux de la recherche

Le génome humain: les enjeux de la recherche

Le génome humain: les enjeux de la recherche

Le génome humain: les enjeux de la recherche



# TIME

**LOT'S IMPROVEMENT PLAN**

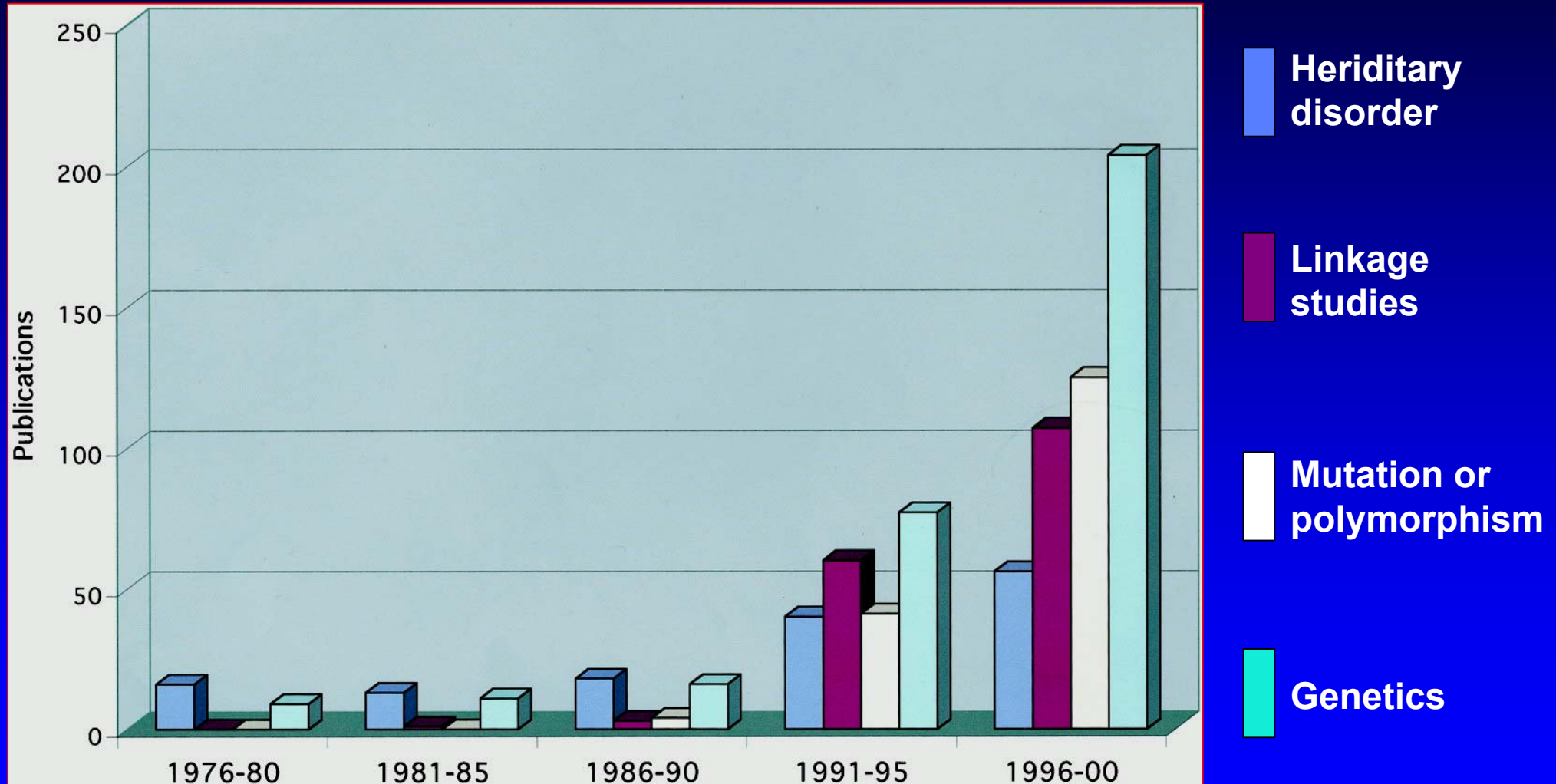
**SPECIAL ISSUE**

## THE FUTURE OF MEDICINE

How genetic engineering will change us in the next century



# Molecular Genetic Research



**TOUS LES ÊTRES HUMAINS  
PARTAGENT LES MÊMES GÈNES**

**MAIS...**

**Small differences in genotype make big differences to phenotype**





**DNA**  
EVIDENCE

# Evidences for a genetic component to sepsis

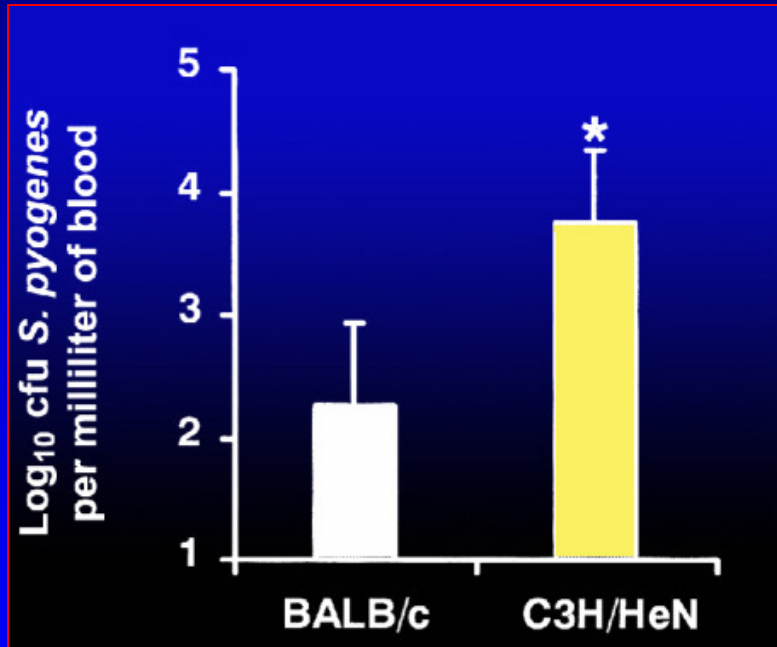
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## Animal Studies

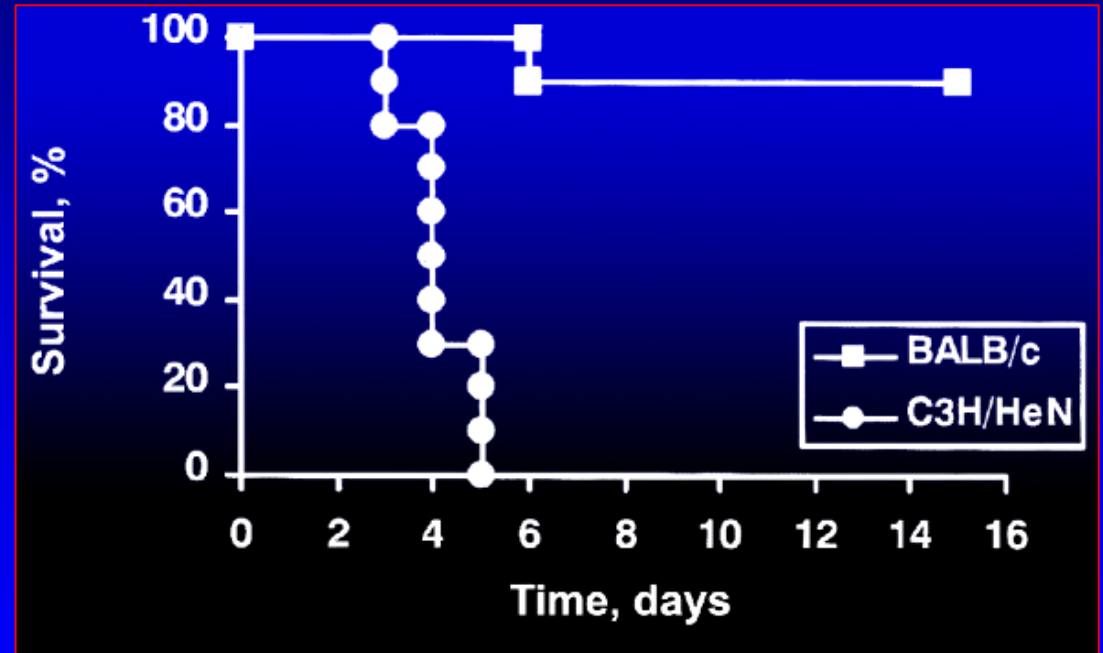
- Susceptibility/resistance to certain infection in mice
- Susceptibility/resistance phenotypes of knock-out mice

# Mice Susceptibility to Infection with Group A Streptococci

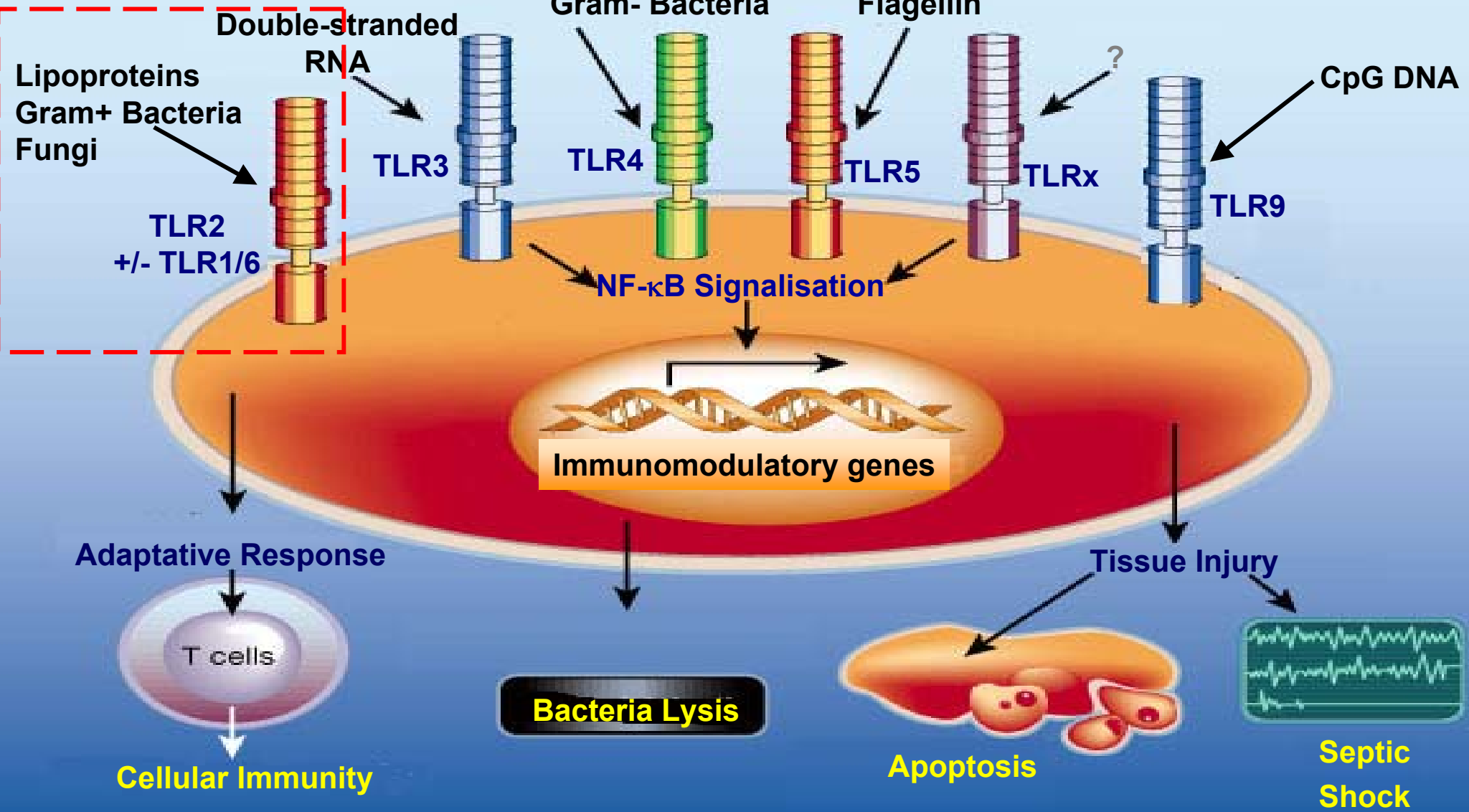
$10^3$  cfu *Strepto* Subcutaneous



d2



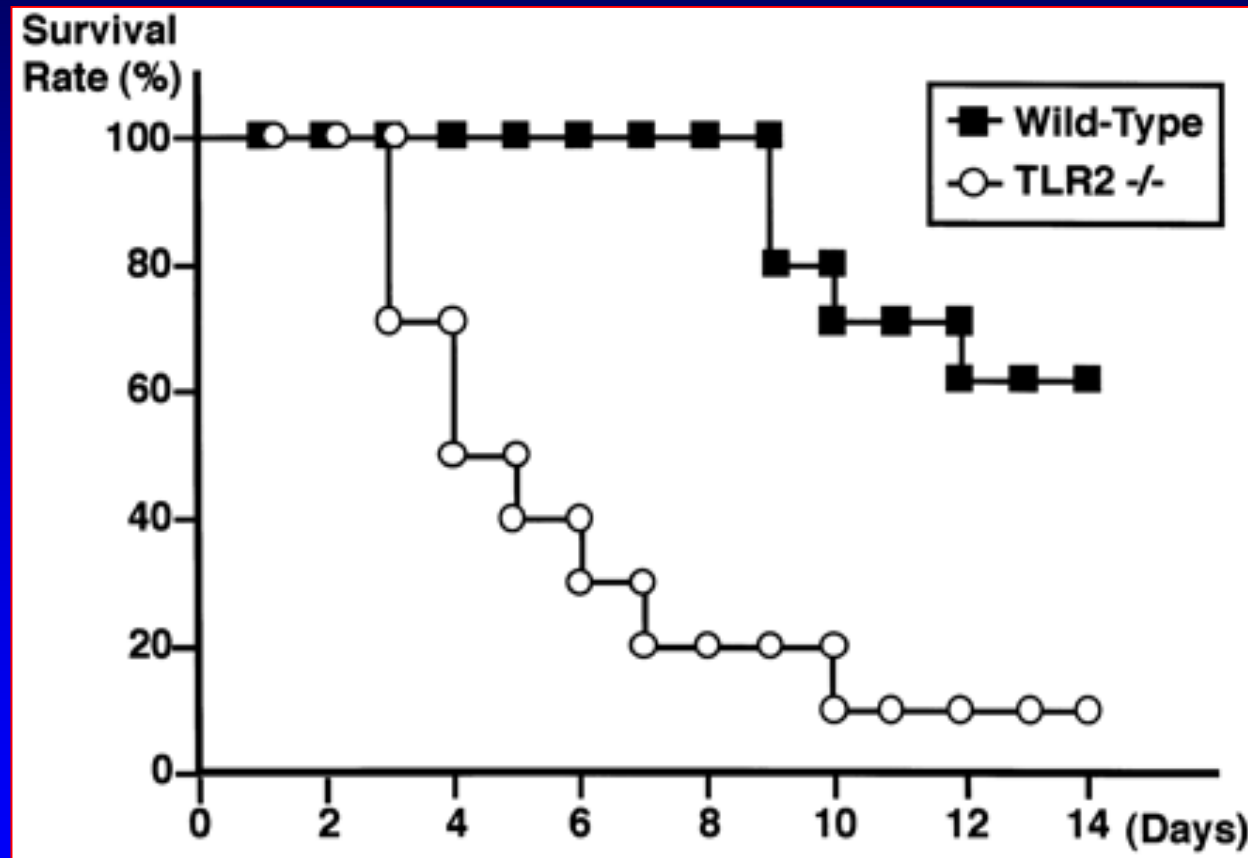
# Monocyte or Dendritic cell





# TLR2-KO Mice and Response to Gram Positive Bacteria

Intravenous infusion of *Staphylococcus aureus*



# Evidences for a genetic component to sepsis

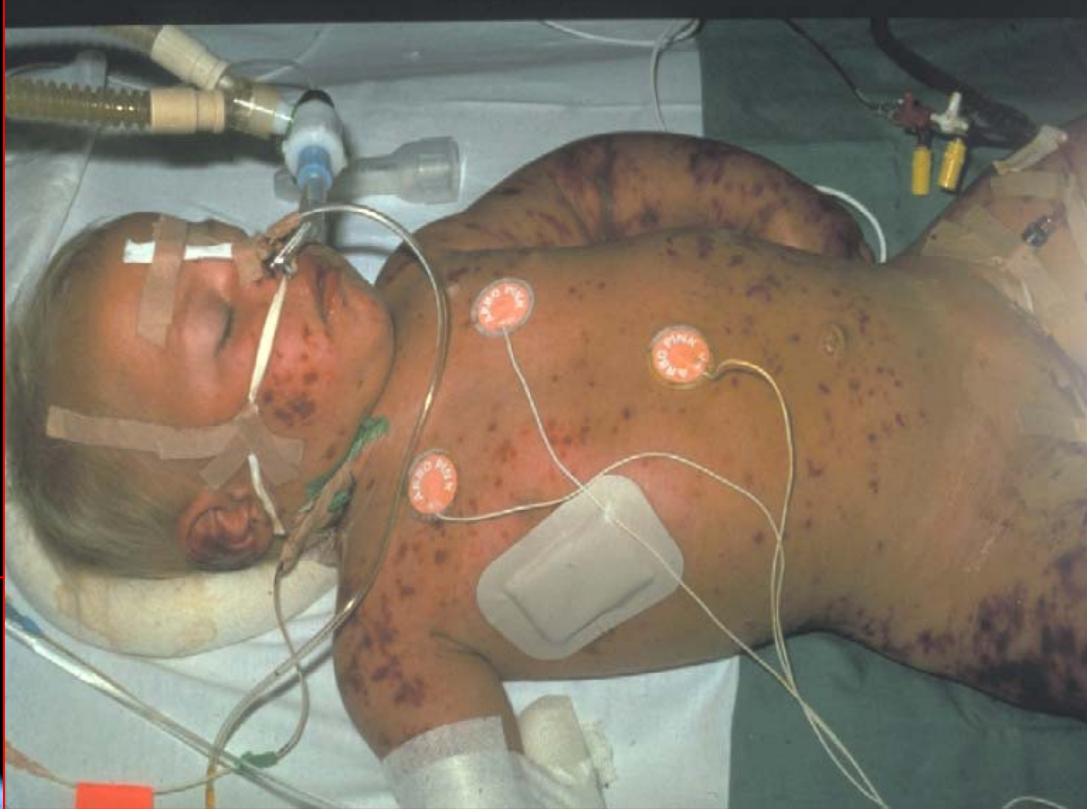
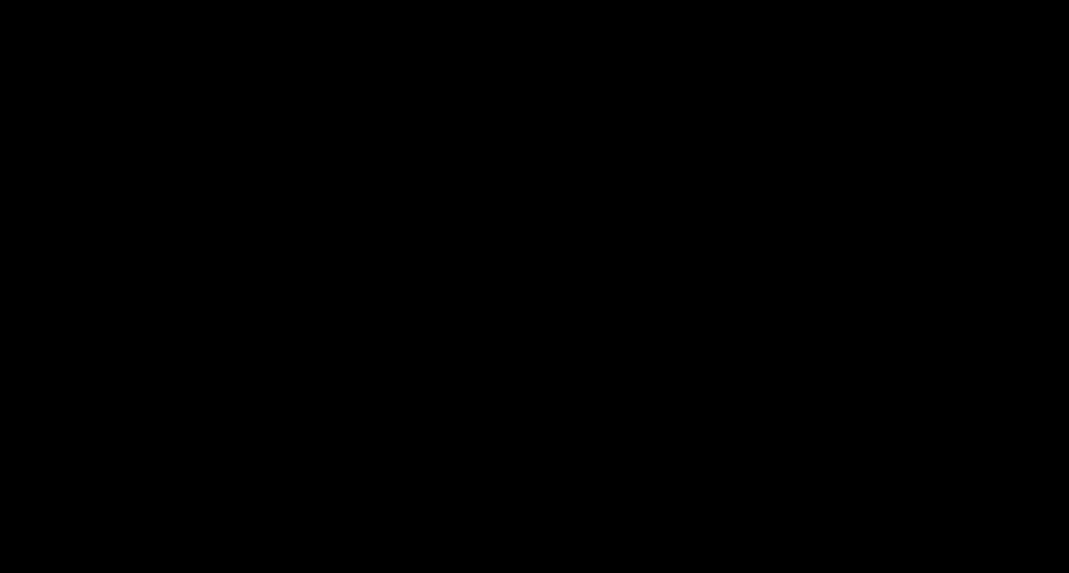
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## Animal Studies

- Susceptibility/resistance to certain infection in mice
- Susceptibility/resistance phenotypes of knockout mice

## Human Studies

- Clinical Evidences
- Ethnic Differences
- Twin Studies
- Adoptee Studies



# Twin Studies

- **Tuberculosis**

Kallmann FJ, Am rev Tuber 1943.  
Comstock GW, Am Rev Respir Dis 1978.

- **Leprosy**

Fine PE, Int J leprosy 1981

- **Helicobacter pylori**

Malaty HM, Ann Intern Med 1994.

- **Malaria**

Jepson AP, J Infect Dis 1995.

- **AIDS**

Chang J, J Virol 1996.



# Genetic and environmental influences on premature death in adult adoptees

| Cause of Death<br>(Parent Dead before the age of 50) | Relative risk for the adoptee<br>to die from the same cause |
|--|---|
| All causes   |   |
| Biologic   | 1.71  |
| Adoptive   | 0.71  |
| <b>Infection</b>                                     |   |
| <b>Biologic</b>                                      | <b>5.8</b>  |
| <b>Adoptive</b>                                      | <b>0.73</b>   |
| Vascular   |   |
| Biologic   | 4.5   |
| Adoptive   | 3.1   |

# Host Genetics of Infectious Diseases

Genetics of Complex Diseases

Mendelian Genetics

Genes

Environmental Influences

Pathogen



P  
H  
E  
N  
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T  
Y  
P  
E  
S

Gene

Pathogen



# Genetics of Phagocyte Immune Defects

## Number

Cyclic neutropenia (AD)  
Congenital agranulocytosis  
(Kostmann syndrome)

## Rolling Deficiency

Type II: Sialyl Lewis<sup>x</sup> (AR)  
Selectin Deficiency (AR)

## Leukocyte Adhesion Deficiency

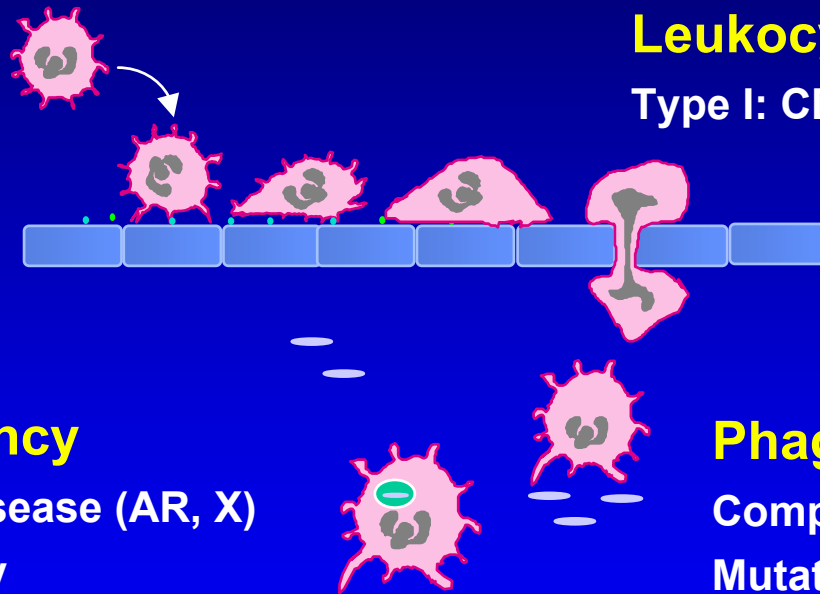
Type I: CD18 (AR);

## Bacterial lysis Deficiency

Chronic Granulomatous Disease (AR, X)  
Myeloperoxidase deficiency  
Neutrophil granule defects

## Phagocytosis Deficiency

Complement deficiencies  
Mutations of MBL



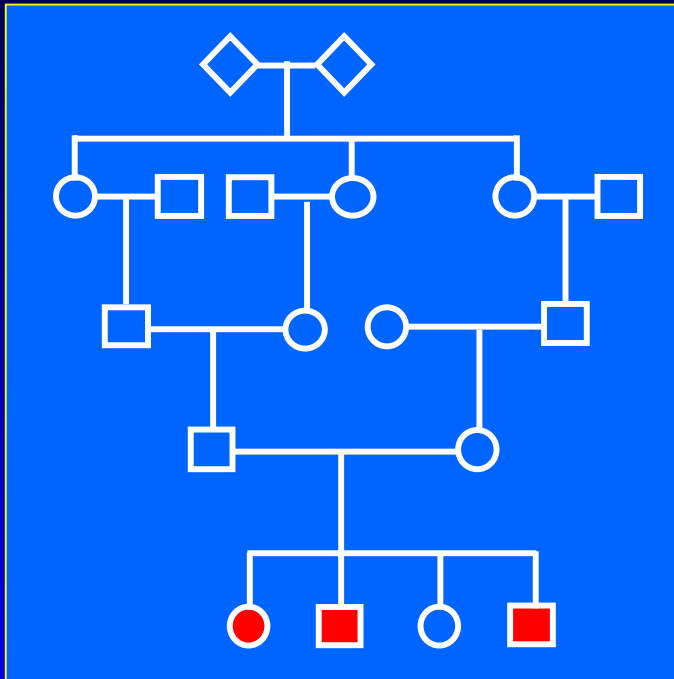
**Recurrent Bacterial Infections**



# Single Gene Defects and Severe Immunodeficiency Disorders

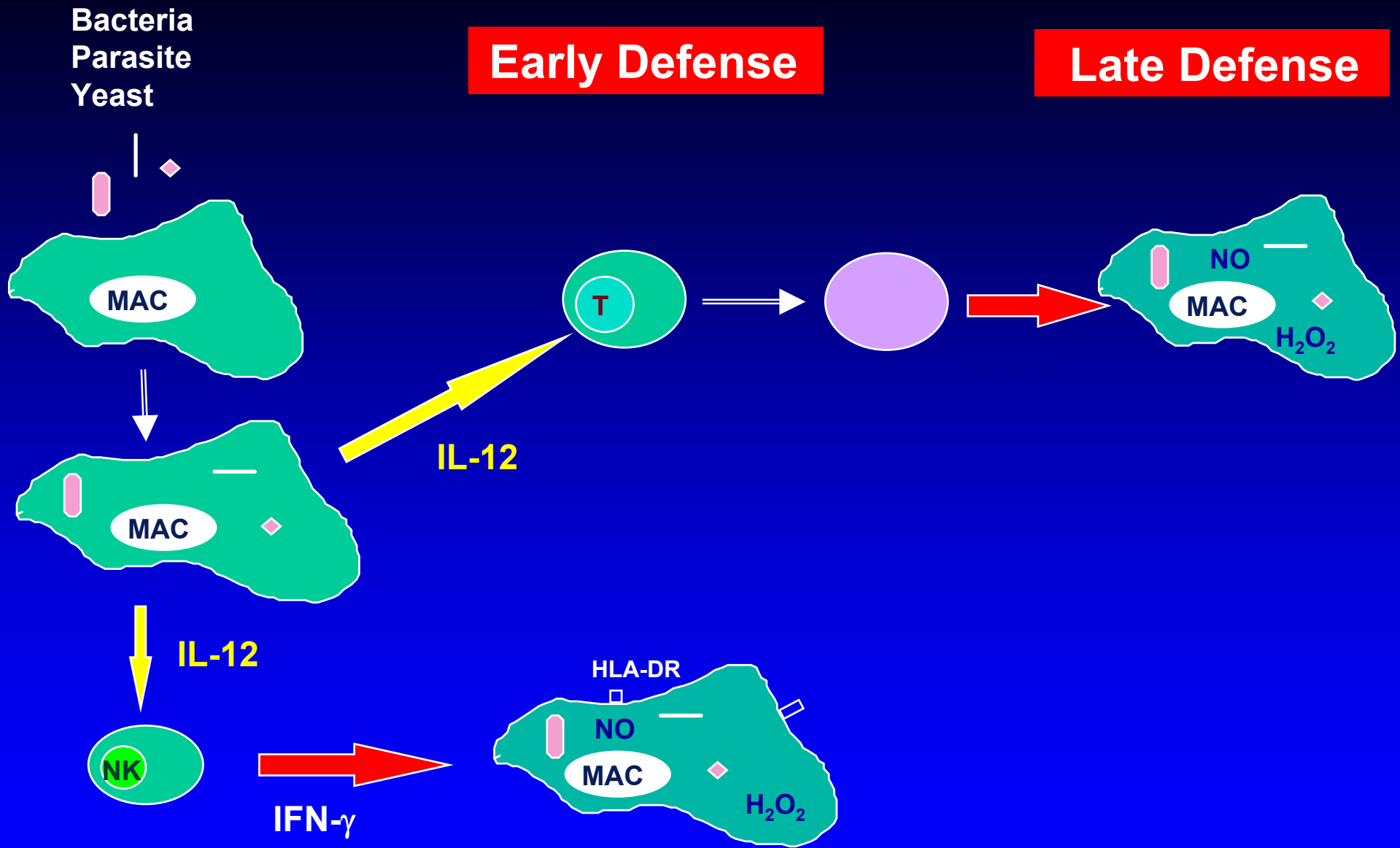
| <b>System involved</b> | <b>Typical clinical syndrome</b>                 | <b>Genetic Defect</b>                                 |
|------------------------|--|---|
| <b>B lymphocyte</b>    | <b>Defective antibody production</b>             | <b>B cell tyrosine kinase<br/>CD40 ligand</b>         |
| <b>T lymphocyte</b>    | <b>Defective humoral and cellular immunity</b>   | <b>IL-2 receptor</b>                                  |
| <b>Neutrophil</b>      | <b>Defective phagocytosis</b>                    | <b>Cytochrome b<br/><math>\beta</math> 2 integrin</b> |
| <b>Macrophage</b>      | <b>Susceptibility to mycobacterial infection</b> | <b>Interferon <math>\gamma</math> receptor</b>        |
| <b>Complement</b>      | <b>Recurrent <i>Neisseria</i> infections</b>     | <b>Terminal complement components</b>                 |

# Single Gene Defects and Severe Tuberculosis



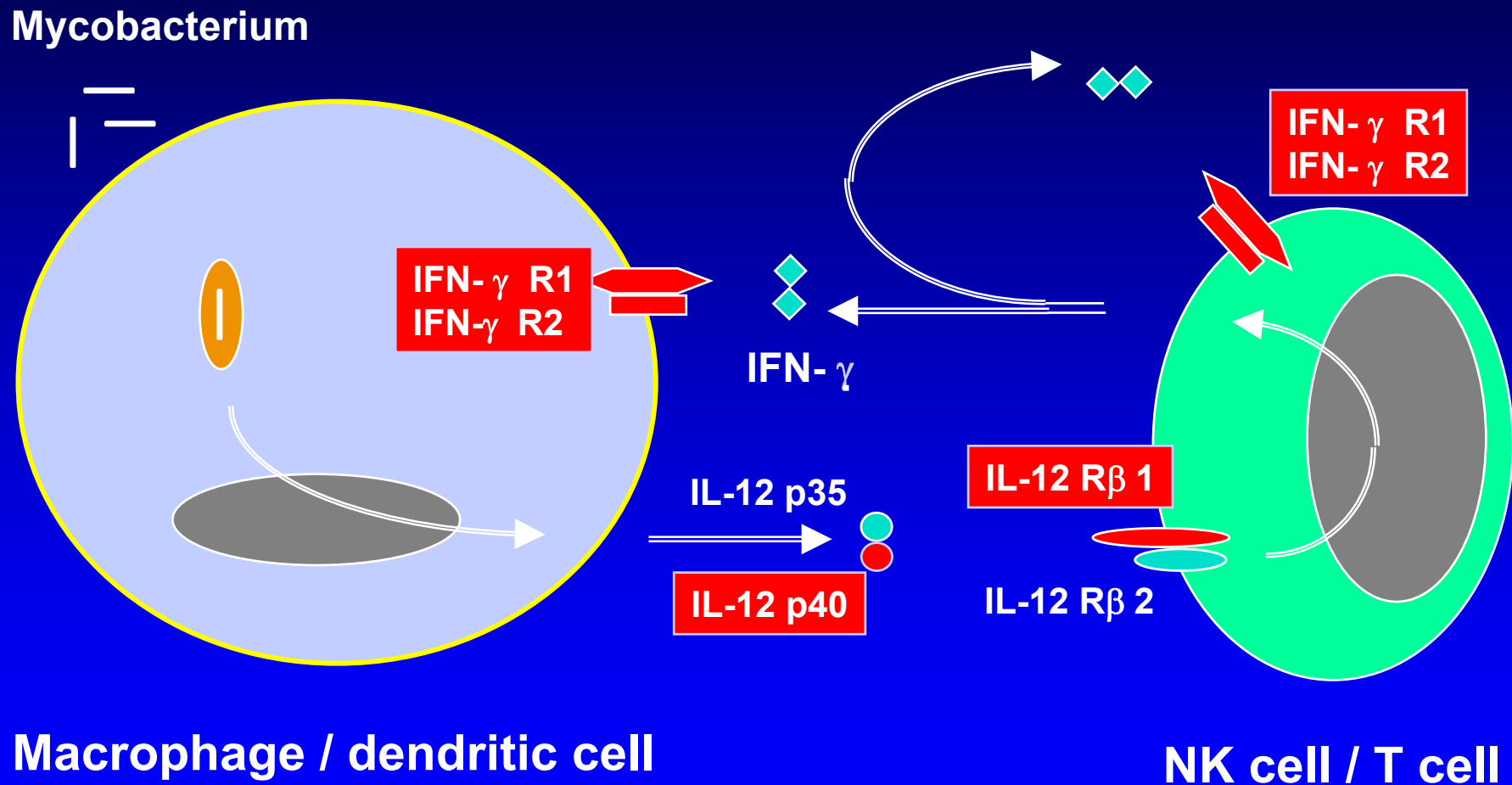
- Parental consanguinity
- Affected siblings
- Familial forms of disseminated infections with weakly pathogenic mycobacteria

**Search for recessive genetic disorders**



(Biron et Gazzinelli. *Curr. Op. Immuno.* 1995;7:485-496)

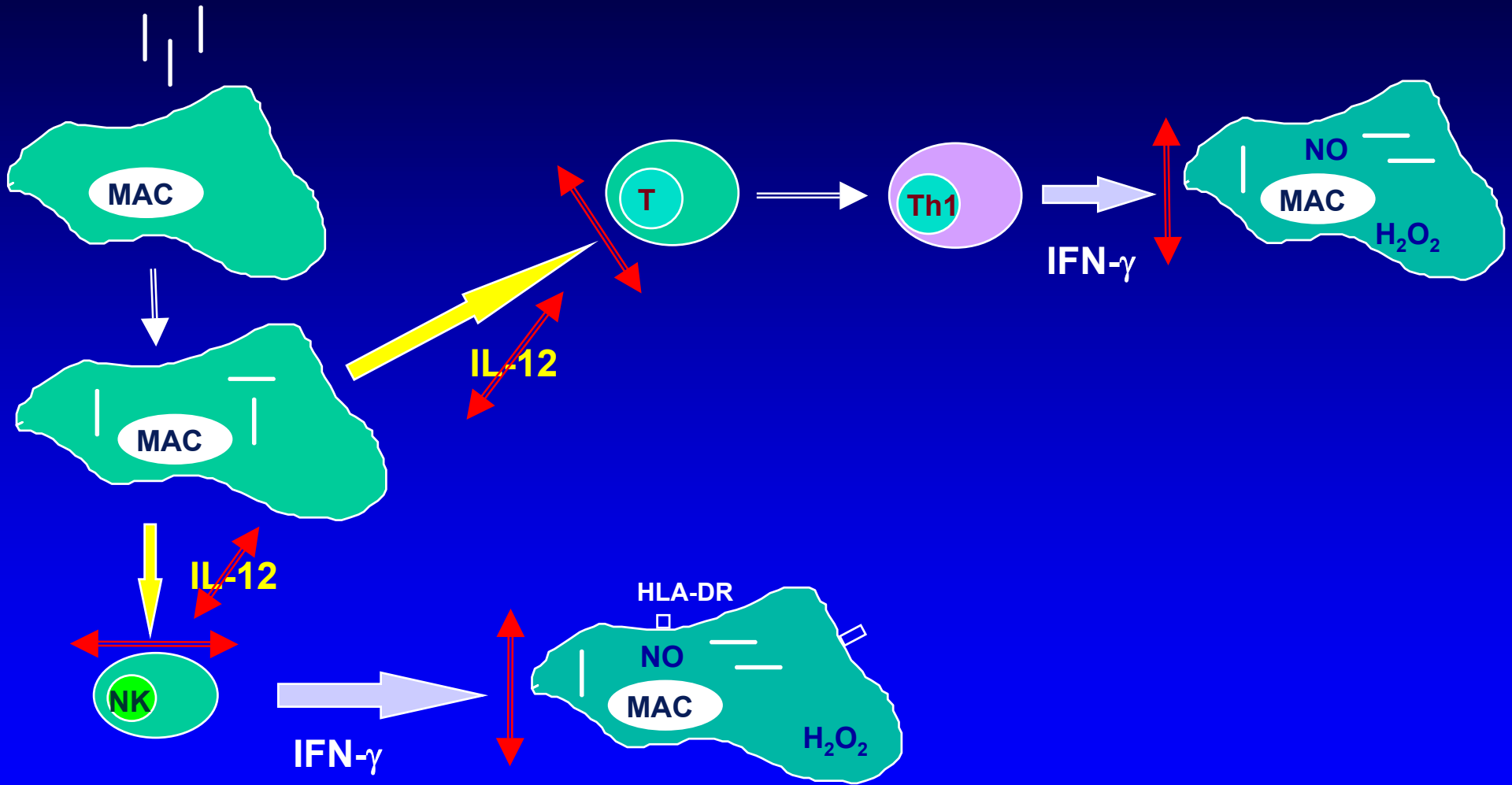
# Mendelian susceptibility to mycobacterial infection in man



**Mycobacteria**

**Early Defense**

**Late Defense**



# Host Genetics of Infectious Diseases

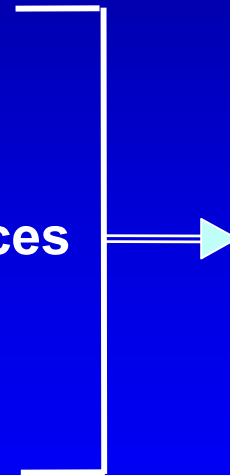
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## Genetics of Complex Diseases

Genes

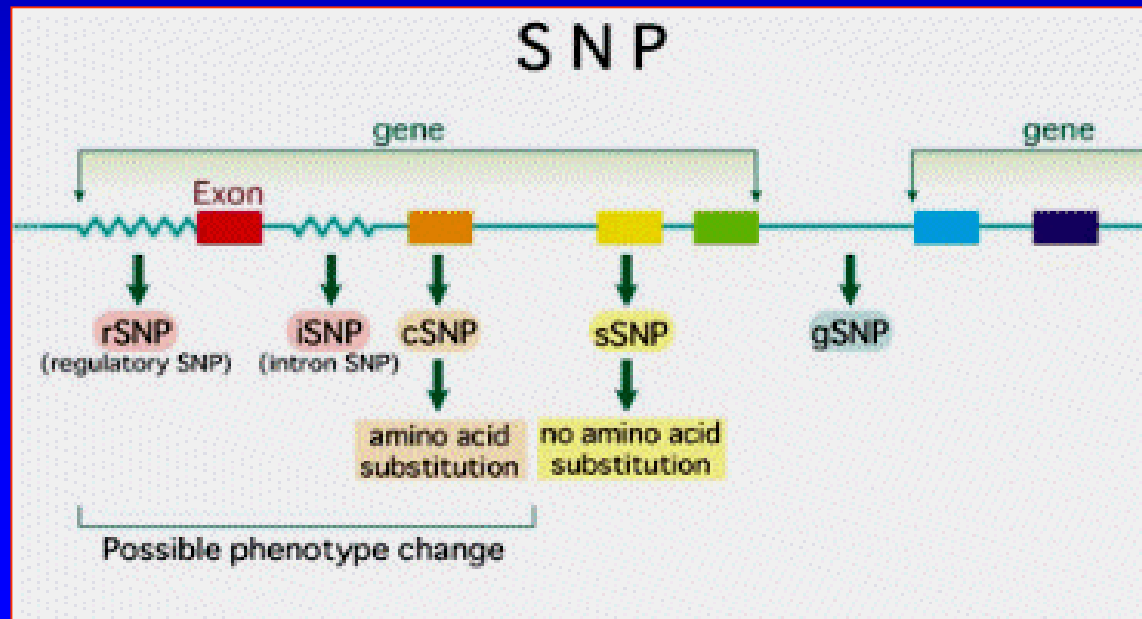
Environmental Influences

Pathogen



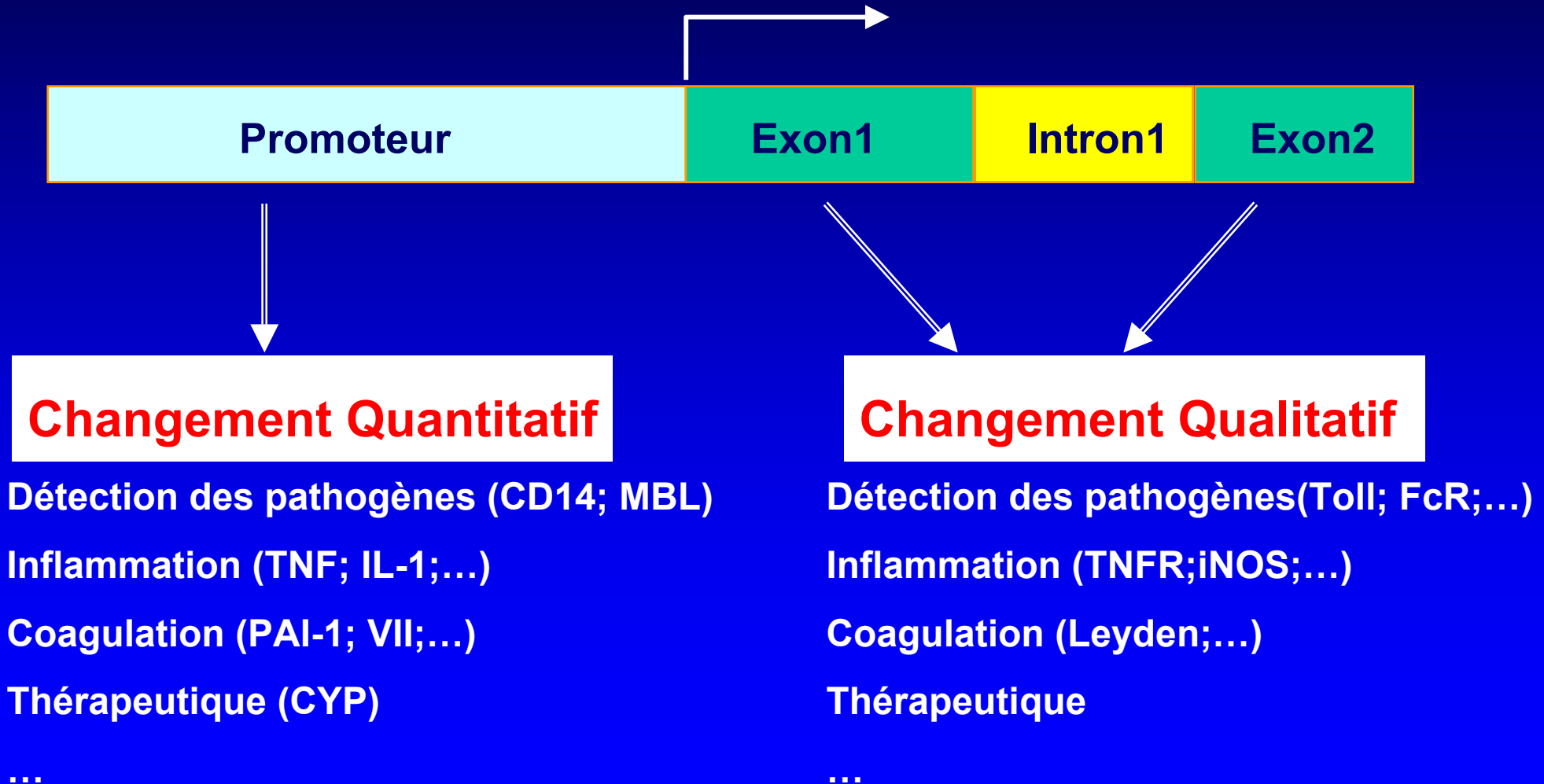
P  
H  
E  
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O  
T  
Y  
P  
E  
S

# Polymorphismes Génétiques





# Polymorphismes génétiques fonctionnels



# Background vs. Functional SNPs

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S O T M ! A  
I E R E G  
M A S E T N P

Before  
DNA  
Sequencing

DNA  
Sequence

**IMPORTANT MESSAGE !**

Variation 1

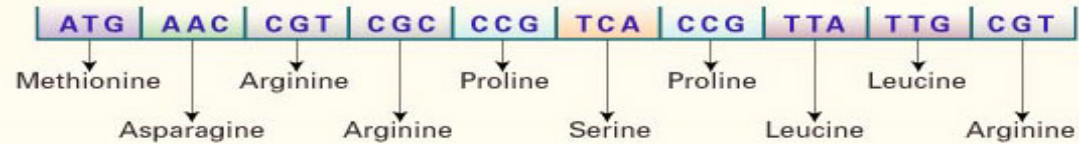
**IMPERTANT MESSAGE !**

Variation 2

***IMPORTANT MASSAGE !***

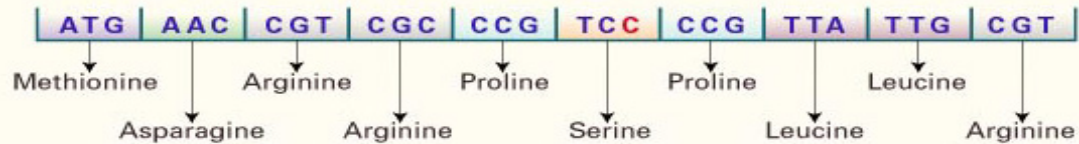
A

## Normal sequence



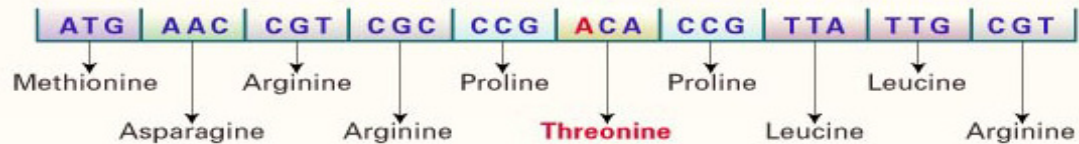
B

## Silent mutation



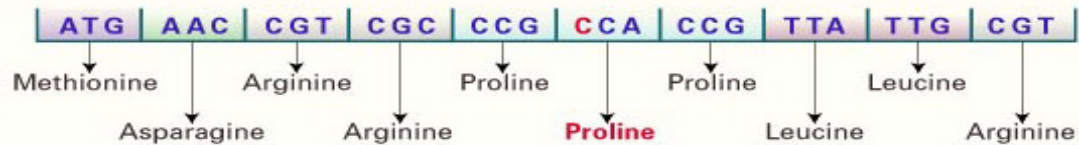
C

## Conservative missense mutation



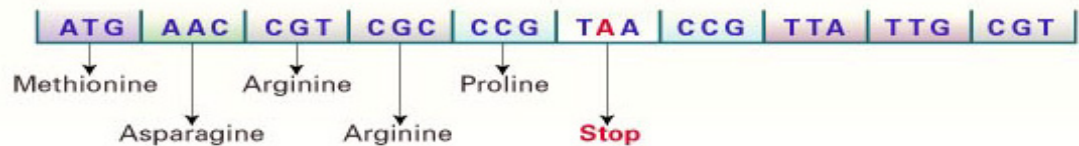
D

## Nonconservative missense mutation



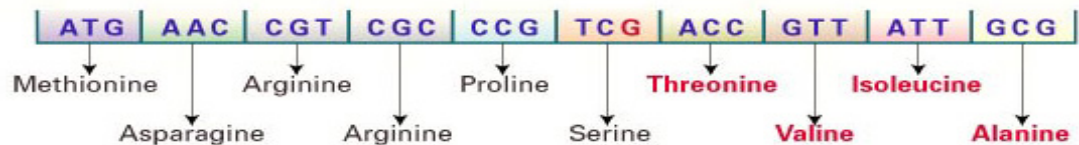
E

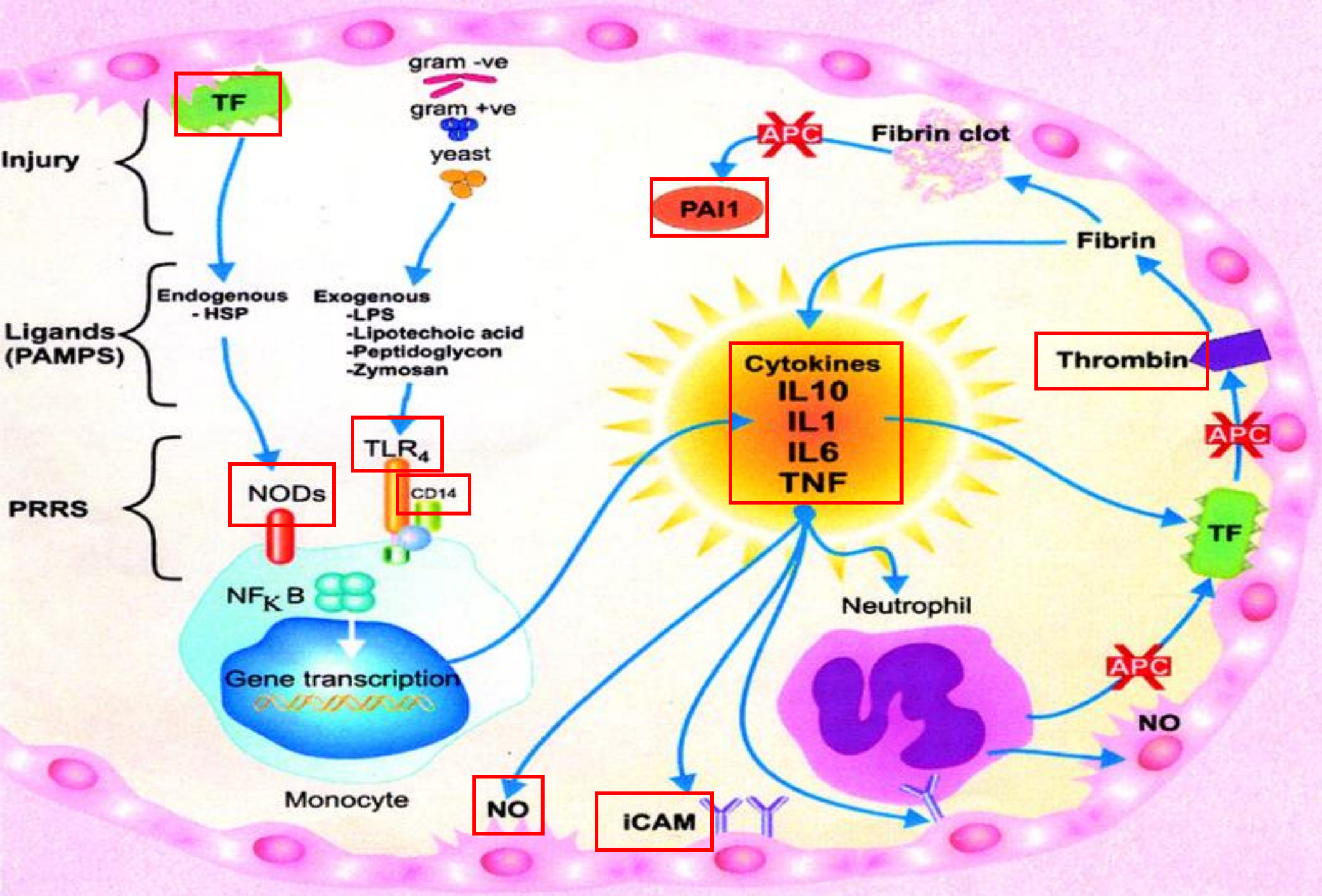
## Nonsense mutation



F

## Frame-shift mutation



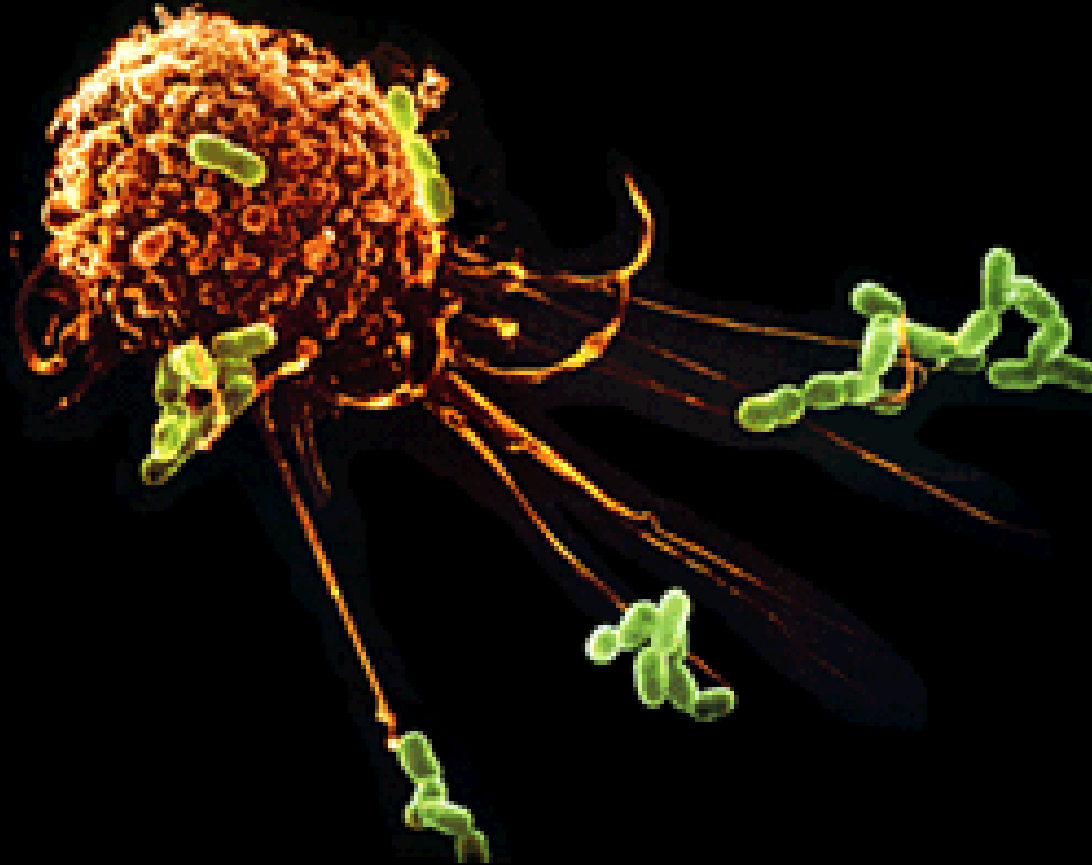


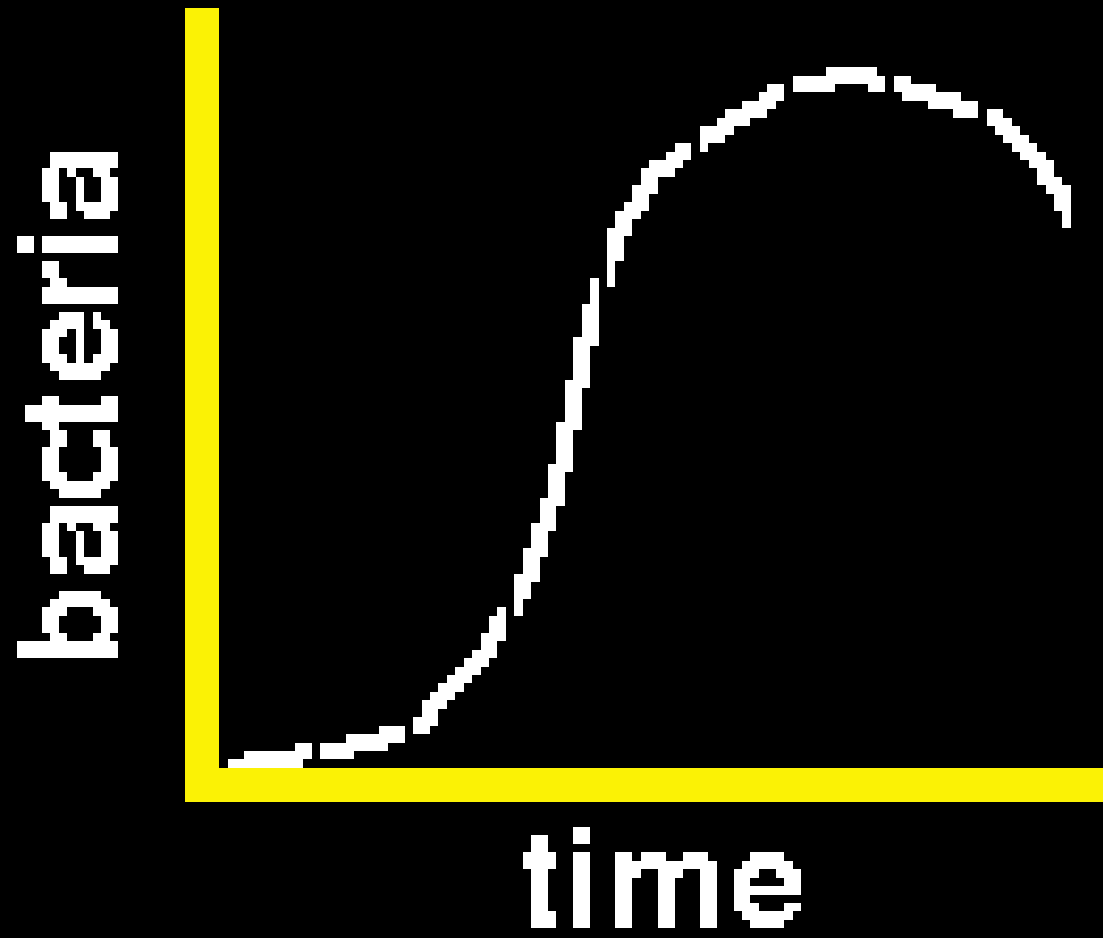


# Genetic Polymorphisms and Severe Sepsis

| Gene                     | Susceptibility and/or Outcome                    |
|--------------------------|--|
| Mannose Binding Lectin   | Meningococemia, Pneumococemia<br>Severe sepsis   |
| Toll-Like Receptor 4/2   | Gram negative/positive Septic Shock              |
| Toll-Like Receptor 5     | Legionnaire's Disease                            |
| CD14                     | Septic Shock                                     |
| FC $\gamma$ RII Receptor | Meningococemia; Pneumococemia                    |
| TNF locus                | Meningococemia<br>Septic Shock; Cerebral Malaria |
| IL-18                    | Severe Sepsis                                    |
| IL-10                    | Severe Sepsis, Meningococemia                    |
| IL-6                     | Severe sepsis                                    |
| IL-1 locus               | Severe Sepsis                                    |
| IL-4                     | Viral Pneumonia                                  |
| Caspase 12               | Severe Sepsis                                    |
| PAI-1                    | Meningococemia; Severe sepsis                    |
| Factor V Leiden          | Meningococemia; Severe sepsis                    |

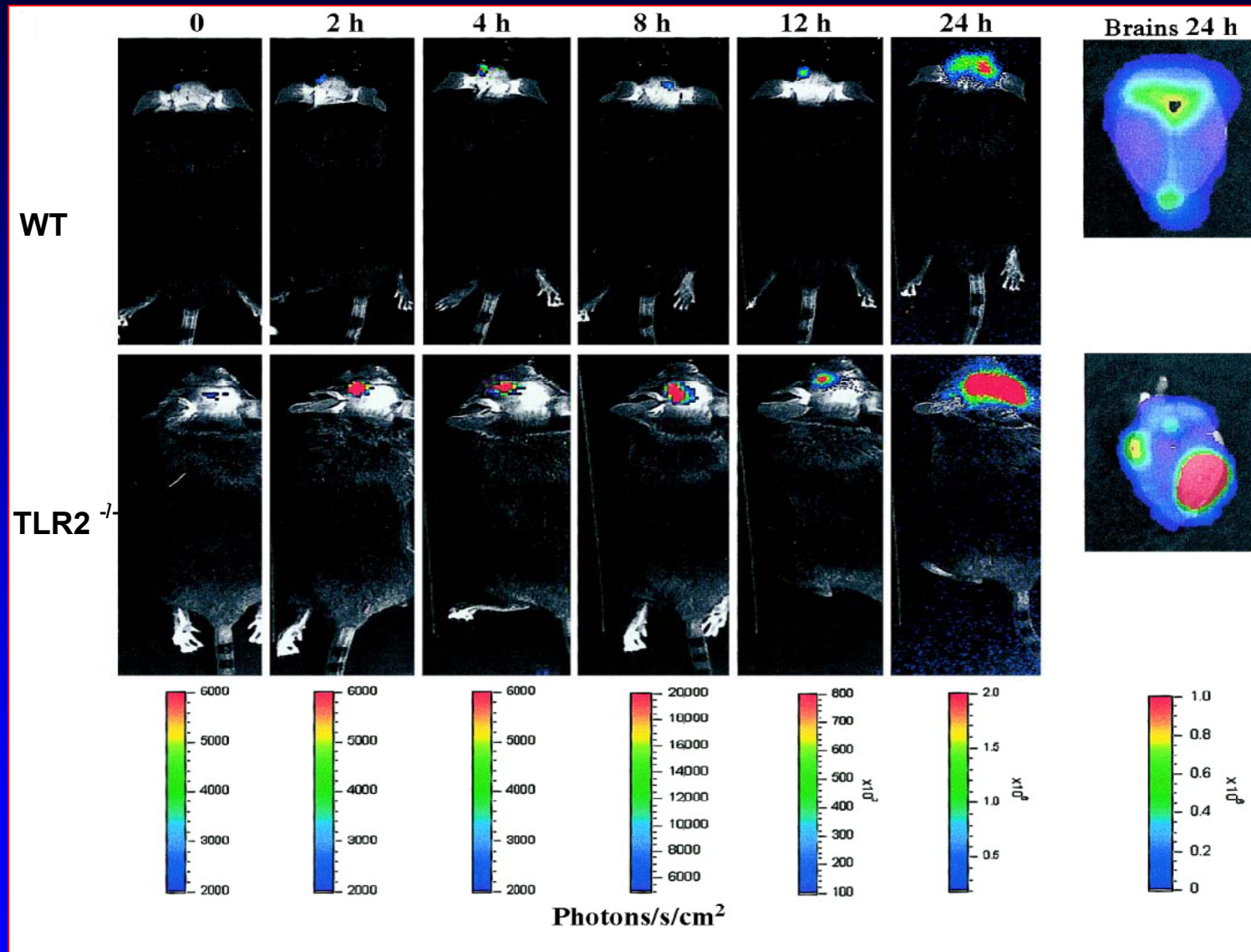
# Pathogen Detection





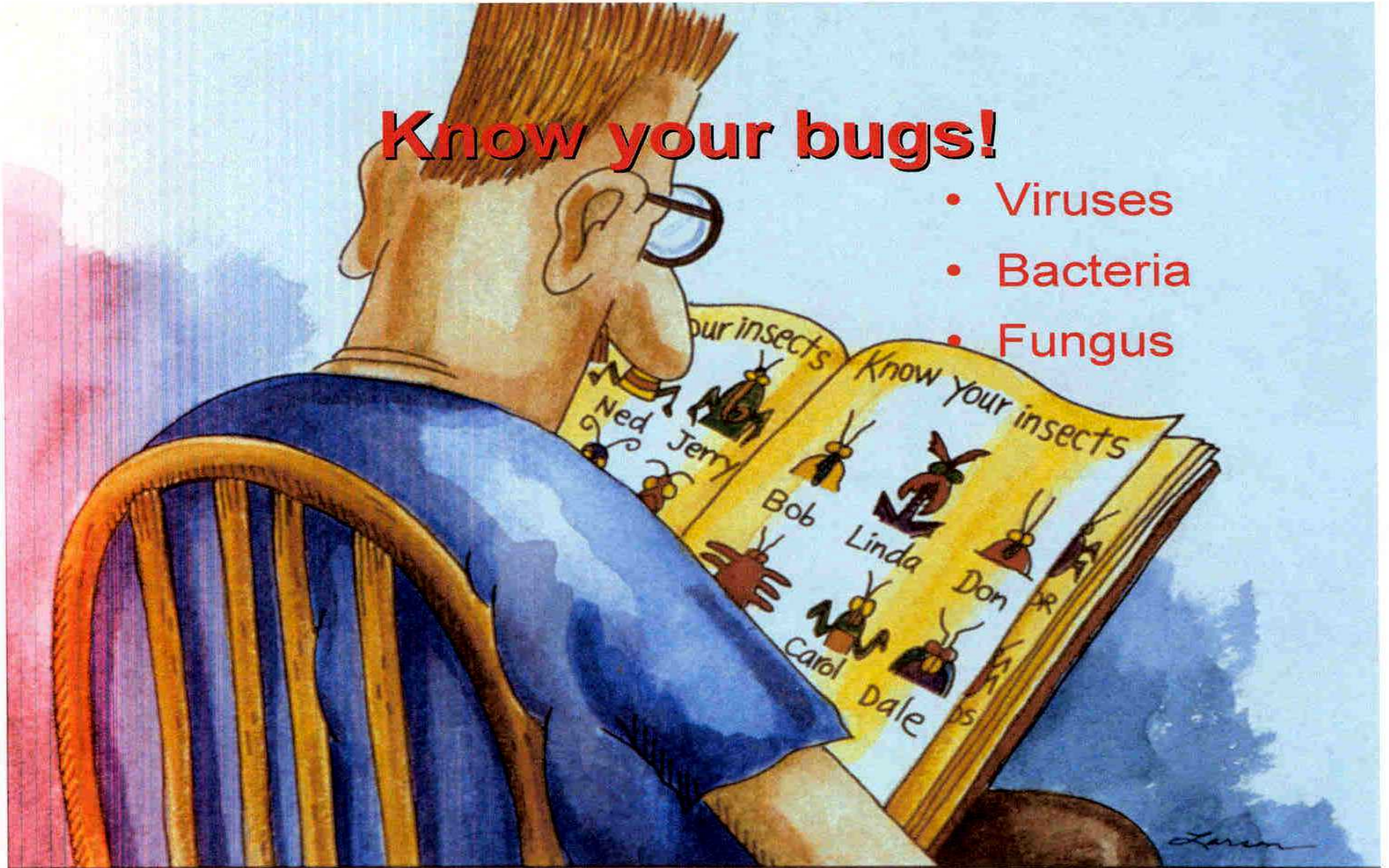


# TLR2 and *Streptococcus pneumoniae* meningitis

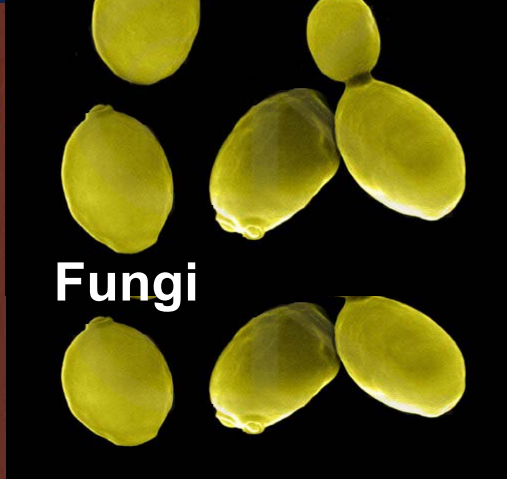
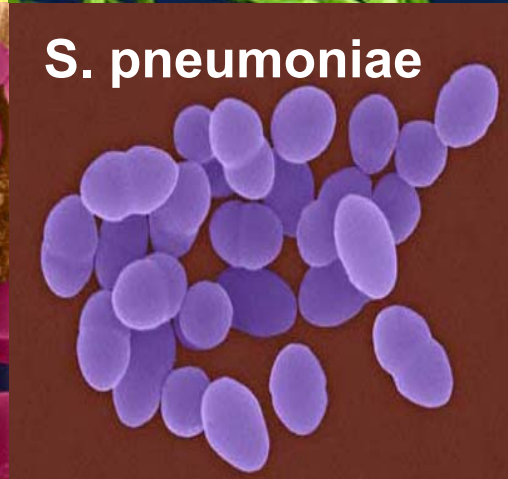
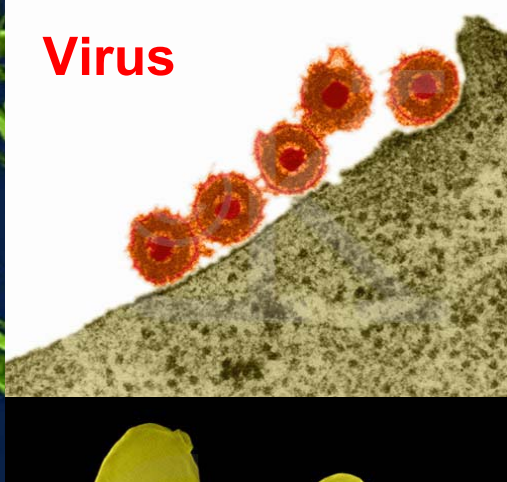
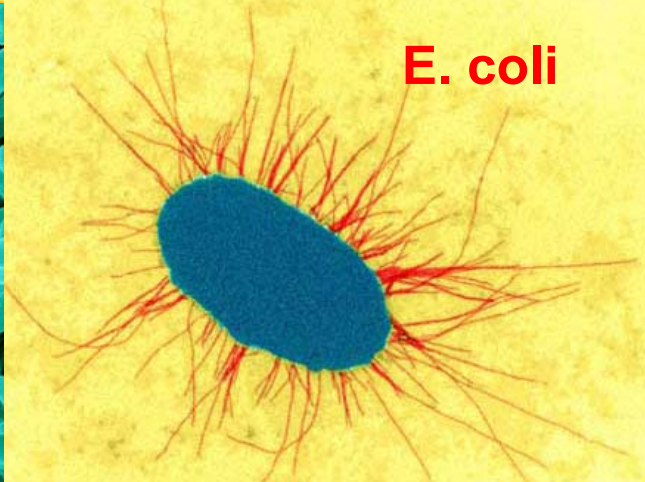
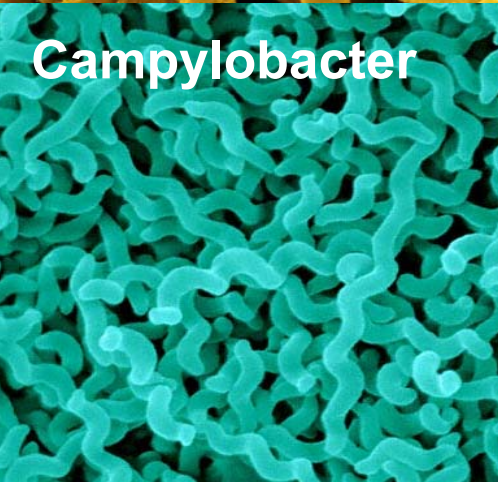
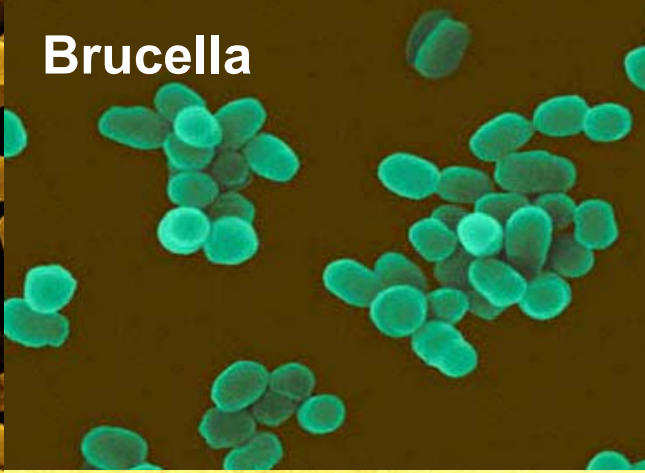


# Know your bugs!

- Viruses
- Bacteria
- Fungus

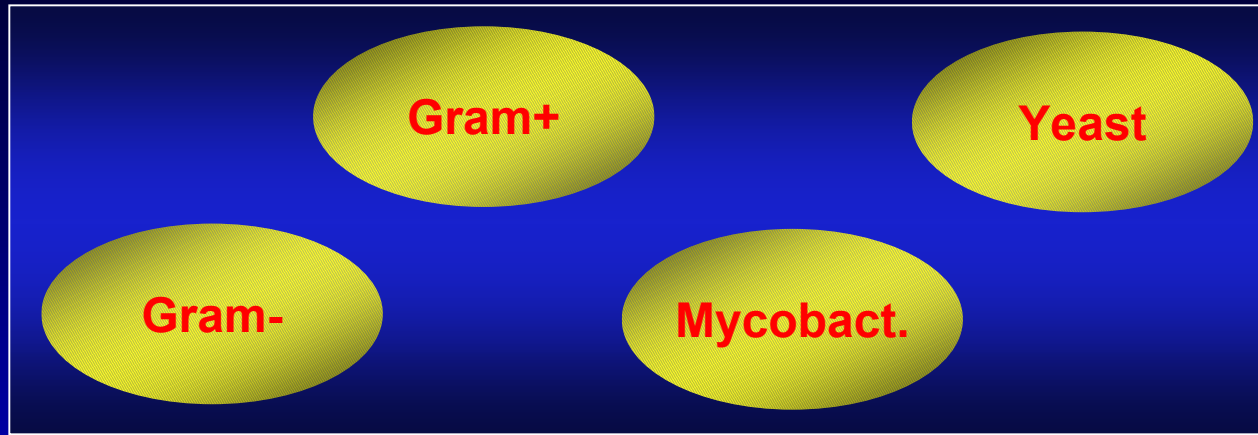




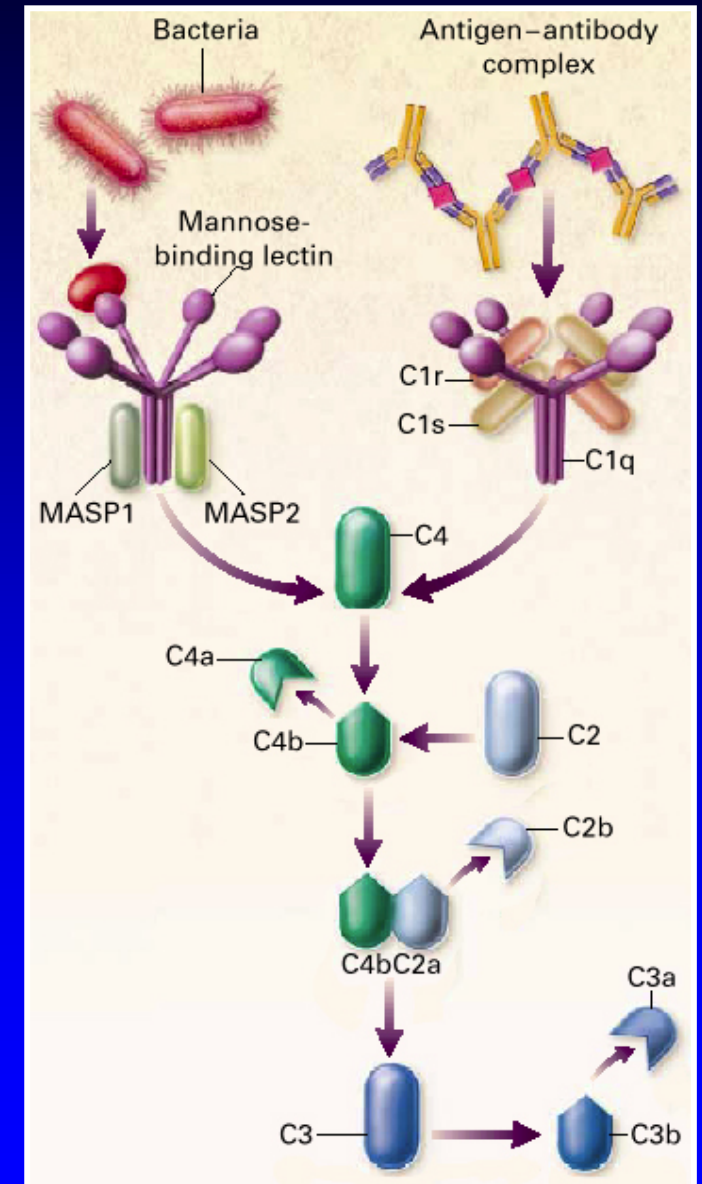




# Mannose-Binding Lectin



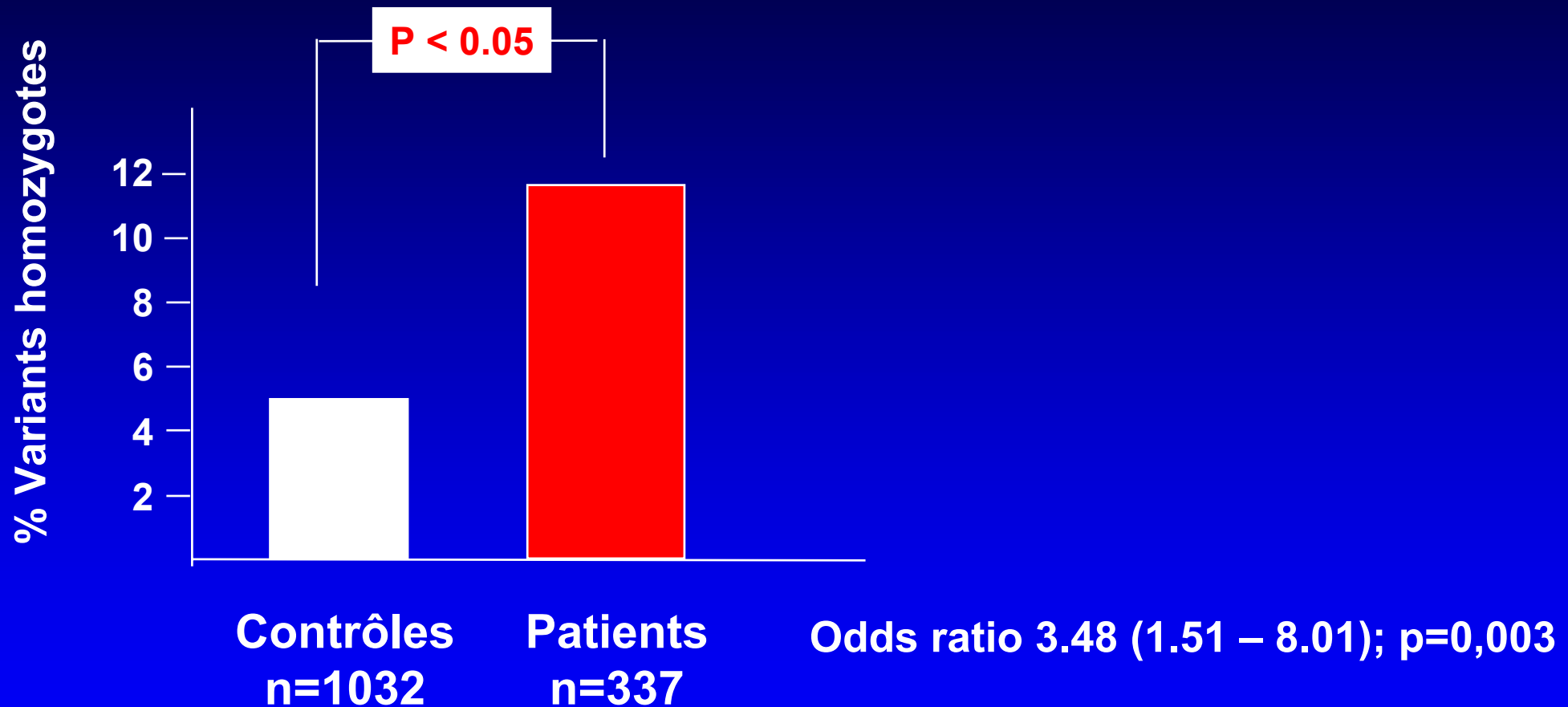
- Collectin
- Structural homology with C1q
- Associated to 2 serine proteases
- Variability:
  - Point mutations codons 52, 54, 57
  - Polymorphisms in the promoter



# **Mannose-binding Lectin Polymorphisms & The Risk of Infections**

- **Repeated bacterial and fungal infections**
  - Sumiya et al., Lancet 1991
  - Summerfeld et al., Lancet 1995
  - Garred et al., Lancet 1995
  - Summerfeld et al., BMJ 1997
- **Infections after chemotherapy**
  - Neth et al., Lancet 2001
  - Peterslund et al., Lancet 2001
- **Increased severity of lung disease and low survival in cystic fibrosis**
  - Garred et al., J. Clin. Invest. 1999
- **Meningococcal disease**
  - Hibberd et al., Lancet 1999

# MBL genotype and risk of invasive pneumococcal disease

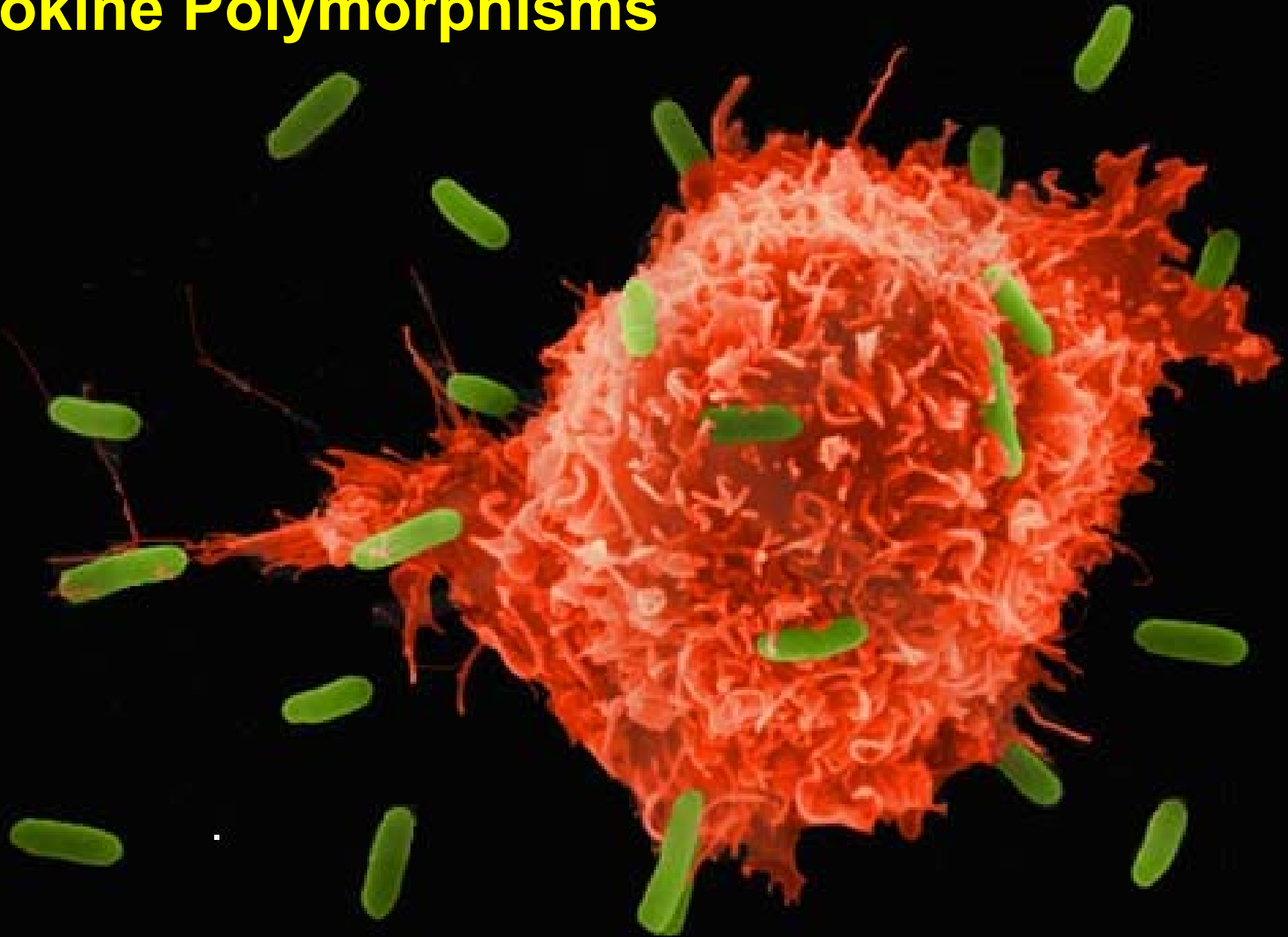


# Clinical potential of mannose-binding lectin-replacement therapy

**J.A. Summerfield<sup>1</sup>**

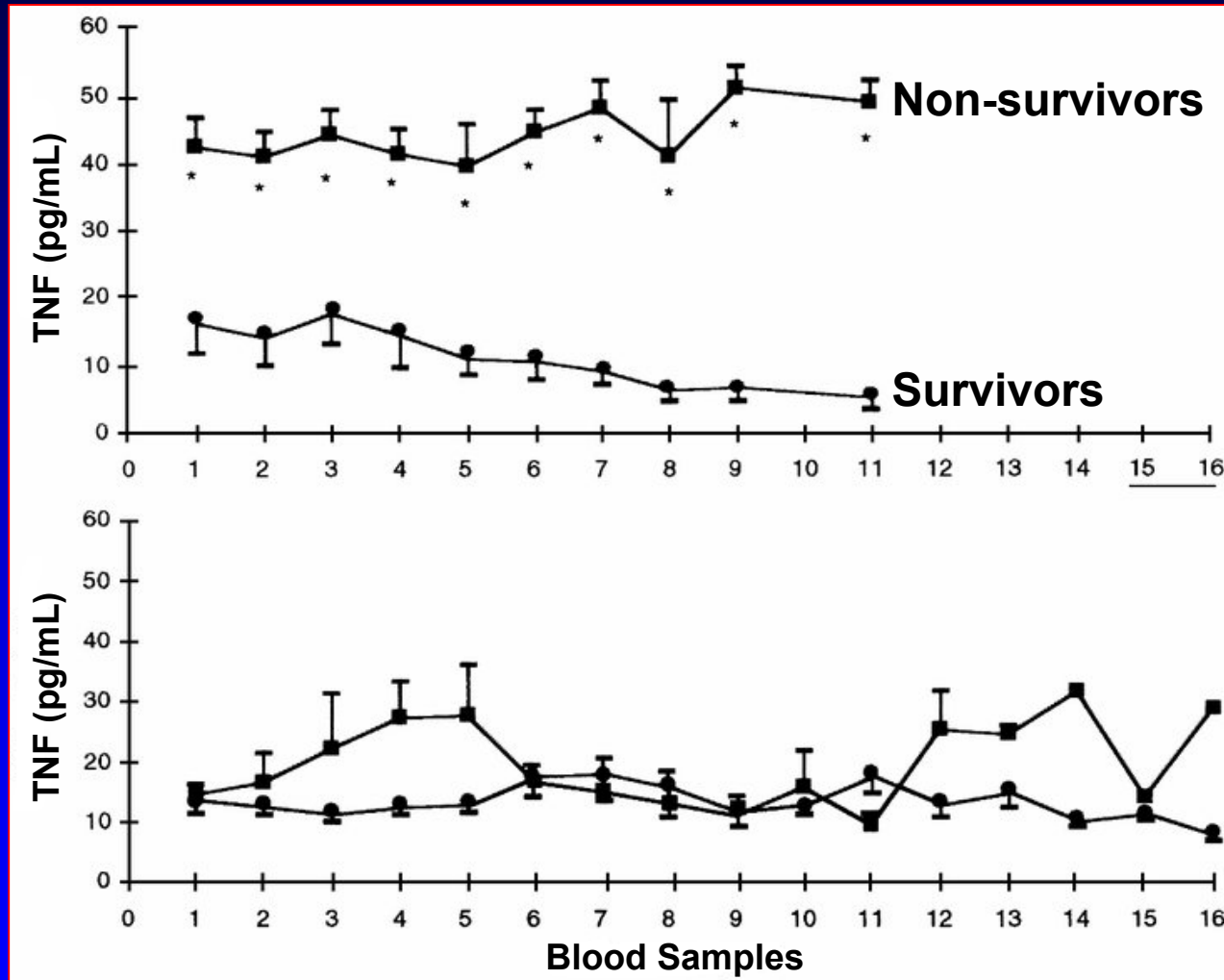
Division of Medicine, Faculty of Medicine, Imperial College London, St Mary's Campus, London W2 1NY, U.K.

# Cytokine Polymorphisms





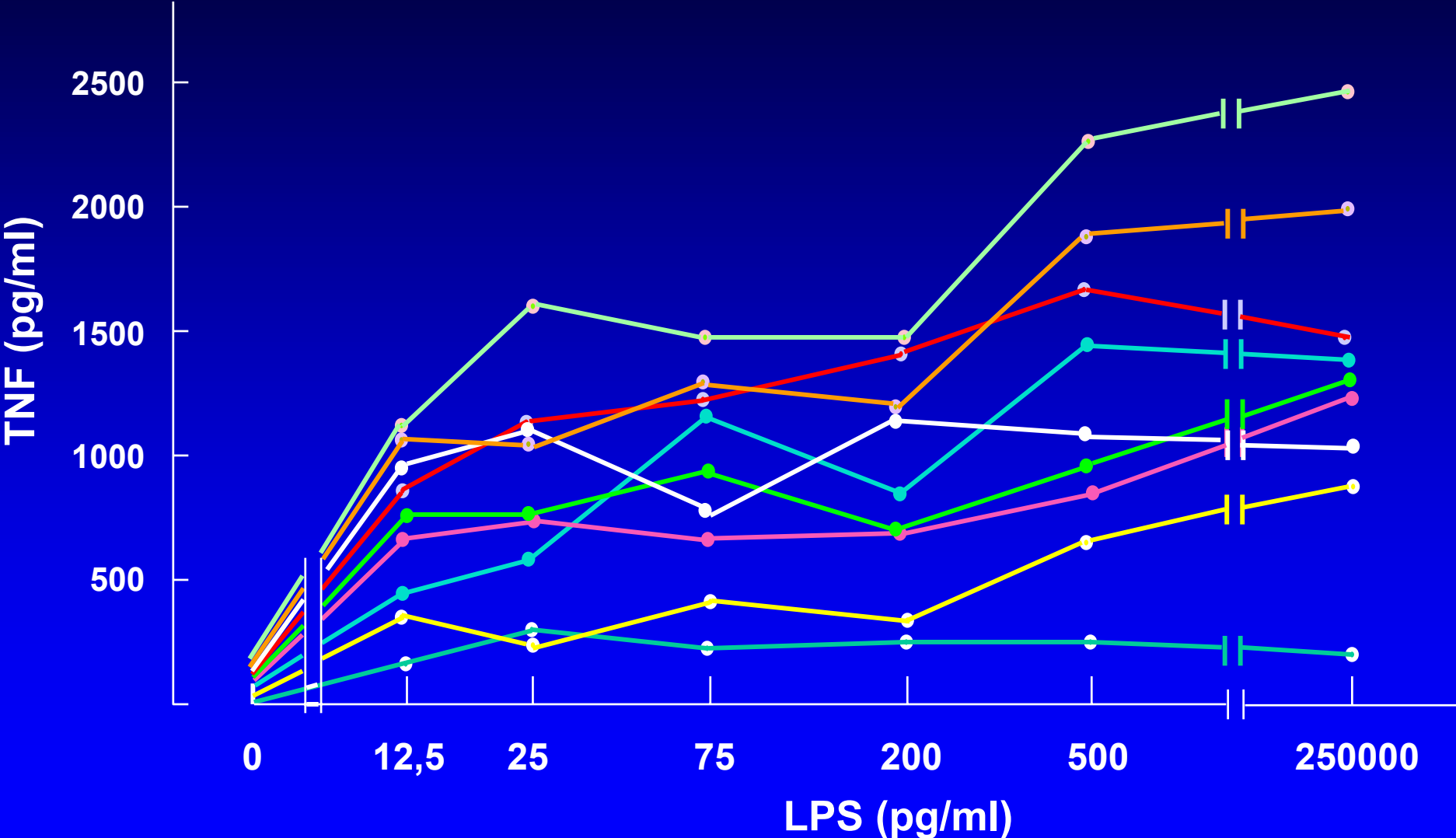
# TNF plasma levels and mortality



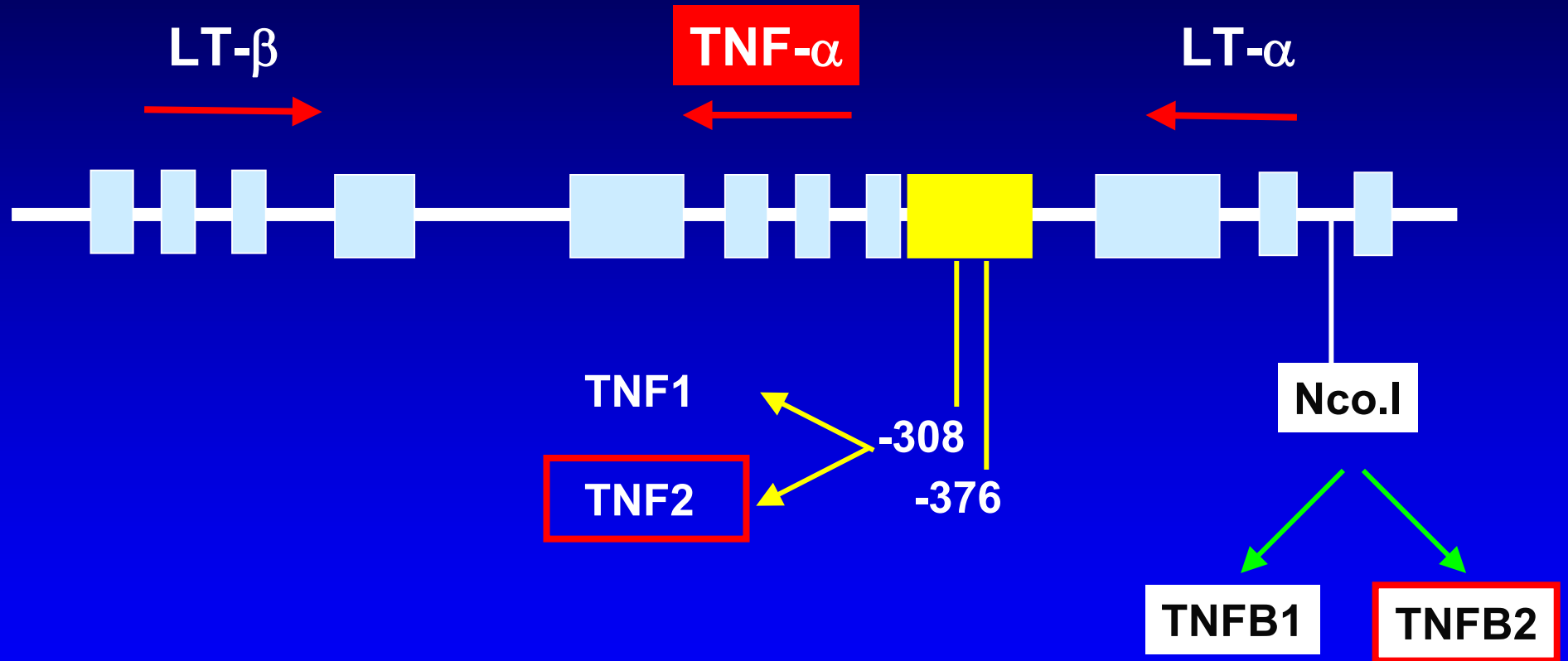
Septic shock

Trauma

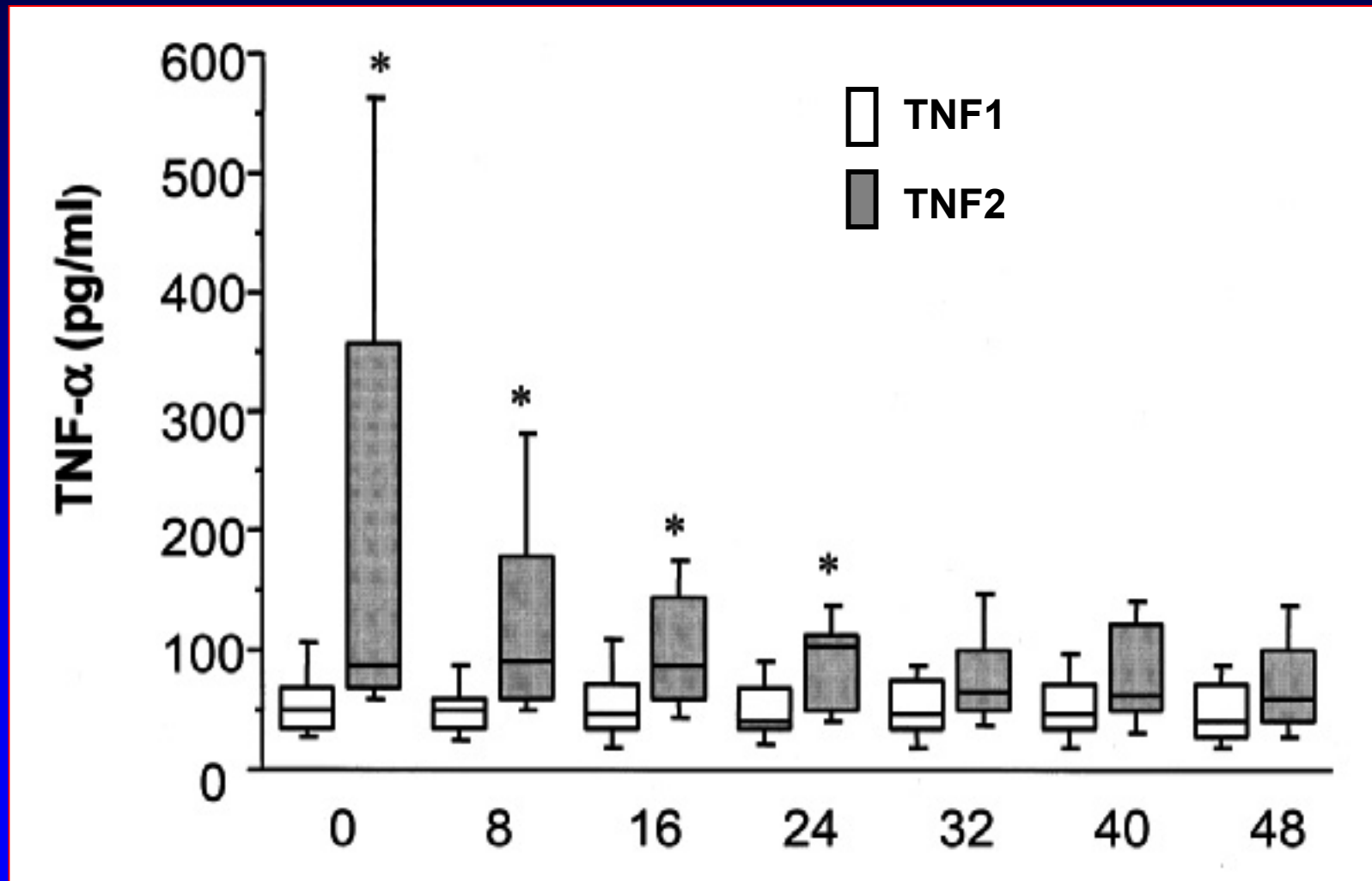
# Interindividual Differences in TNF- $\alpha$ Secretion



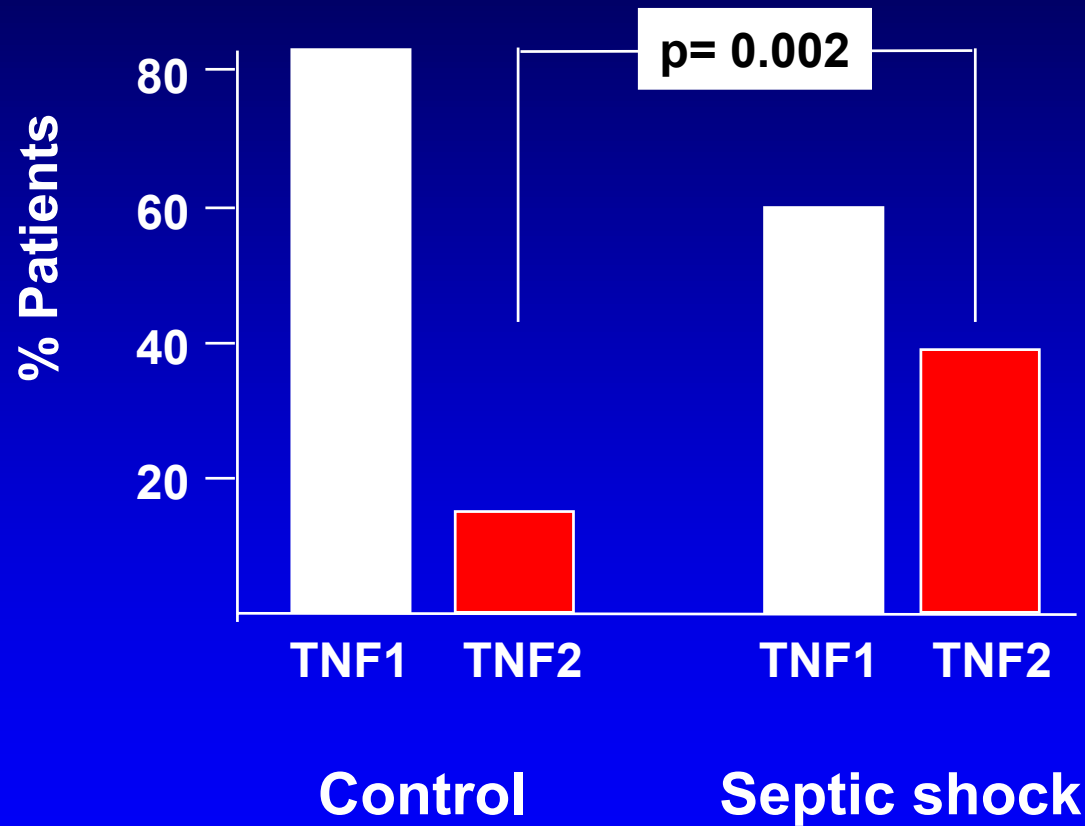
# TNF locus



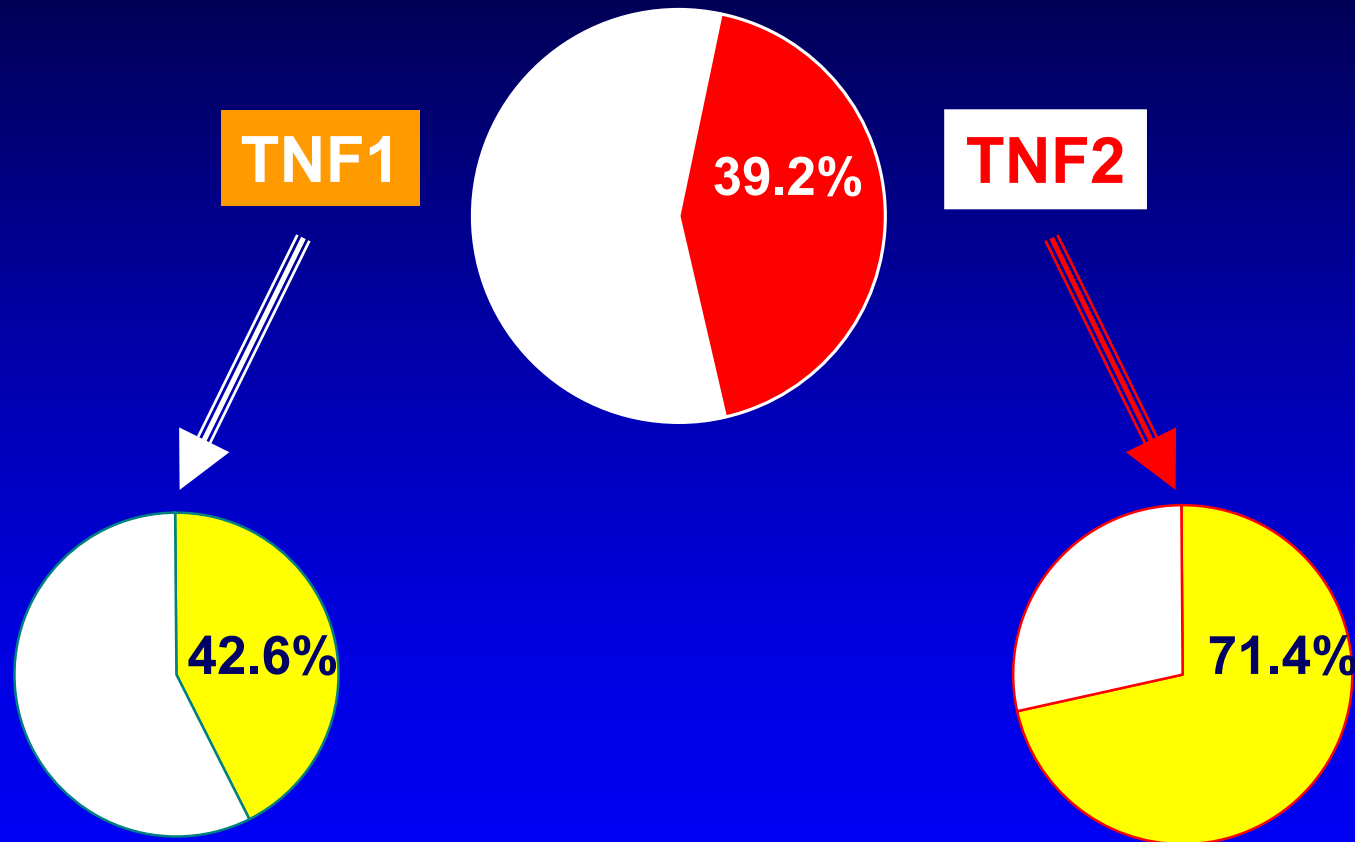
# Association of TNF2 with TNF levels in Septic Shock



# TNF2 polymorphism and septic shock susceptibility



# TNF2 polymorphism and septic shock outcome



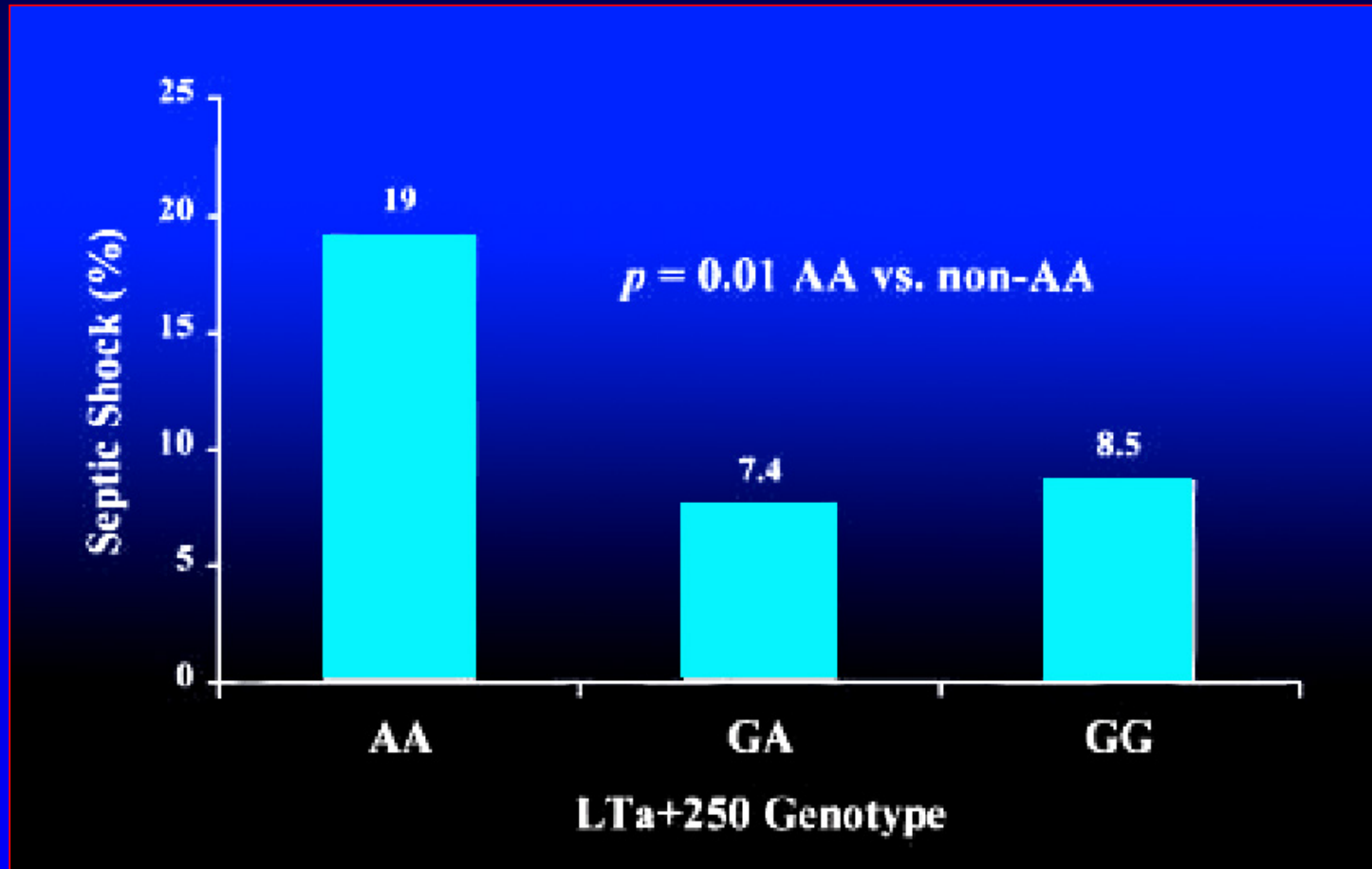
# TNF2 polymorphism and septic shock mortality

| Characteristics               | TNF1<br>(n=54) | TNF2<br>(n=35) | p            |
|-------------------------------|----------------|----------------|--------------|
| Age [mean. $\pm$ SD]          | 57 $\pm$ 15    | 59 $\pm$ 16    | ns           |
| SAPS II [mean. $\pm$ SD]      | 54 $\pm$ 17    | 56 $\pm$ 22    | ns           |
| OSF [mean. $\pm$ SD]          | 3 $\pm$ 1      | 2.8 $\pm$ 1    | ns           |
| <b>Observed mortality (%)</b> | <b>42.6</b>    | <b>71.4</b>    | <b>0.008</b> |
| Predicted mortality (%)       | 52.1           | 52.8           | ns           |

# Community-Acquired Pneumonia and TNF polymorphisms

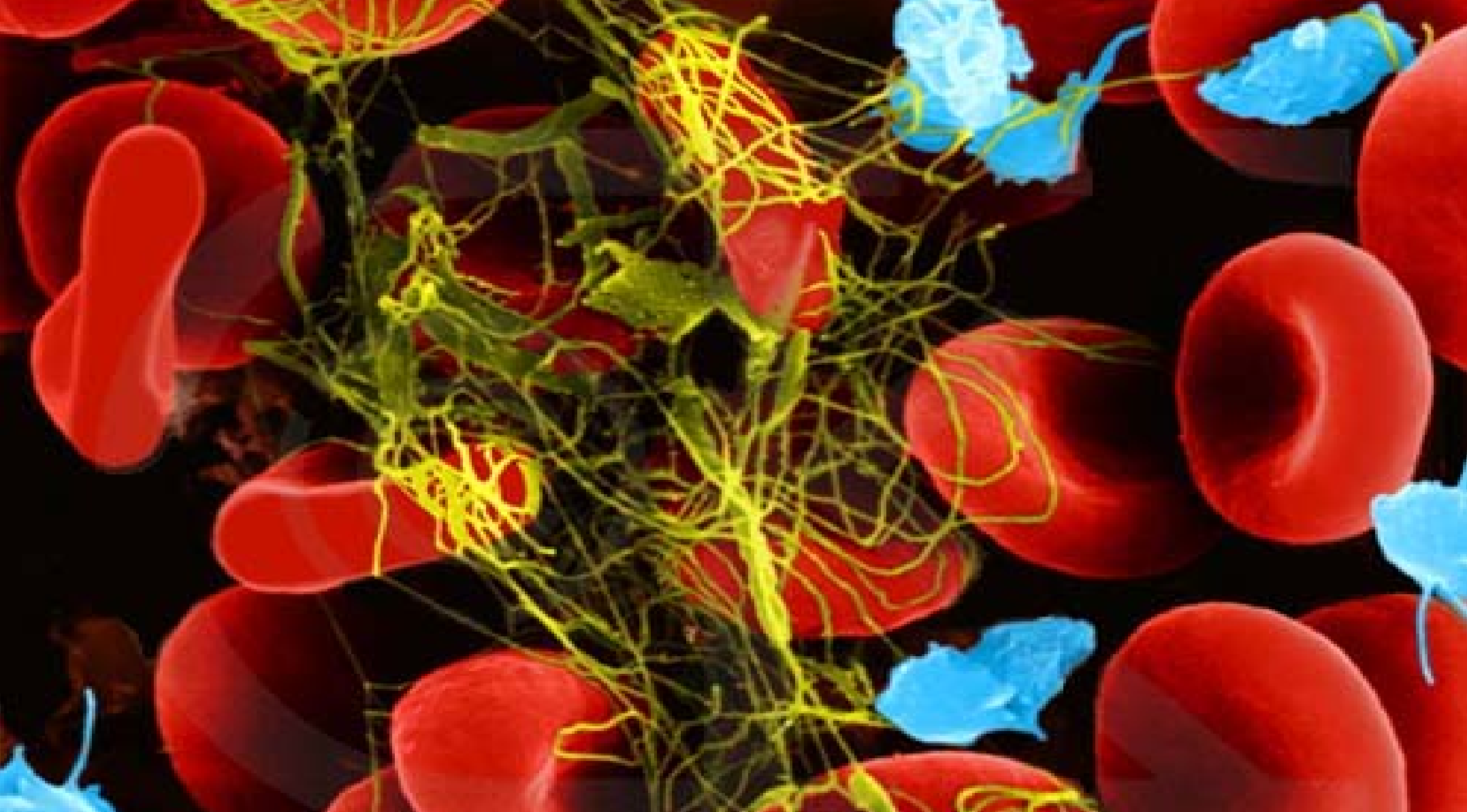
280 CAP

No association with mortality rate



LTα+250 AA genotype RR= 2.48 (1.28 – 4.78), Age-adjusted RR = 3.64 (1.28 – 10.66)





# Coagulation Polymorphisms

# Cytokines

Generation of thrombin mediated by tissue factor

Impairment of anticoagulant pathways

Suppression of fibrinolysis

TF  $\xrightarrow{+}$  Thr  $\xrightarrow{+}$  Fibrin

Low levels of ATIII  
Prot C, Prot S  
Insufficient TFPI

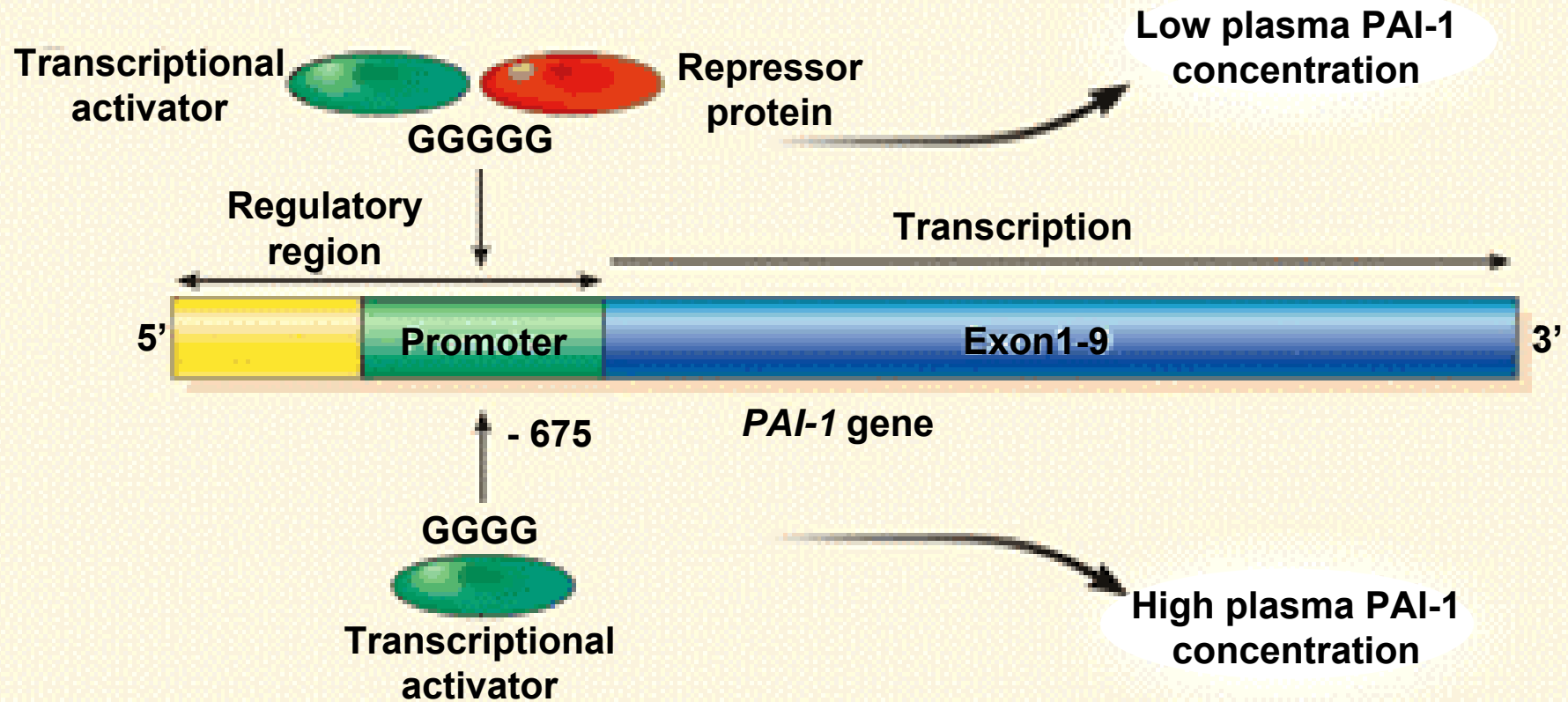
PAI-1  $\xrightarrow{-}$  t-PA

Formation of fibrin

Inadequate removal of fibrin

Thrombosis of small and midsize vessels

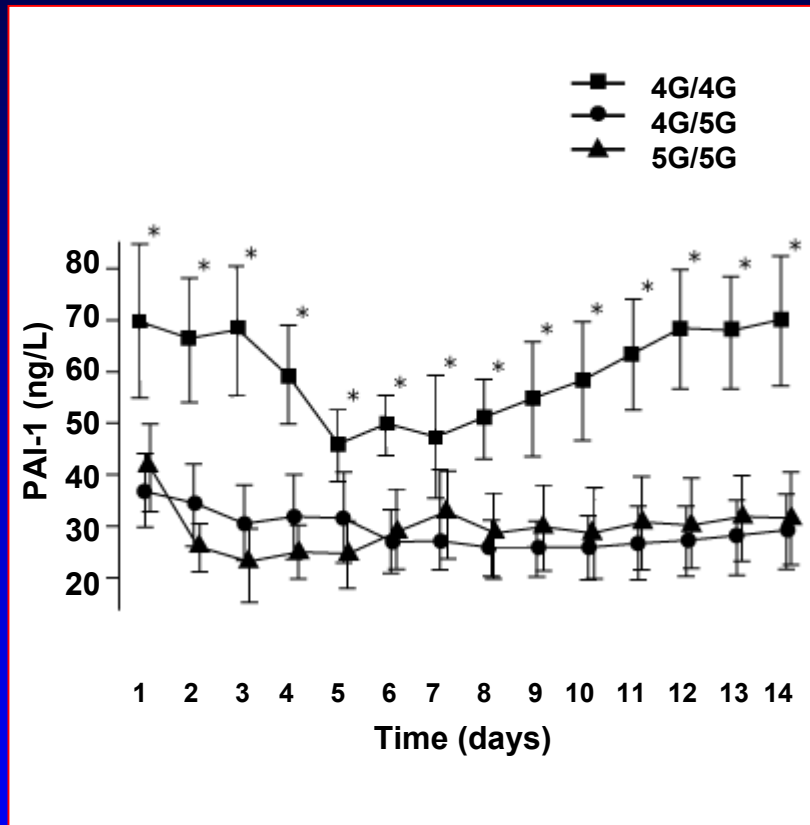
# 4G/5G PAI-1 Polymorphism



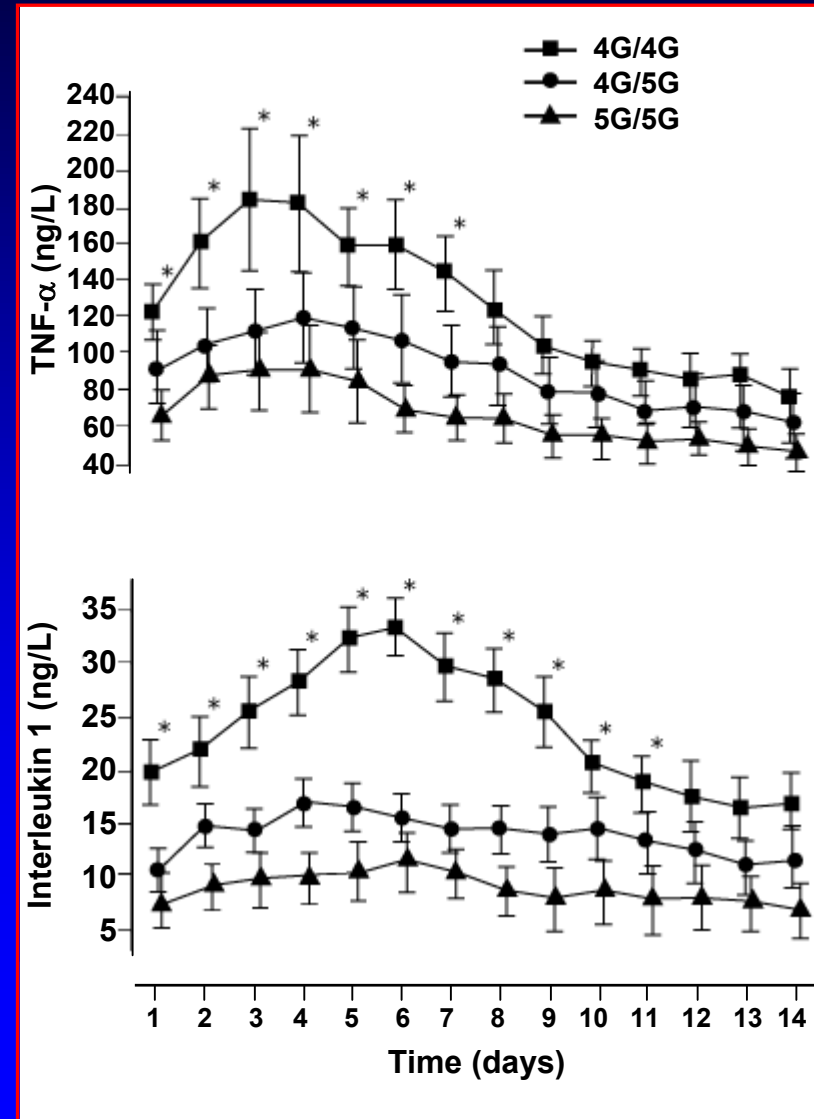
# Genetics and Trauma Outcome



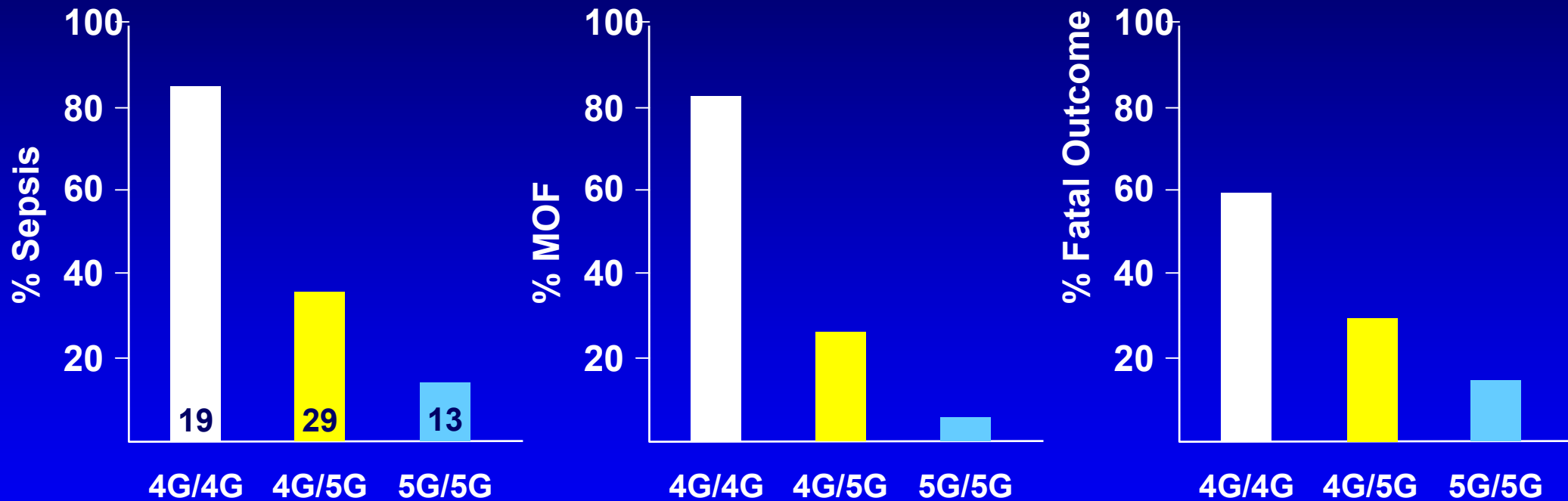
# 4G/5G promoter polymorphism in the PAI-1 gene and severe trauma patients



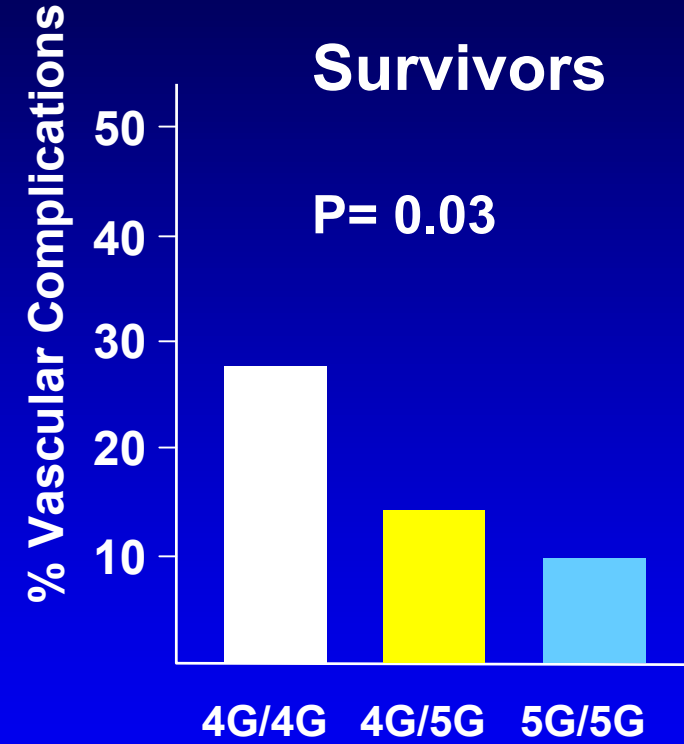
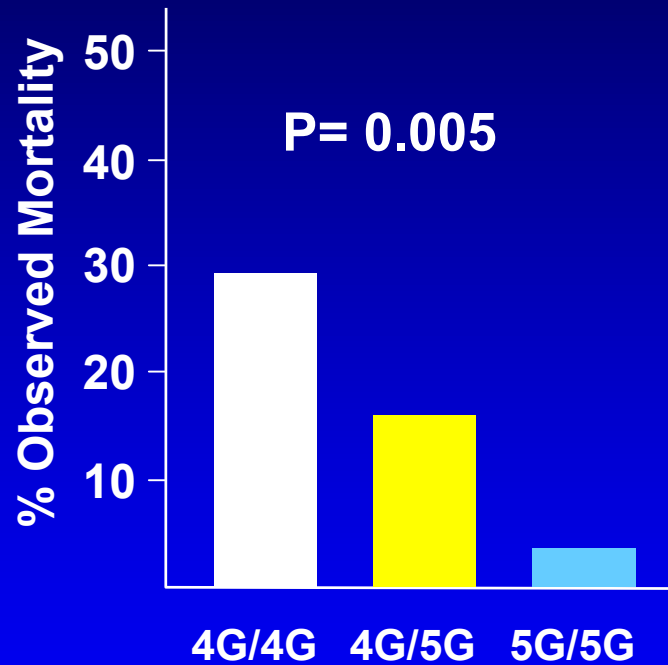
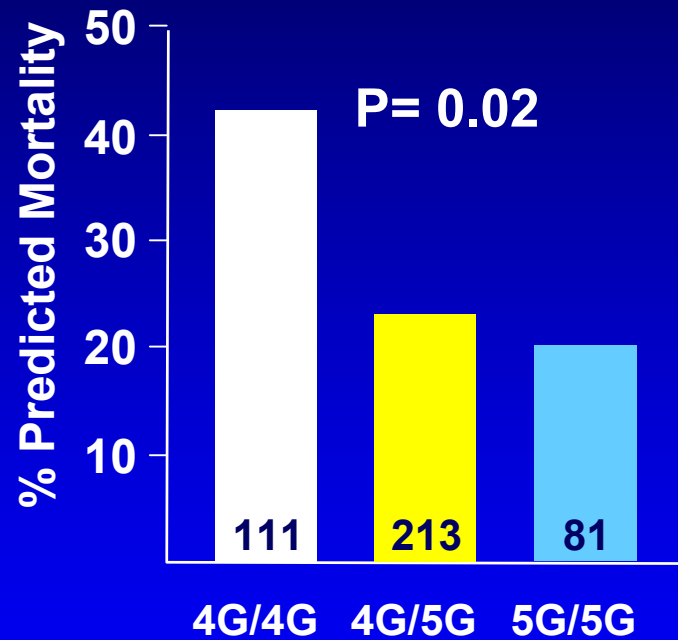
Menges, Lancet 2001;357:1096



# 4G/5G promoter polymorphism in the PAI-1 gene and severe trauma patients



# 4G/5G PAI-1 Polymorphism and Meningococcal Disease







# Perspectives and Conclusions

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- ⇒ Screening of a high number of polymorphisms in large cohorts
  - ⇒ SNPs or haplotype
  - ⇒ Micro-arrays, Taqman, Mass Spectroscopy, ...

**Yamada Y et al. *N Engl J Med* 2002; 347: 1916-23.**

⇒ **2819 patients with myocardial infarction**

⇒ **2242 controls**

⇒ **112 polymorphisms of 71 candidate genes**

**PAI-1, connexin 37, stromelysin**

# Perspectives et Conclusions

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- **Screening of a high number of polymorphisms in large cohorts**
  - ⇒ **UK: 1000 Patients – Peritonitis**
  - ⇒ **UK: 2000 Patients – Community-Acquired Pneumonia**
  - ⇒ **USA: 2000 Patients – Severe Sepsis**
  - ⇒ **USA: 1500 Patients – Severe Sepsis**
  - ⇒ **France: 3500 Patients – Nosocomial Pneumonia**
  - ⇒ **France: 3500 Severe Trauma**
  - ⇒ **Australia ?**
  - ⇒ **Japan ?**

# Génotypage à Haut Débit



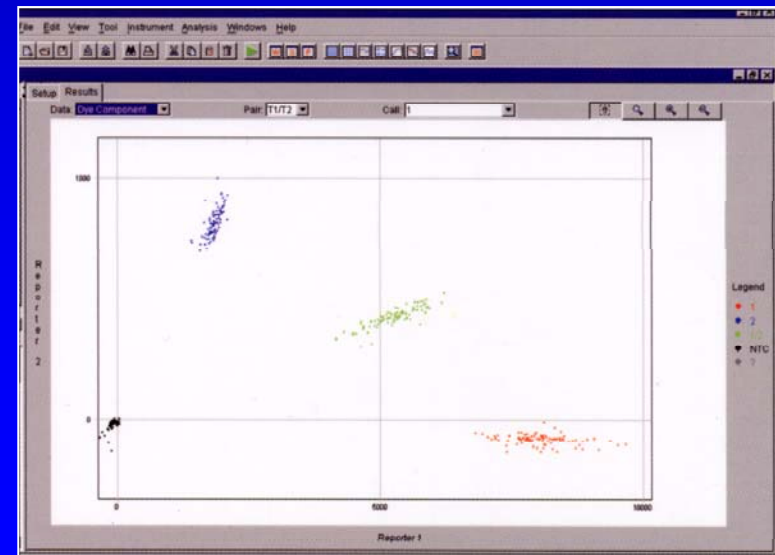
20'



30'



90'



# Perspectives and Conclusions

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⇒ Screening of a high number of polymorphisms

⇒ Identify potential markers of susceptibility, severity, and clinical outcome

Genetic profiling → Individual risk assessment

→ Prevention, Vaccination

→ To tailor prescriptions to each patient

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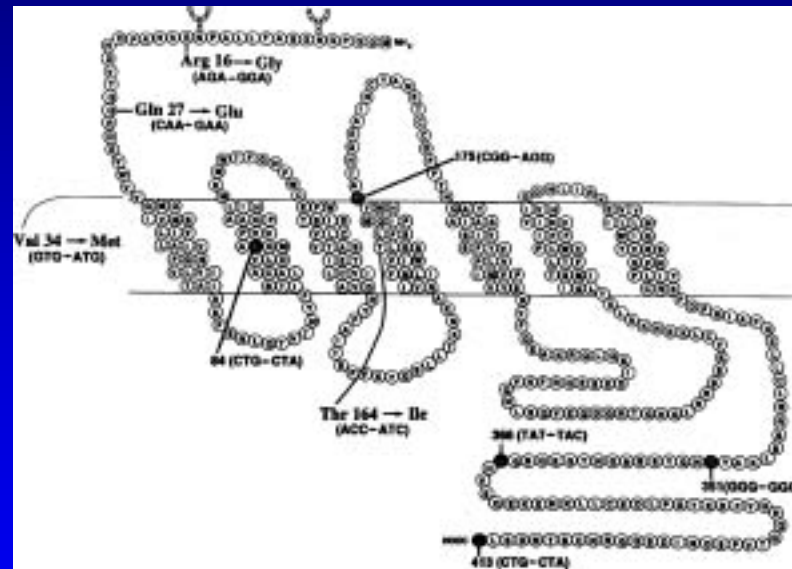
→ To tailor prescriptions to each patient

⇒ Stratification of patients by genotype in the design of treatment trials

⇒ Identify potential markers for responders vs non-responders

# Use of regularly scheduled albuterol treatment in asthma: genotype-stratified, randomised, placebo-controlled cross-over trial

Elliot Israel, Vernon M Chinchilli, Jean G Ford, Homer A Boushey, Reuben Cherniack, Timothy J Craig, Aaron Deykin, Joanne K Fagan, John V Fahy, *Lancet* 2004; 364: 1505-12

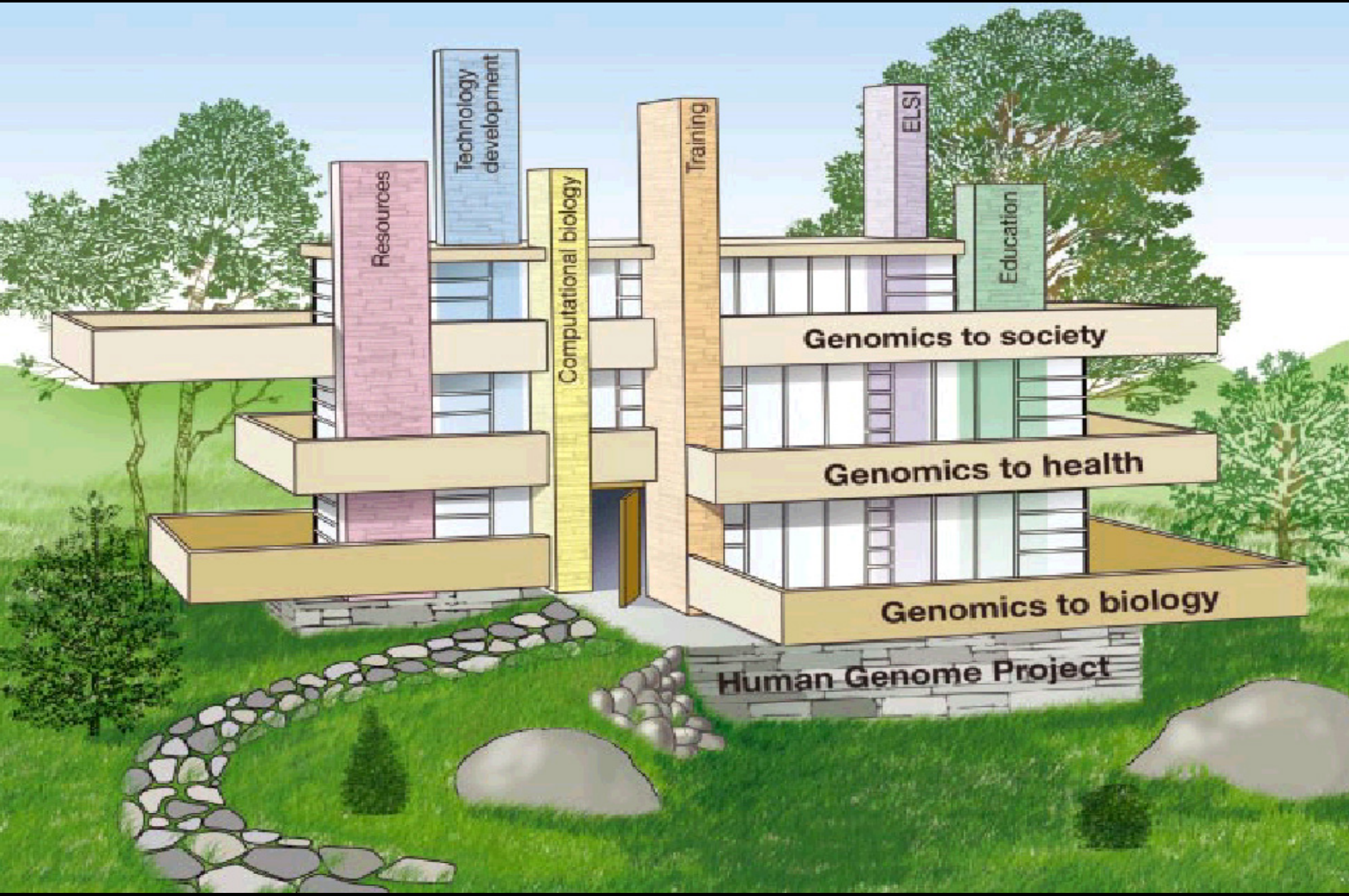


**Interpretation** Genotype at the 16th aminoacid residue of the  $\beta_2$ -adrenergic receptor affects the long-term response to albuterol use. Bronchodilator treatments avoiding albuterol may be appropriate for patients with the Arg/Arg genotype.

PUTTING SCIENCE  
RIGHT  
TO WORK!







Resources

Technology  
development

Computational biology

Training

ELSI

Education

Genomics to society

Genomics to health

Genomics to biology

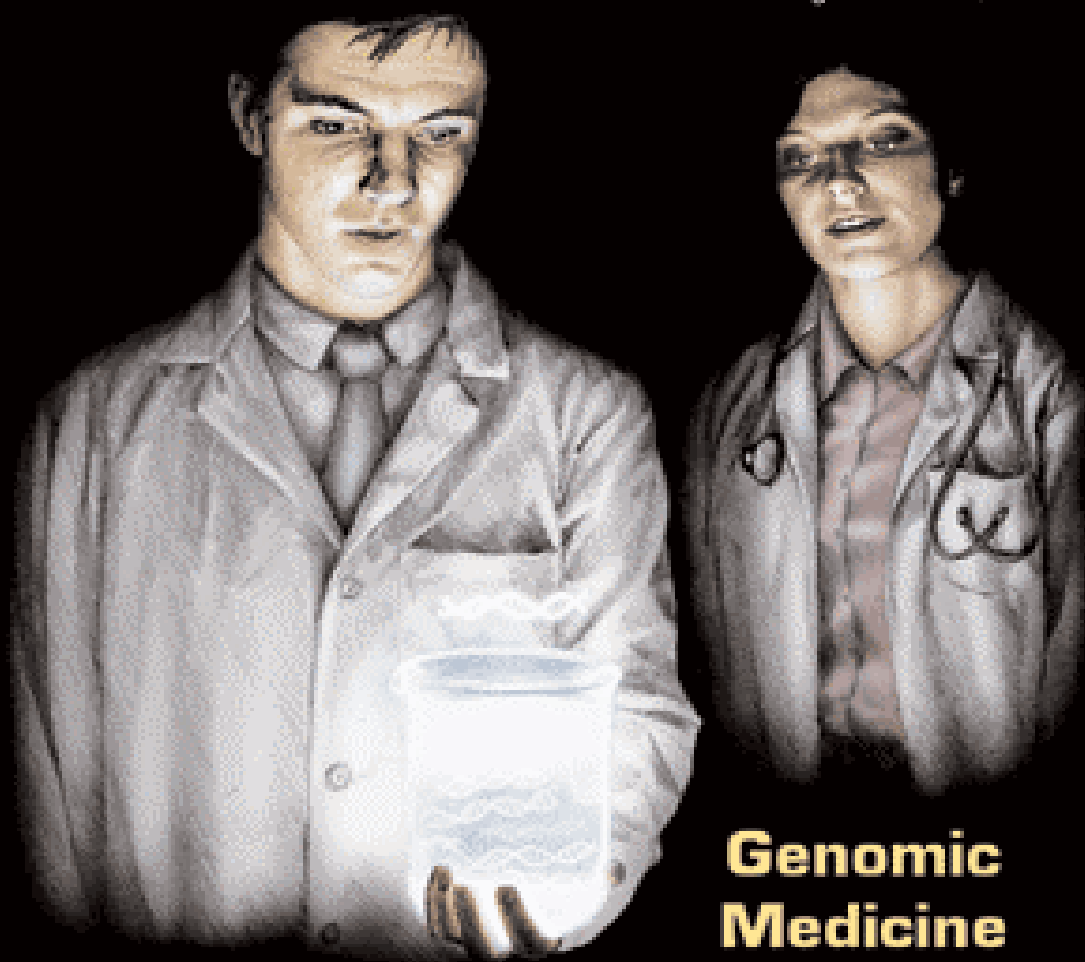
Human Genome Project



24 October 2003

# Science

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## Genomic Medicine



AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE

