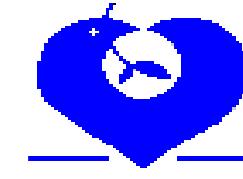


Genetic Factors Governing Susceptibilities to Severe Infections

GSK-Chair of Infectious Diseases

Pr Jean-Paul MIRA



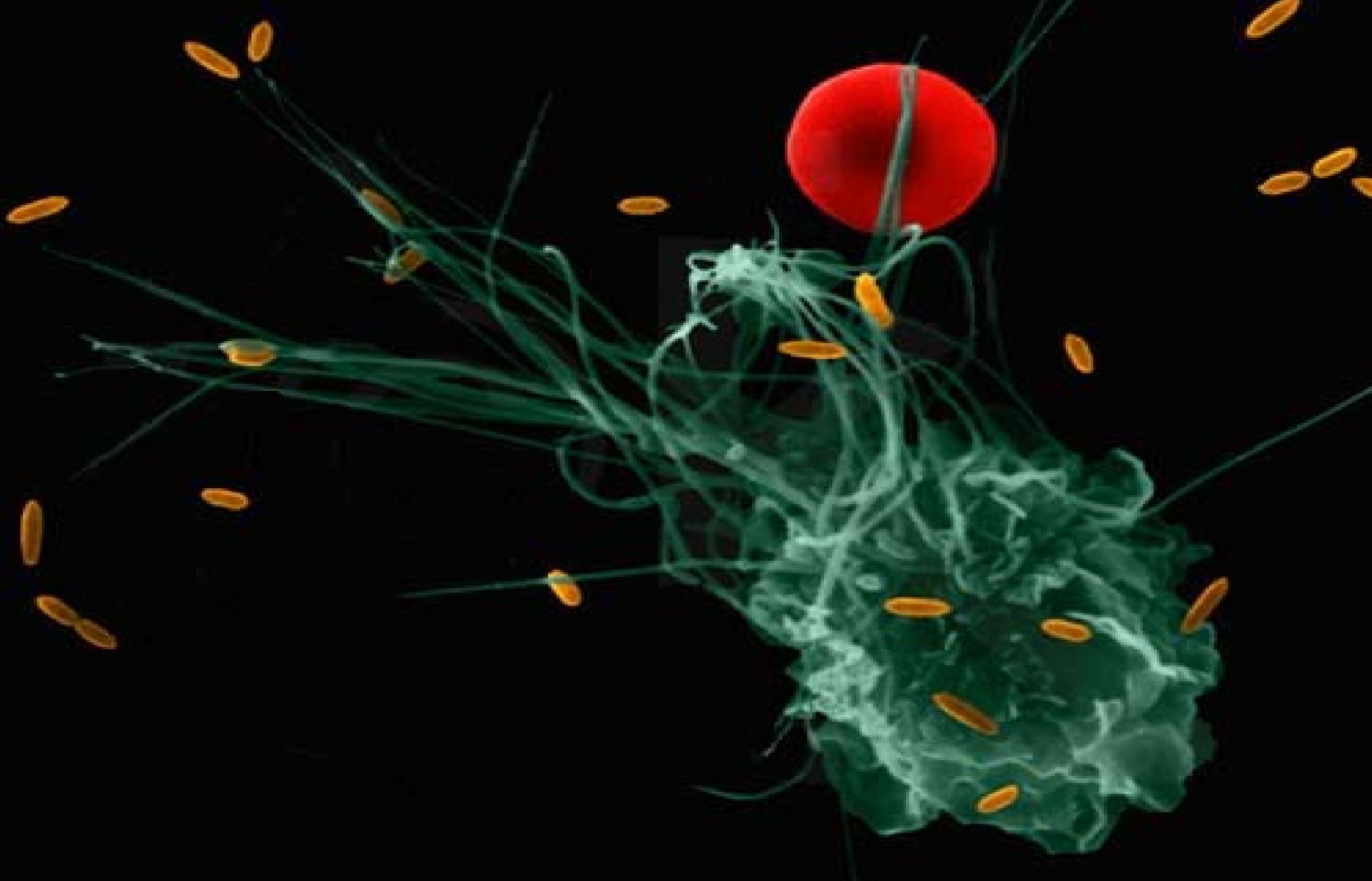
Polymorphisms of Toll Like Receptors and Variability of Innate Immunity

Institute of Cellular Pathology
February 16, 2005

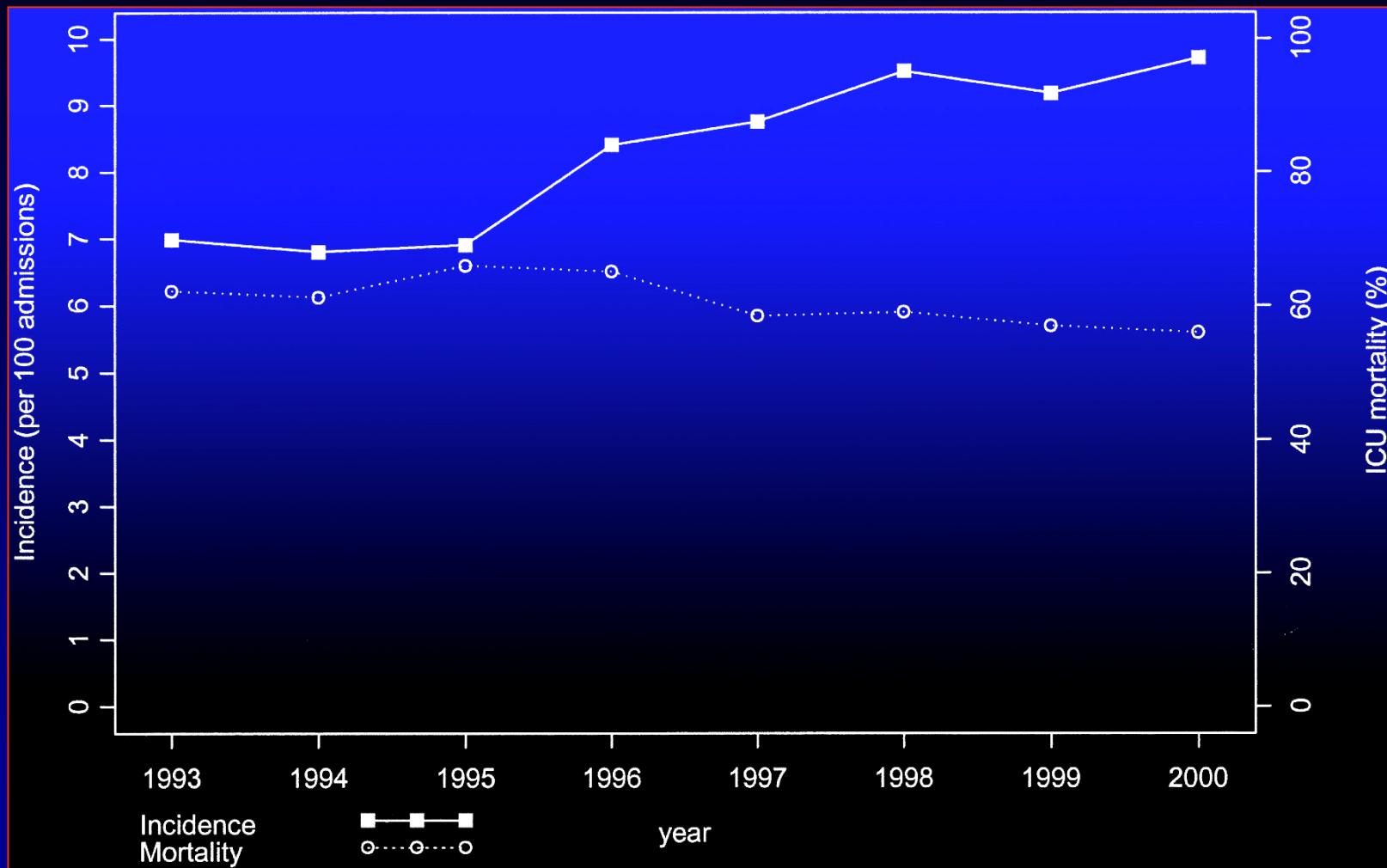
Pr. Jean-Paul MIRA

Medical ICU & Dept. of Cell Biology

Cochin University Hospital & Cochin Institute, Paris, F



Septic Shock Epidemiology



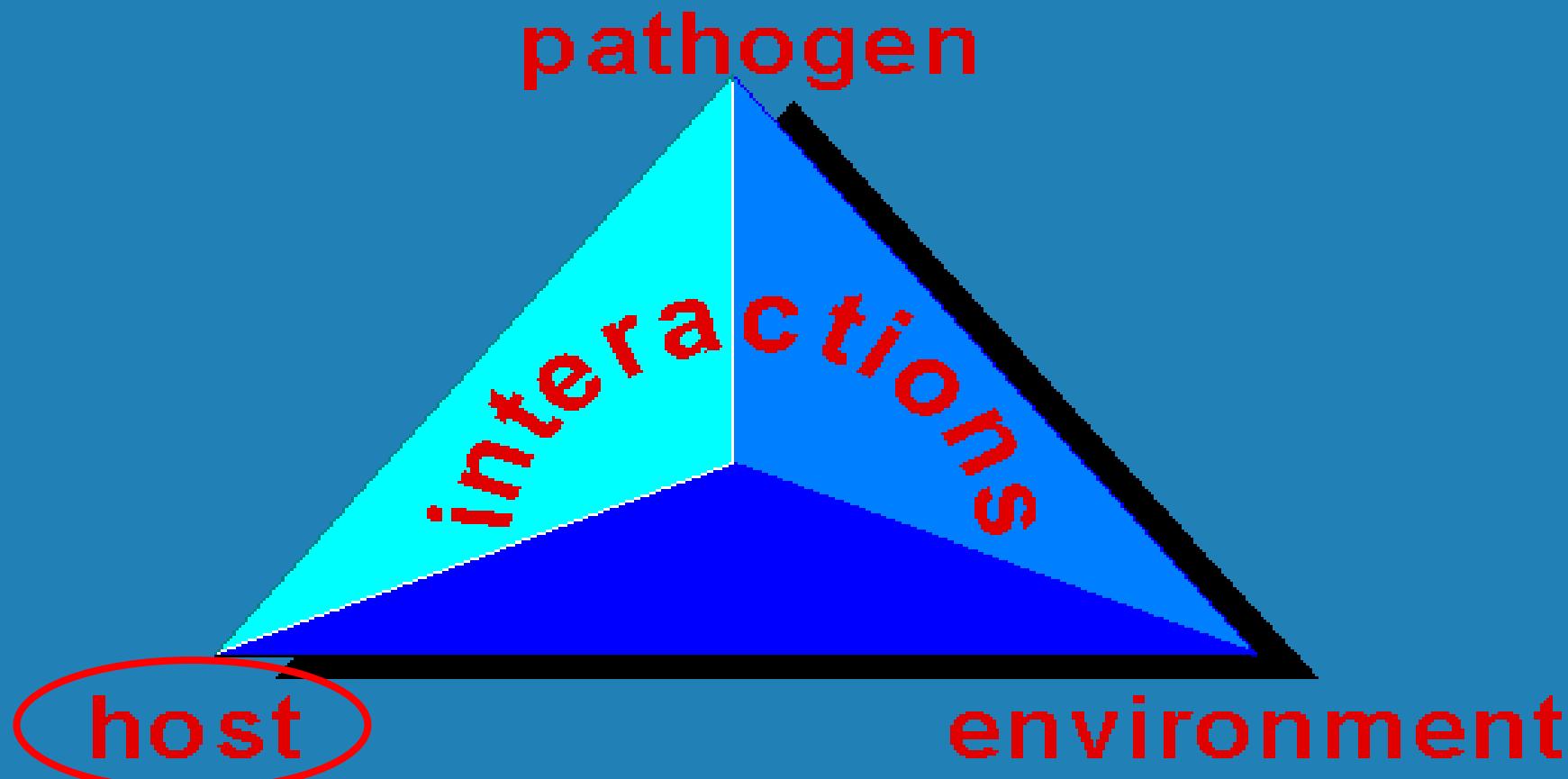
Variability of Severe Sepsis Phenotype



**MIEUX COMPRENDRE
POUR MIEUX GUERIR**

Disease Triangle

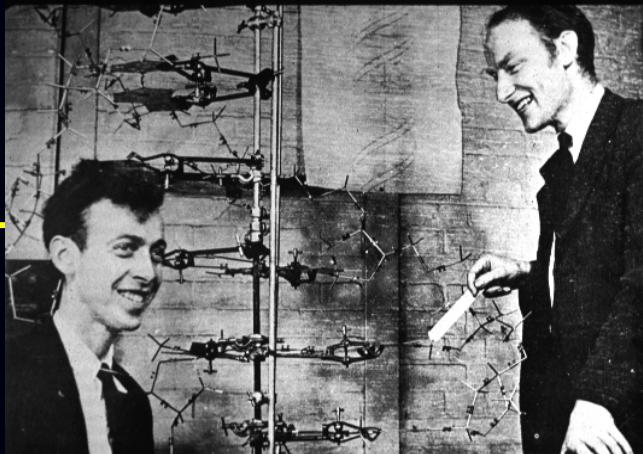
$P(\text{illness}) = f(\text{host, pathogen, environment, interactions})$





« 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-

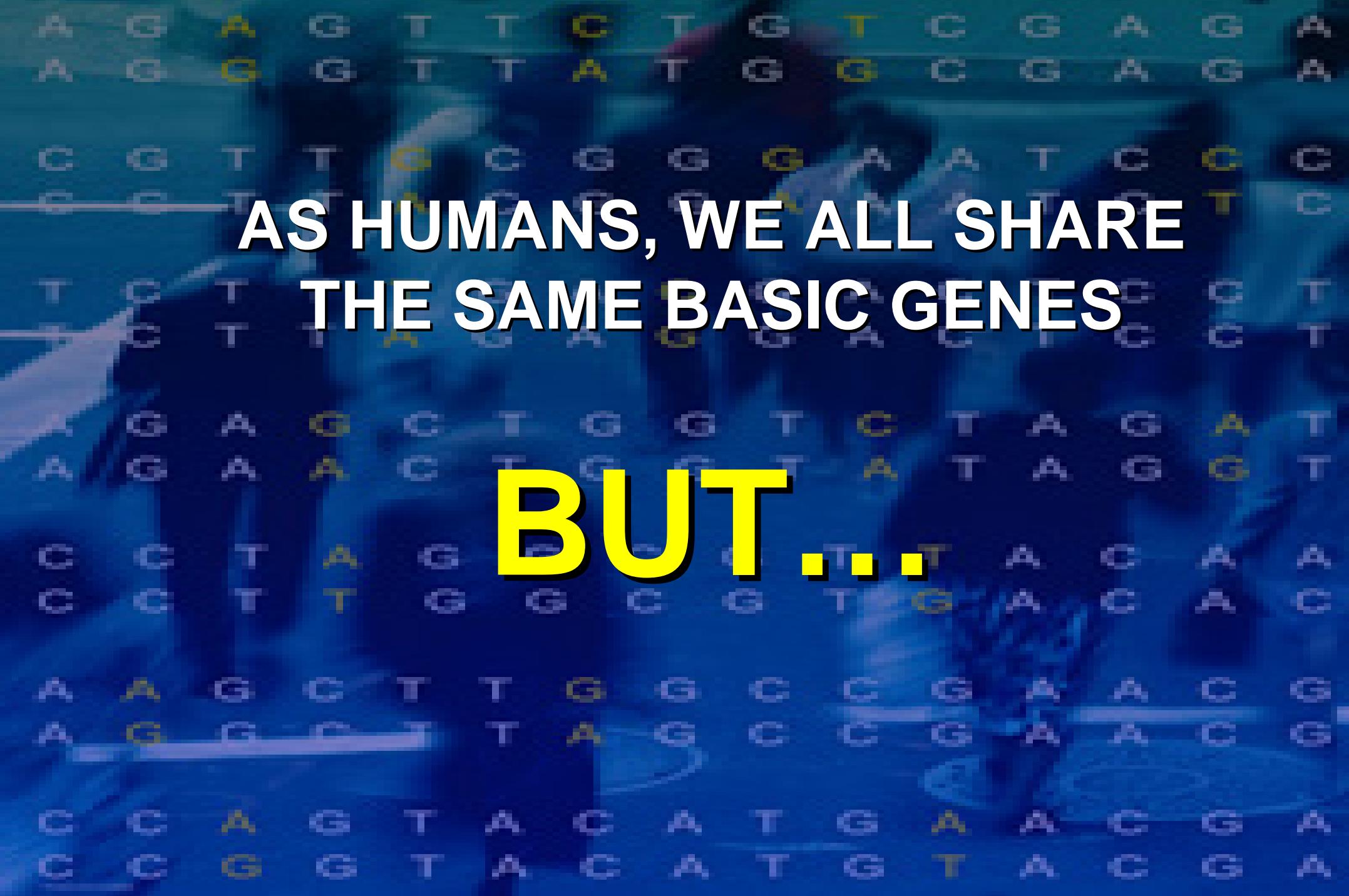


2001-2003



« 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



AS HUMANS, WE ALL SHARE
THE SAME BASIC GENES

BUT . . .



**Very small differences in genotype make beautiful
differences in phenotype...**



Small differences in genotype make big differences to phenotype



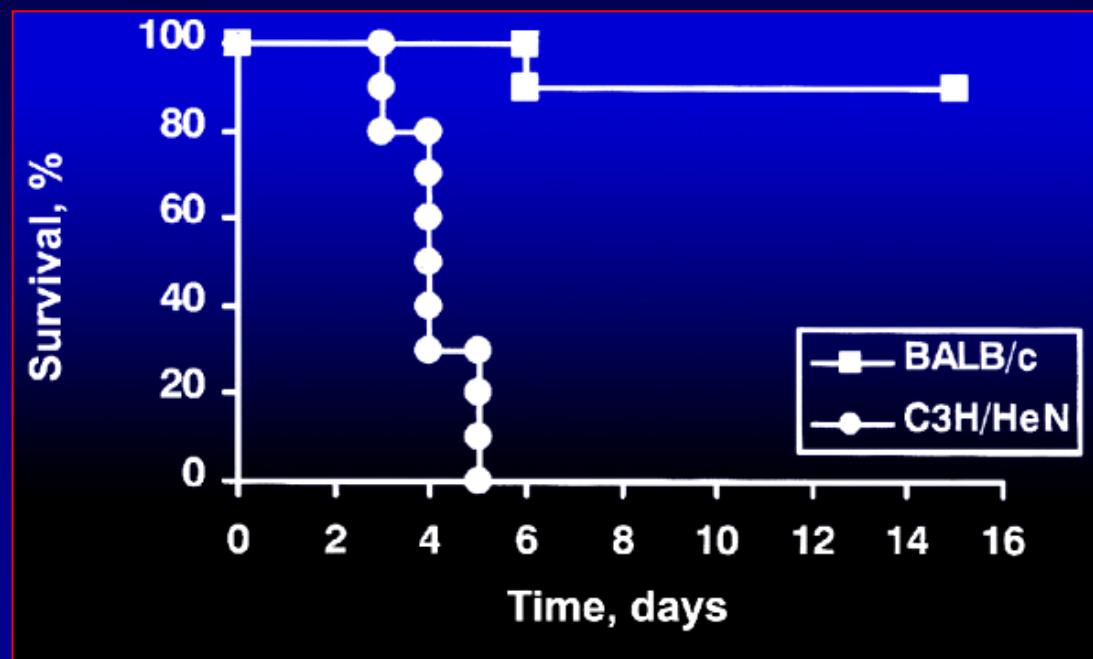
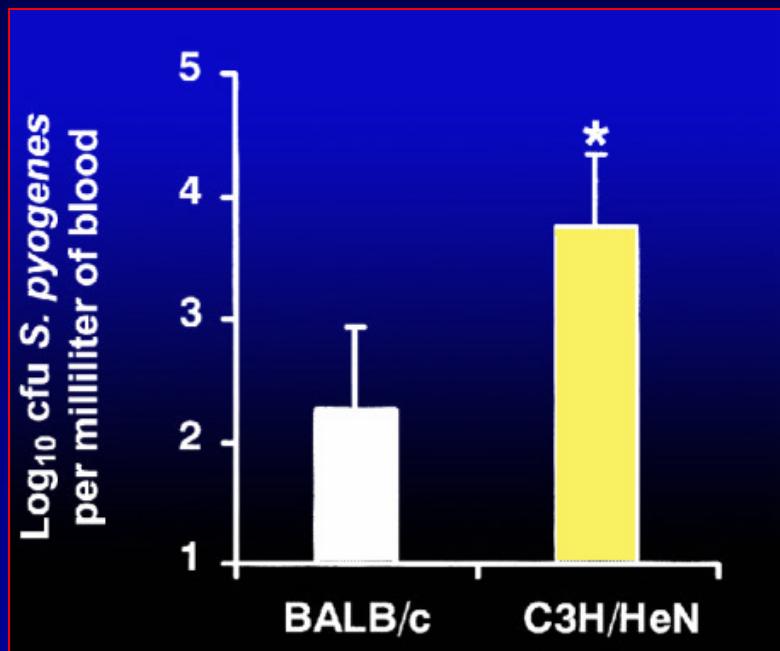
Evidences for a genetic component to sepsis

Animal Studies

- Susceptibility/resistance to certain infection in mice

Mice Susceptibility to Infection with Group A Streptococci

10^3 cfu *Strepto* Subcutaneous



d2

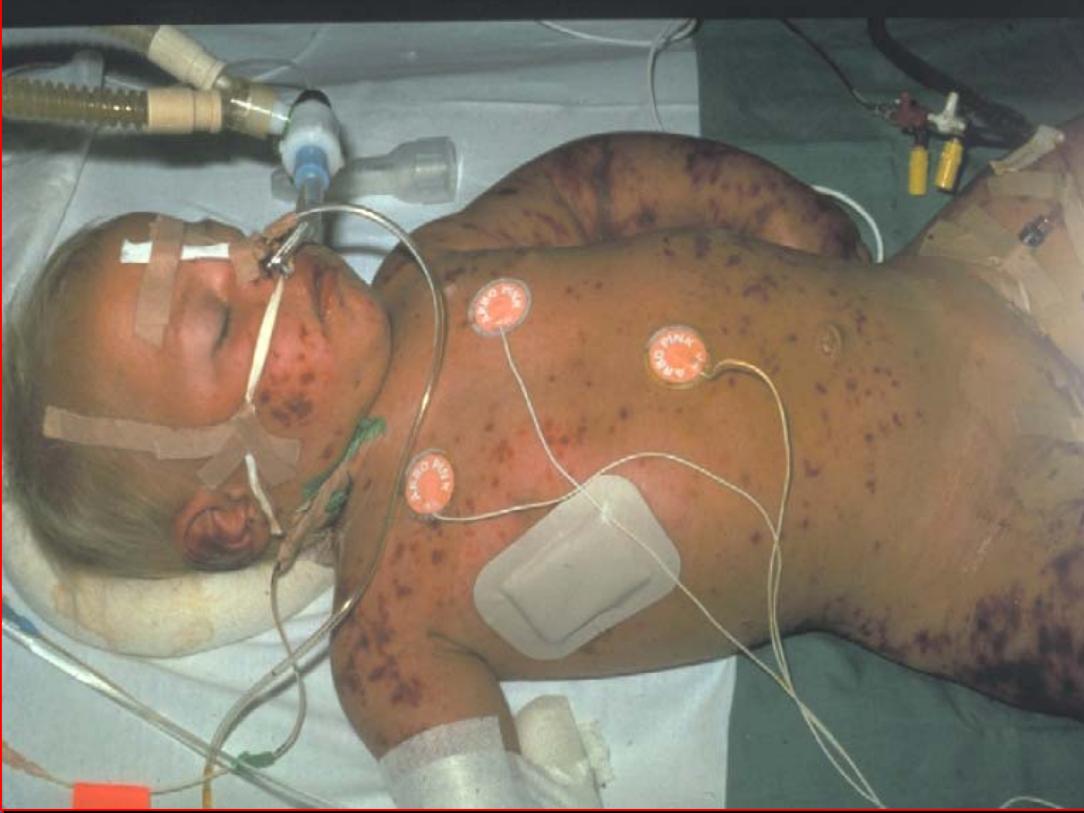
Evidences for a genetic component to sepsis

Animal Studies

- Susceptibility/resistance to certain infection in mice

Human Studies

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



Genetic and environmental influences on premature death in adult adoptees

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

STUDY NATURE AND OBJECTIVES

Large, observational
(characterizing genetic risk
and clinical usefulness)

Small, highly manipulated
(enhancing understanding of the
biology of disease mechanisms)

STUDY METHODS

Population based associations

Genetic association with
clinical outcomes

Case control cohort
comparisons

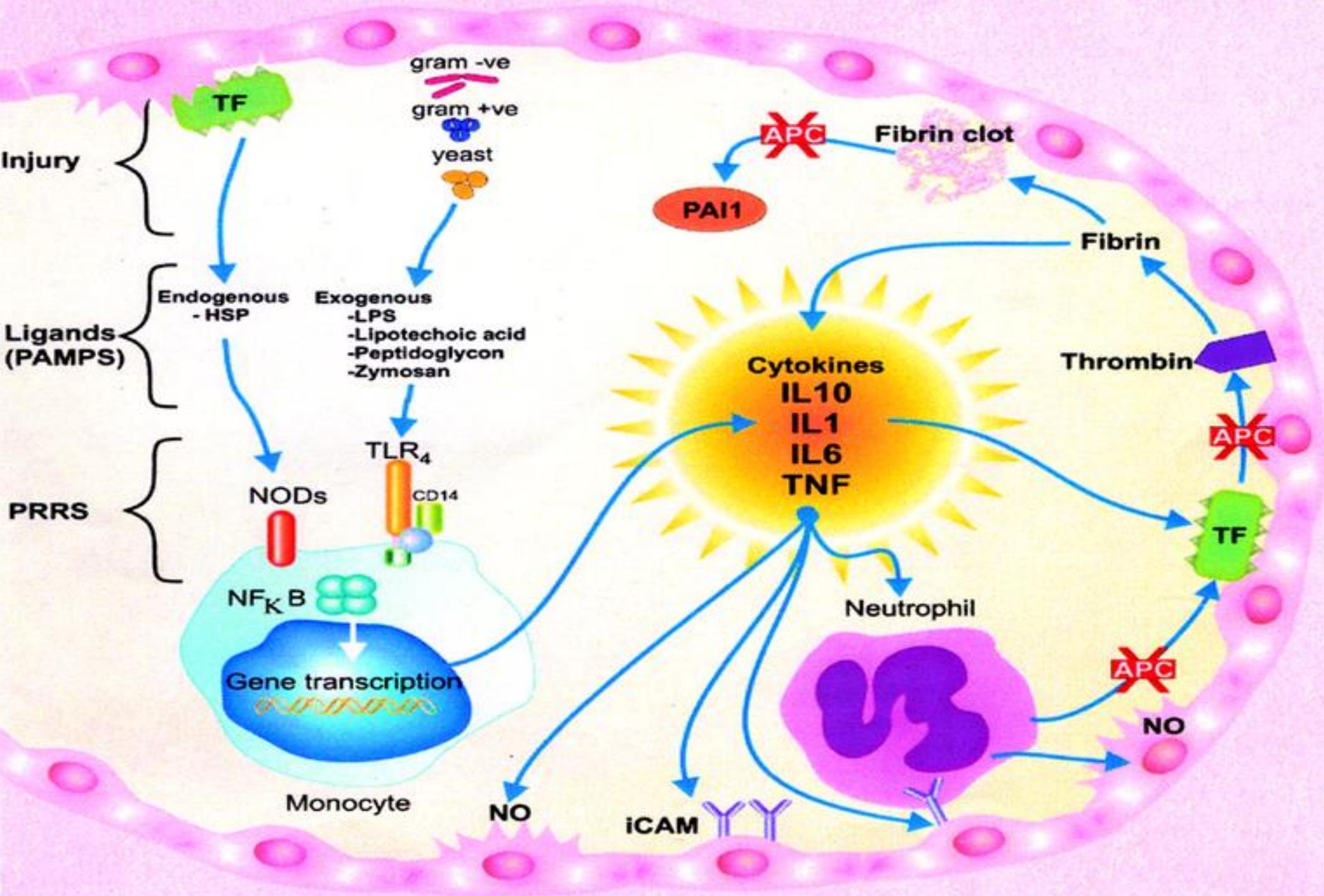
Familial studies

In vivo physiologic responses

In vitro responsiveness

In vitro transfection

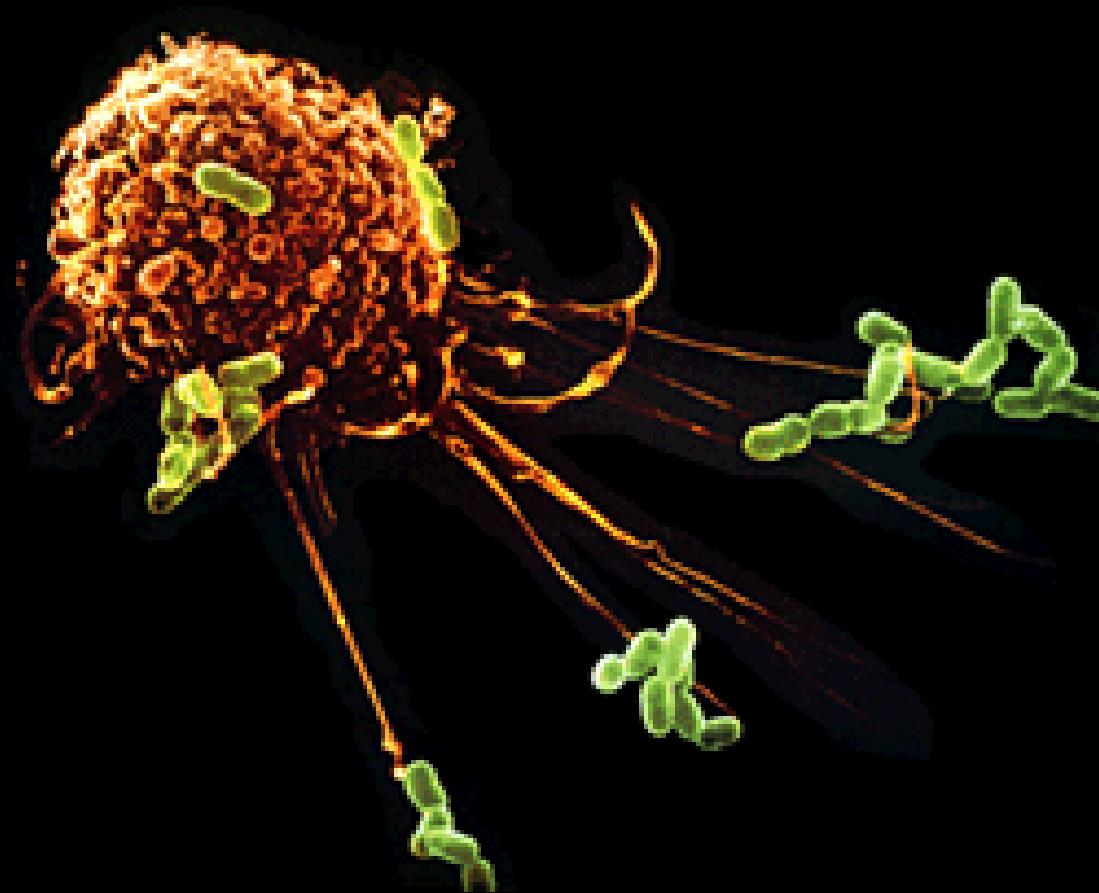
Knockout models

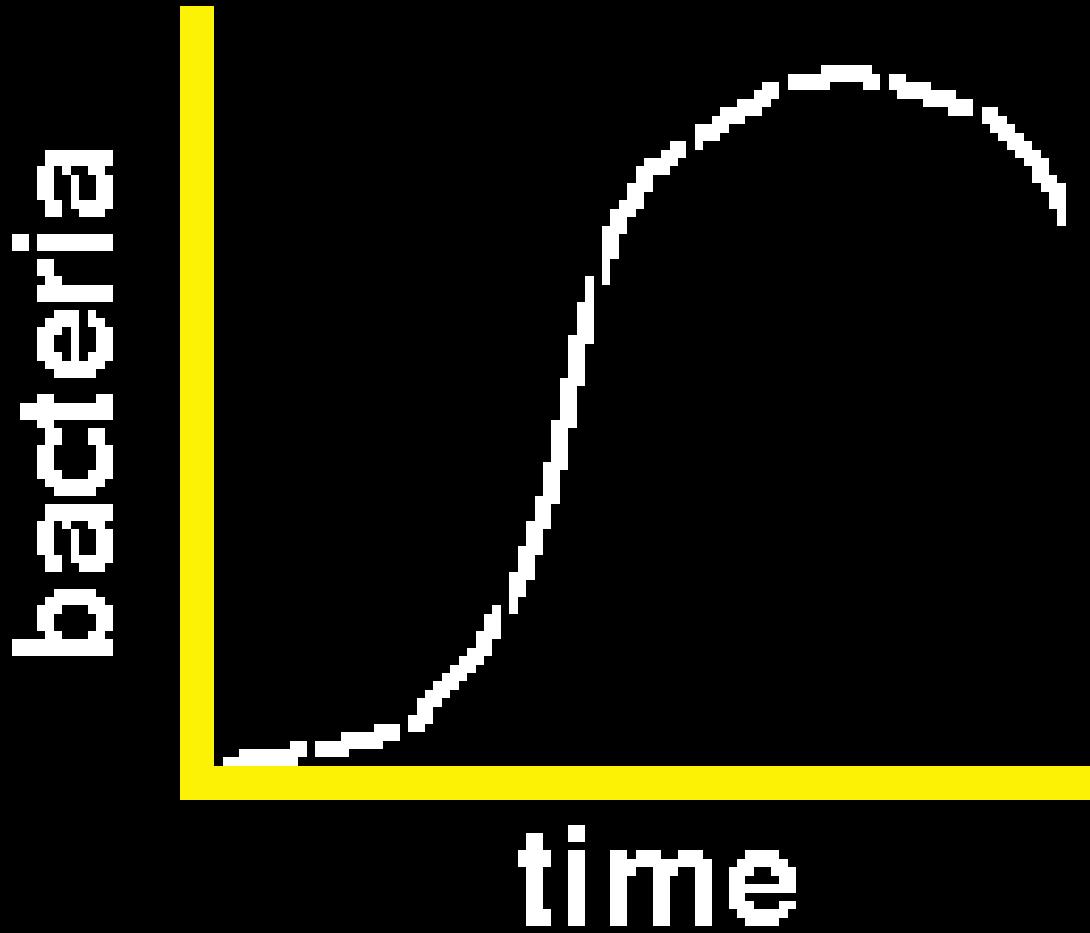


Genetic Polymorphisms and Severe Sepsis

Gene	Susceptibility and/or Outcome
Mannose Binding Lectin	Meningococcemia, Pneumococcemia Severe sepsis
Toll-Like Receptor 4/2	Gram negative/positive Septic Shock
Toll-Like Receptor 5	Legionnaire's Disease
CD14	Septic Shock
FC γ RII Receptor	Meningococcemia; Pneumococcemia
TNF locus	Meningococcemia; Septic Shock; Malaria
IL-18	Severe Sepsis
IL-10	Severe Sepsis, Meningococcemia
IL-6	Severe sepsis
IL-1 locus	Severe Sepsis
IL-4	Viral Pneumonia
Caspase12	Septic shock
PAI-1	Meningococcemia; Severe sepsis
Factor V Leiden	Meningococcemia; Severe sepsis

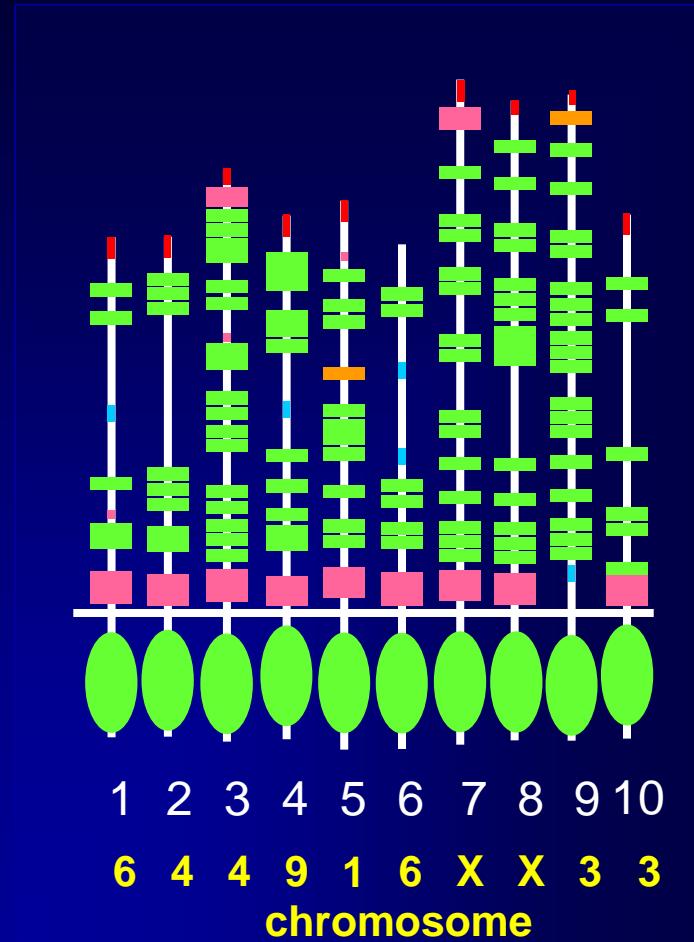
Pathogen Detection



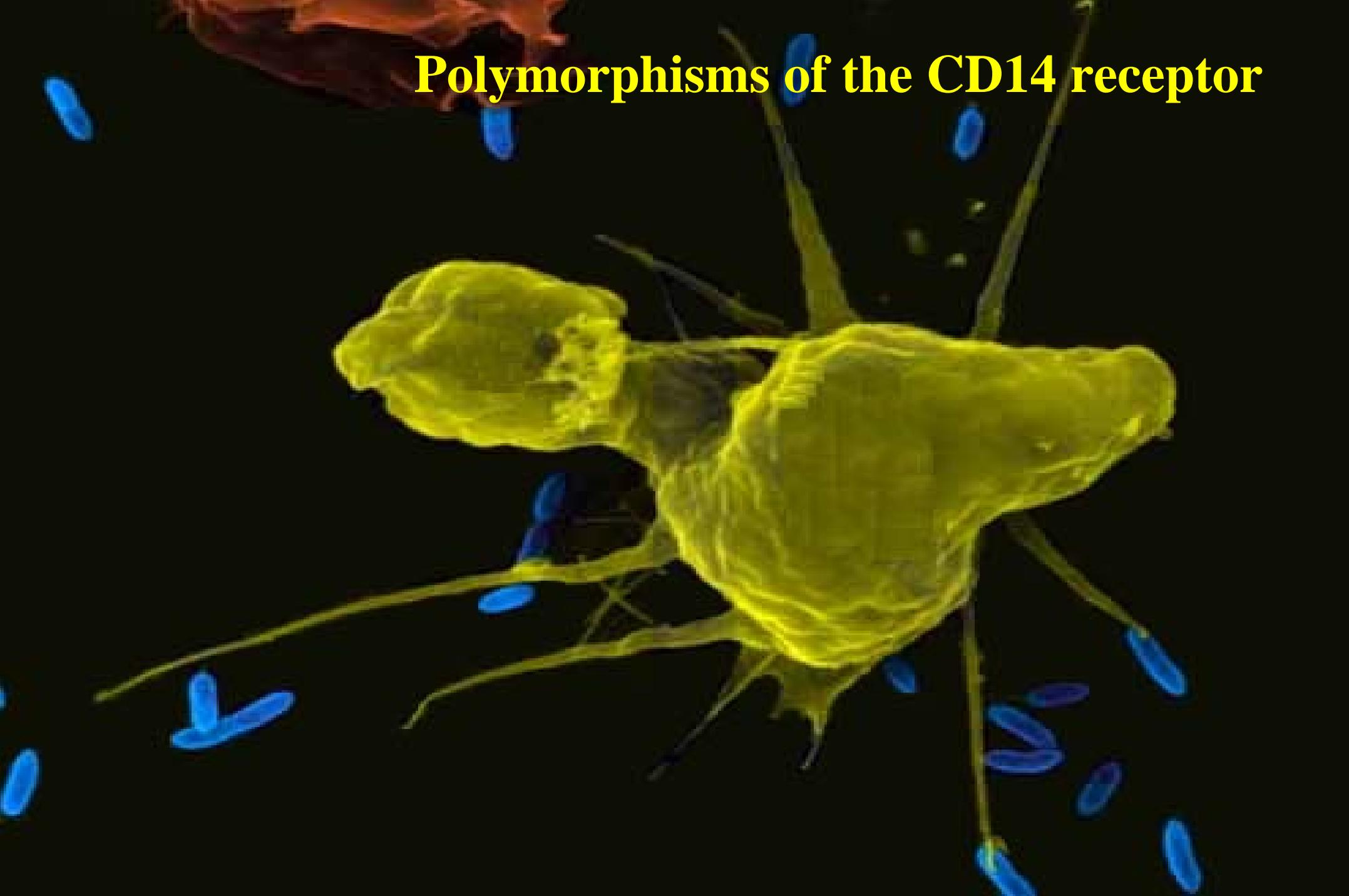


Human Toll-like Receptors

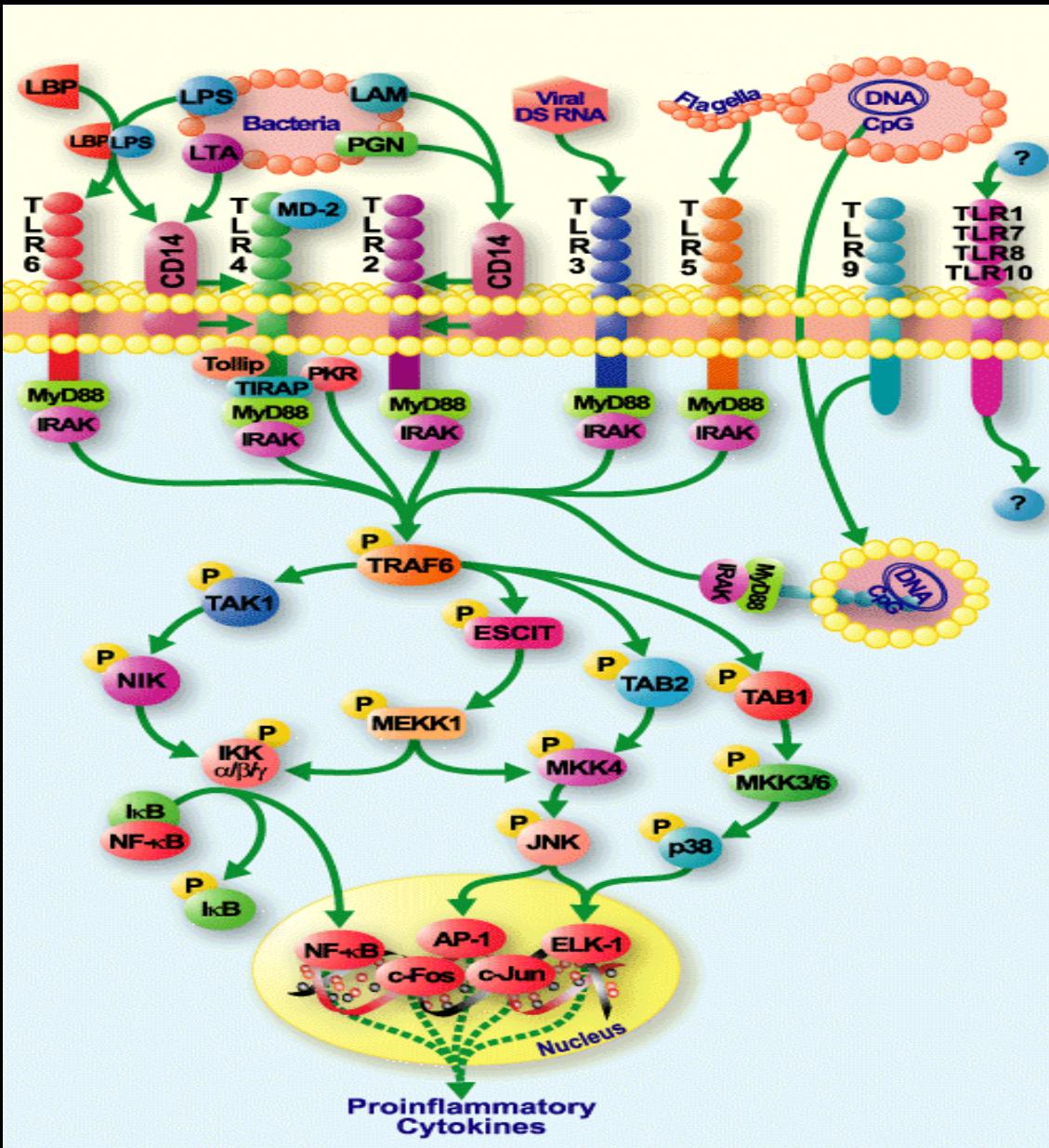
- 10 Receptors (TLR1 – TLR10)
- Specific pathogen detection
- Mediate the innate immune response
- Induce the inflammatory reaction (NF-κB)
- Induce the adaptative immune response
- Resolution of the inflammation (apoptosis)

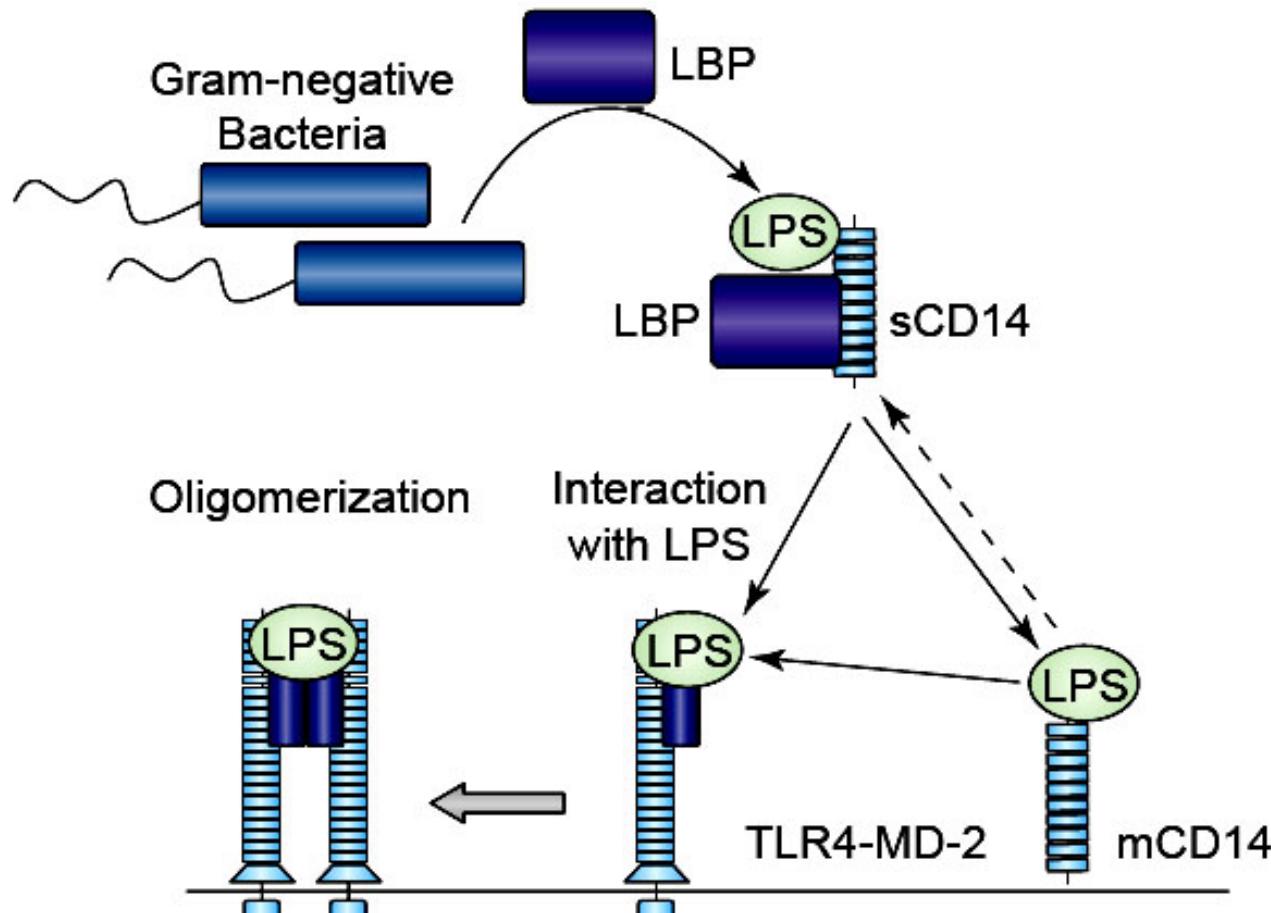


Polymorphisms of the CD14 receptor



CD14 receptor and TLRs

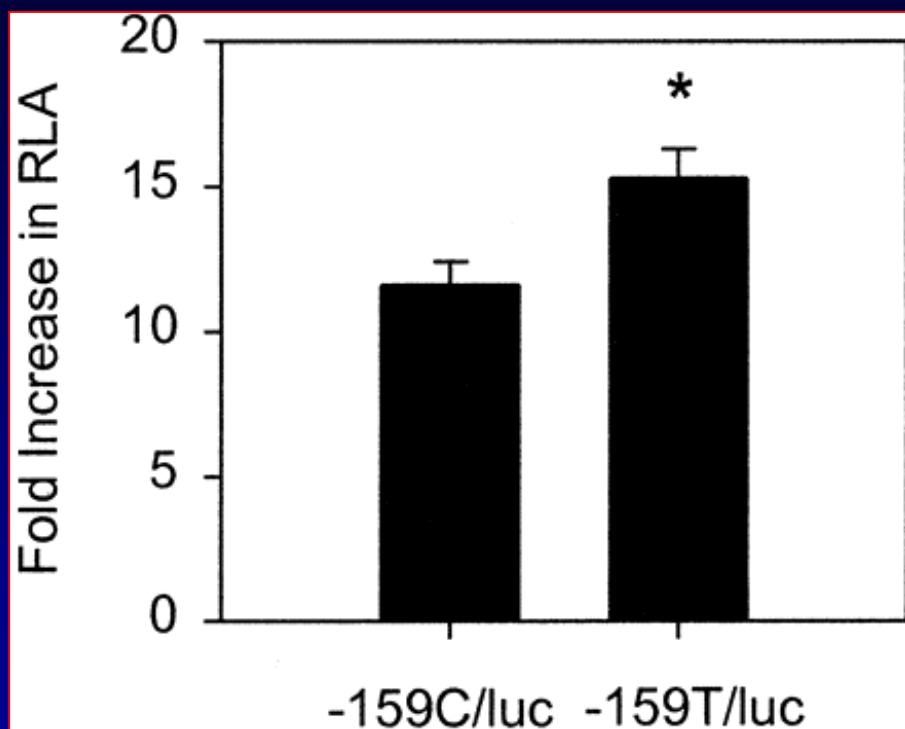




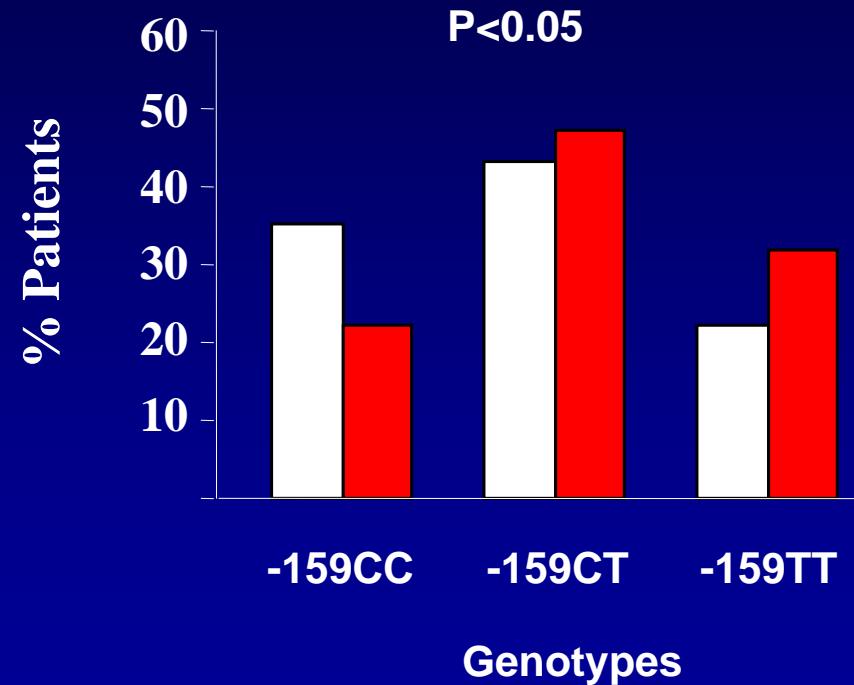
Immediate defense responses
Activating acquired immunity

CD14/159T and Susceptibility to Septic Shock

CD14/159T increases sCD14 and mCD14 levels



■ Control
■ Septic Shock



CD14/159T and Mortality to Septic Shock

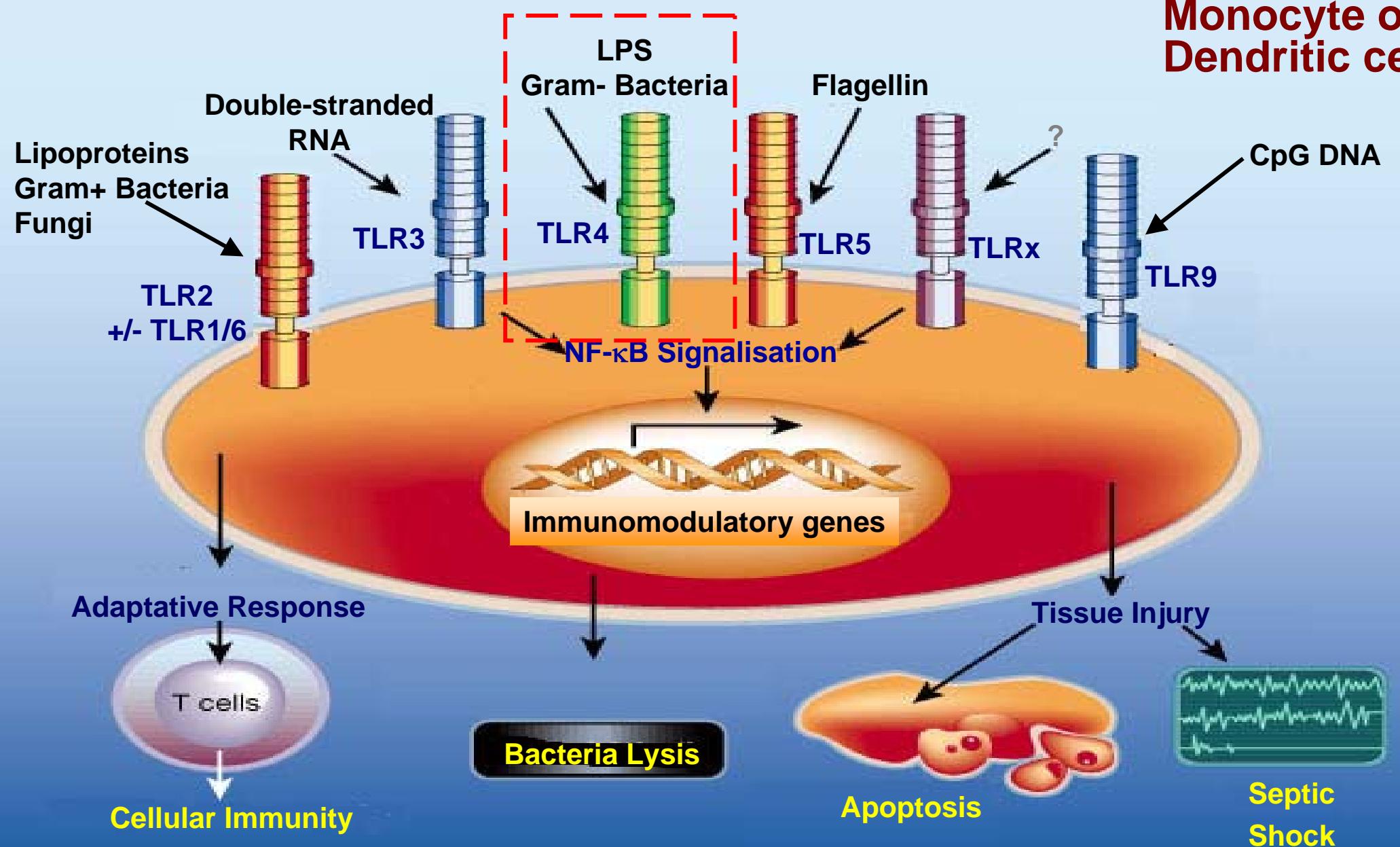
Characteristics	C/C N=19	C/T N=43	T/T N=28	p
Age (mean±SD)	53±15	59±13	59±17	.18
SAPSII (mean±SD)	53±18	56±21	60±19	.21
OSF (mean±SD)	3±1.2	2.8±0.9	3.1±1	.42

CD14/159T and Mortality to Septic Shock

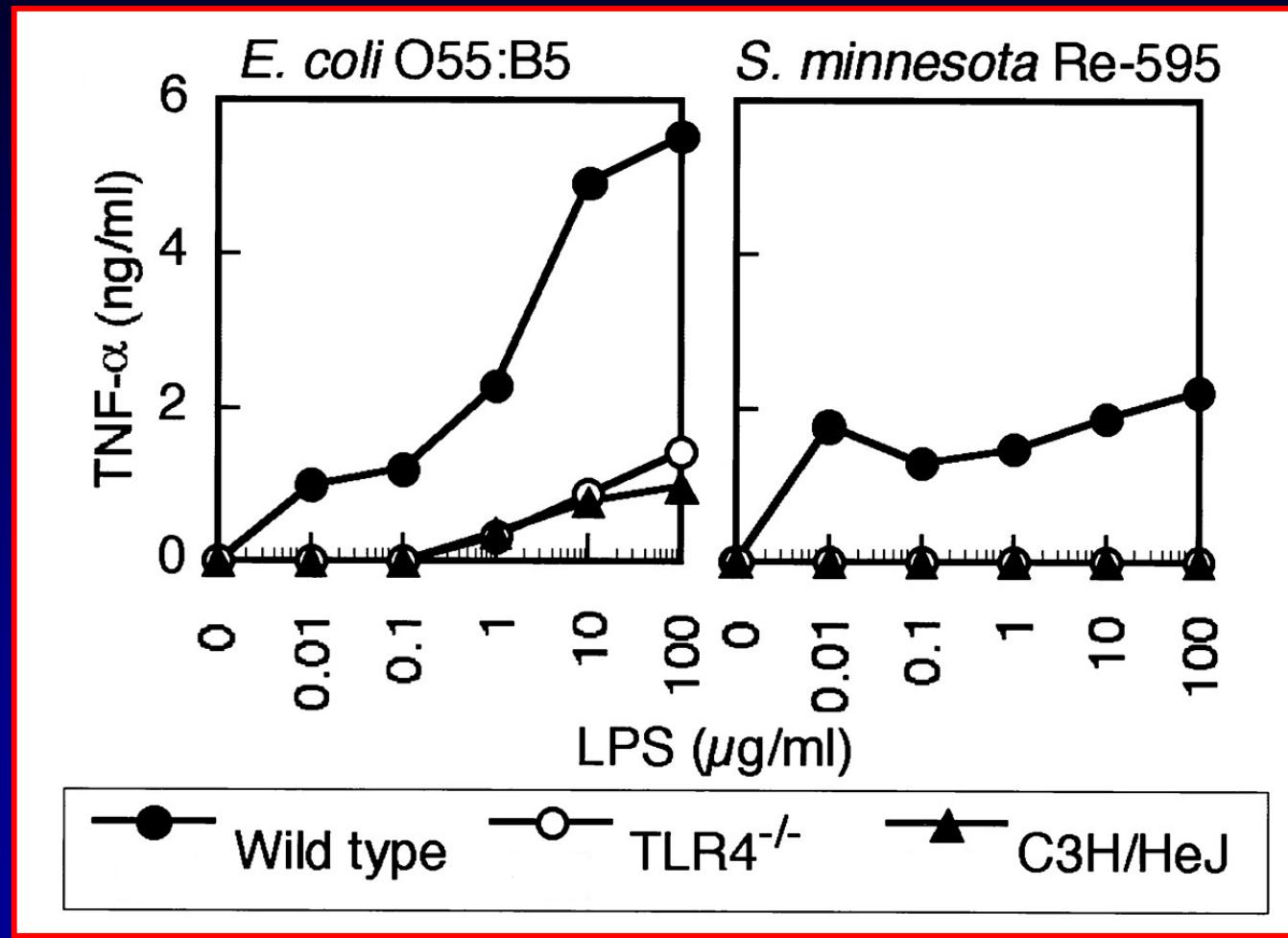
Characteristics	C/C N=19	C/T N=43	T/T N=28	p
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SAPSII (mean±SD)	53±18	56±21	60±19	.21
OSF (mean±SD)	3±1.2	2.8±0.9	3.1±1	.42
Mortality (%)	26.3	58.1	71.4	<.0001

CD14/159TT RR= 5.1; 95%CI [3.2-7.9]

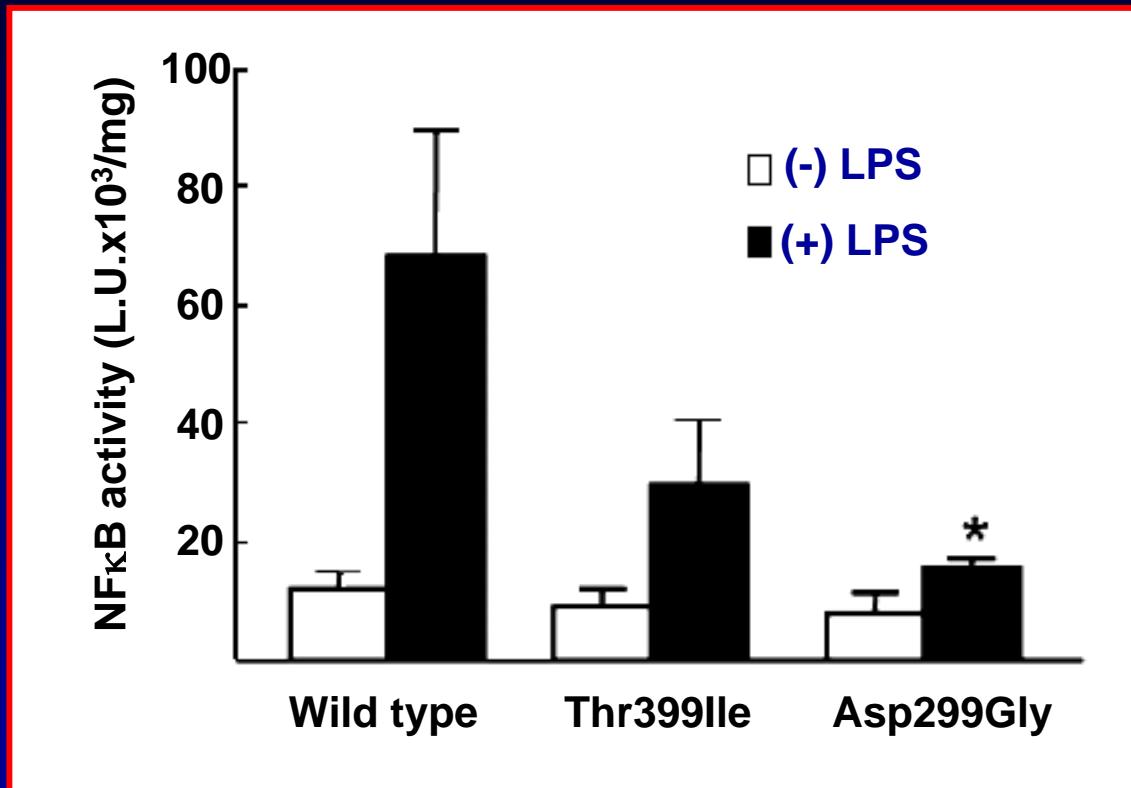
Monocyte or Dendritic cell



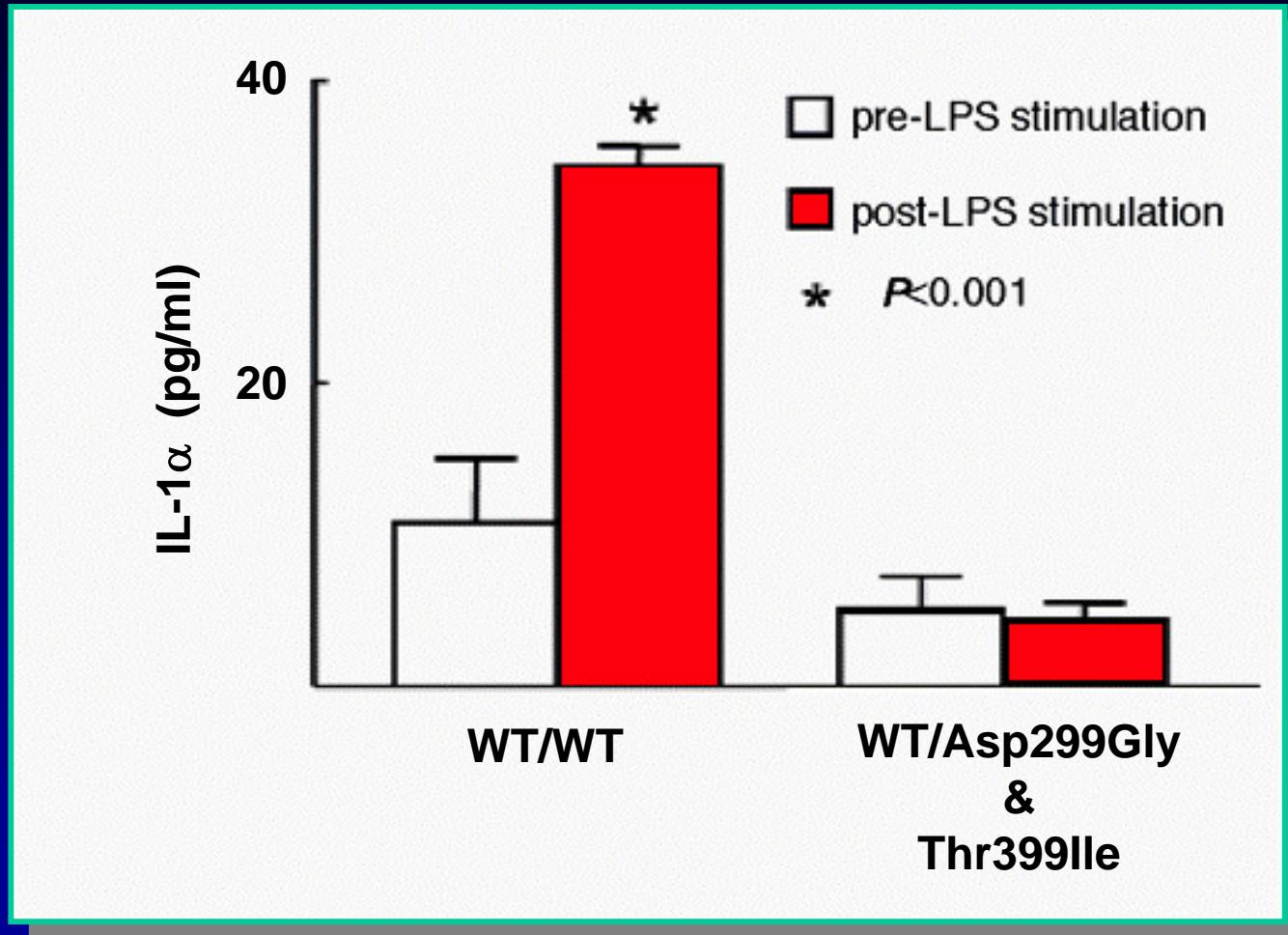
Impaired LPS responsiveness in TLR4^{-/-} macrophages



NF- κ B Activity in Transfected THP-1 cells



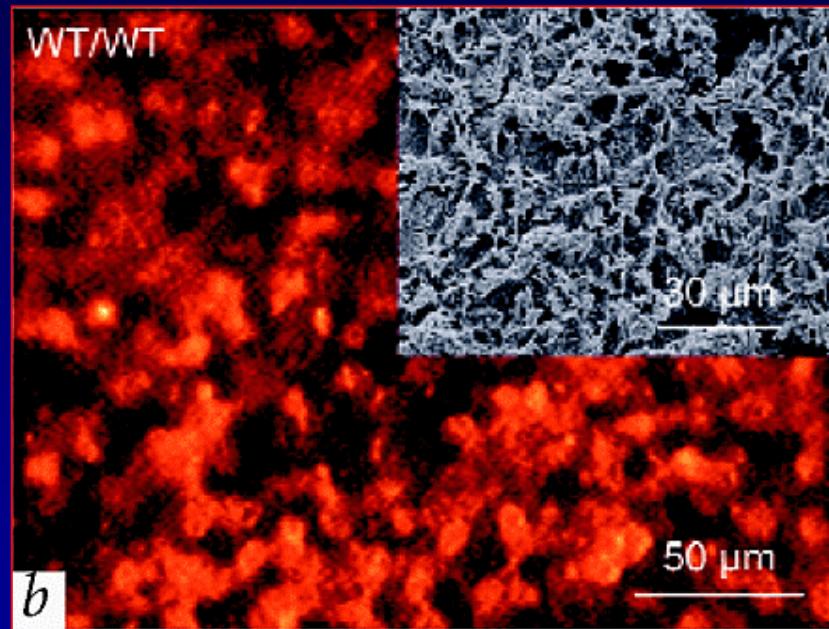
TLR4 mutation and LPS responsiveness



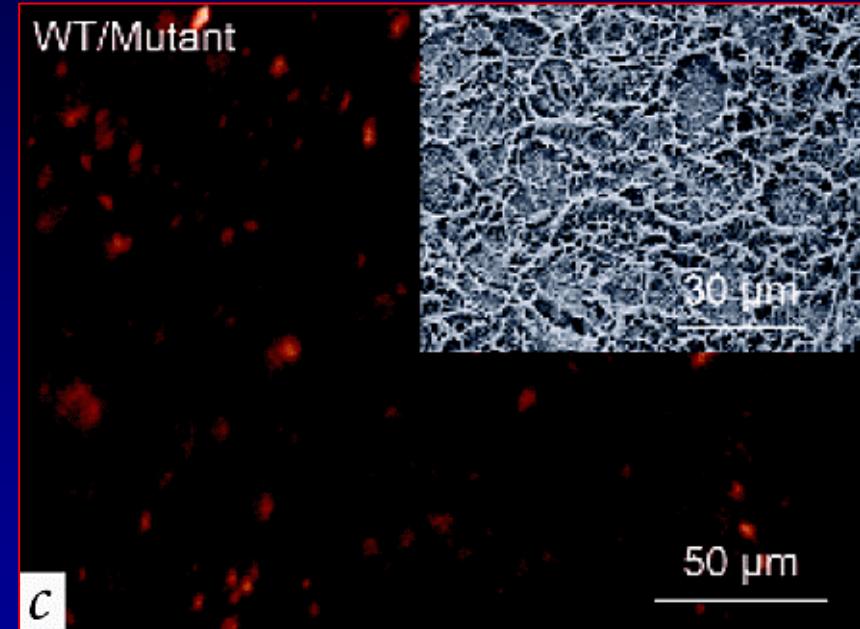
TLR4 Mutant Expression

Human Airway Epithelia

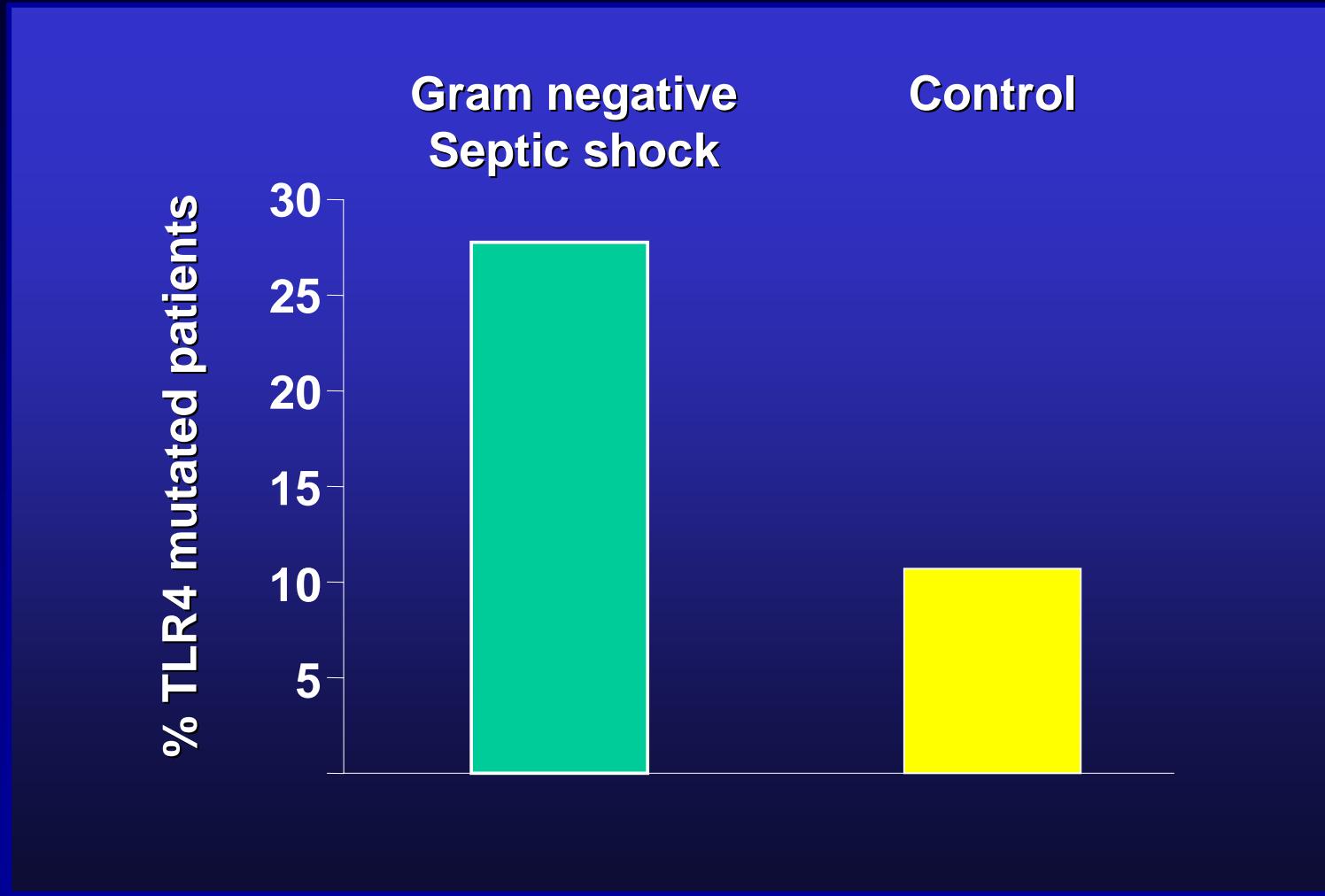
TLR4 WT



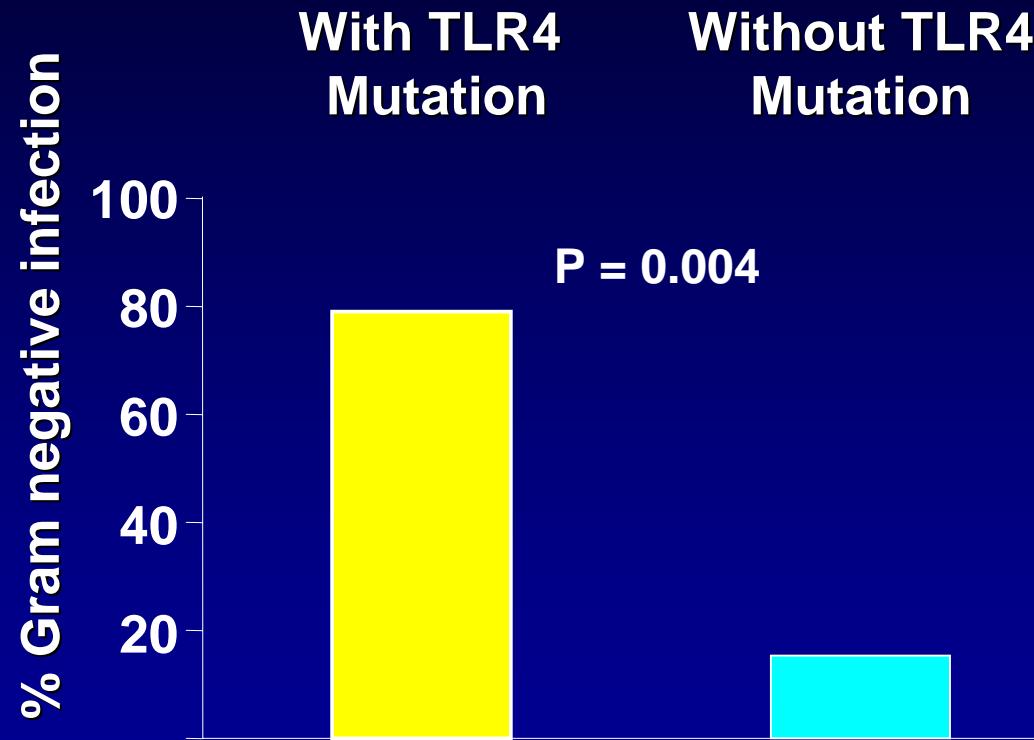
TLR4 WT/299 Gly



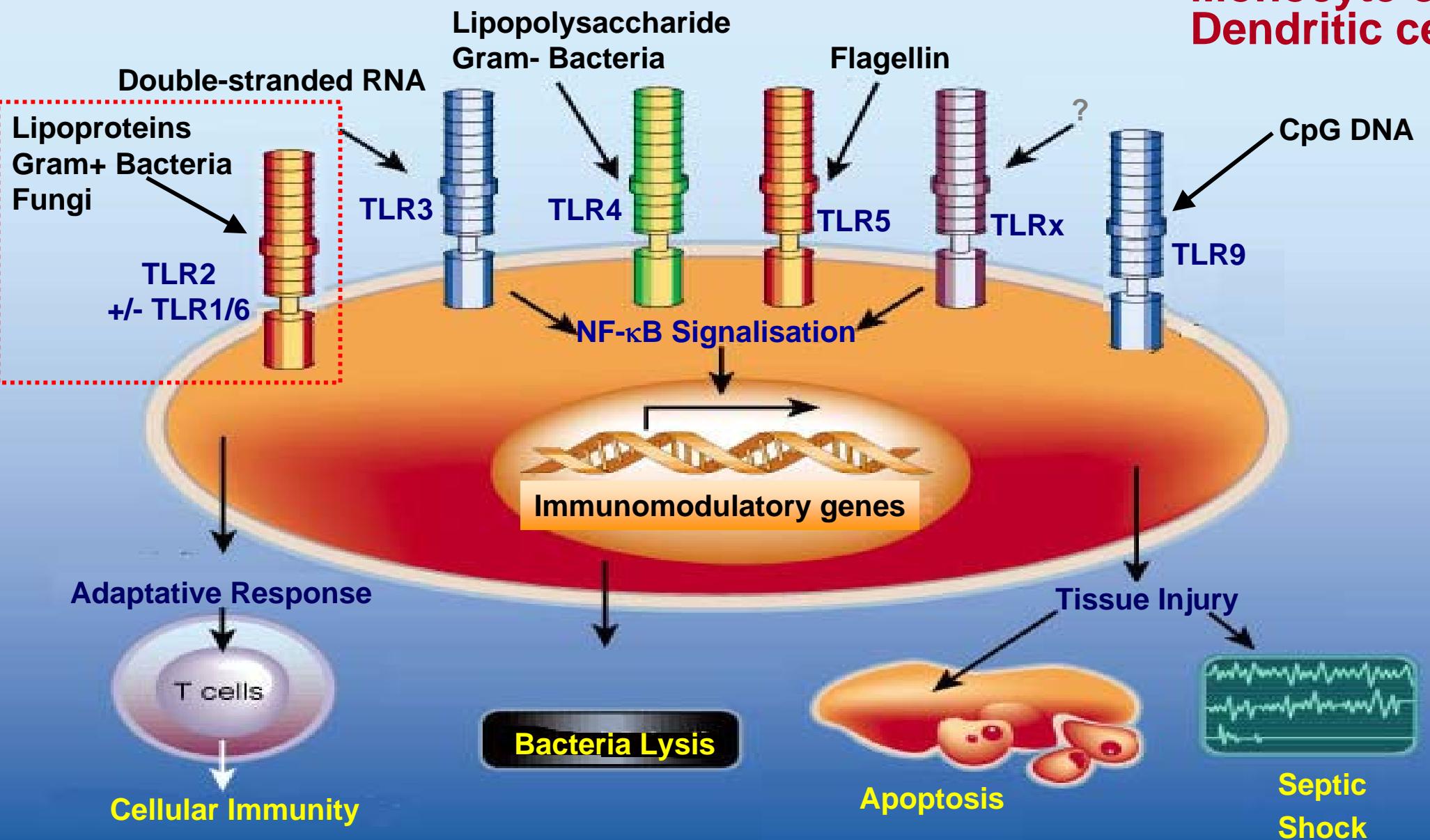
TLR4 Polymorphisms and Septic Shock



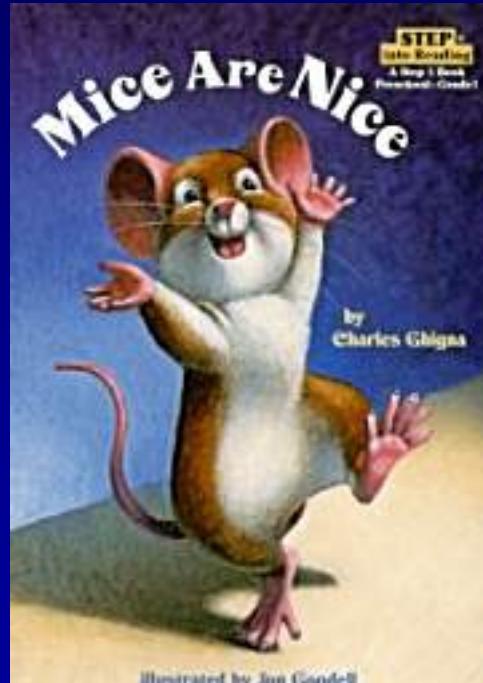
TLR4 Variants and Predisposition to Gram Negative Sepsis



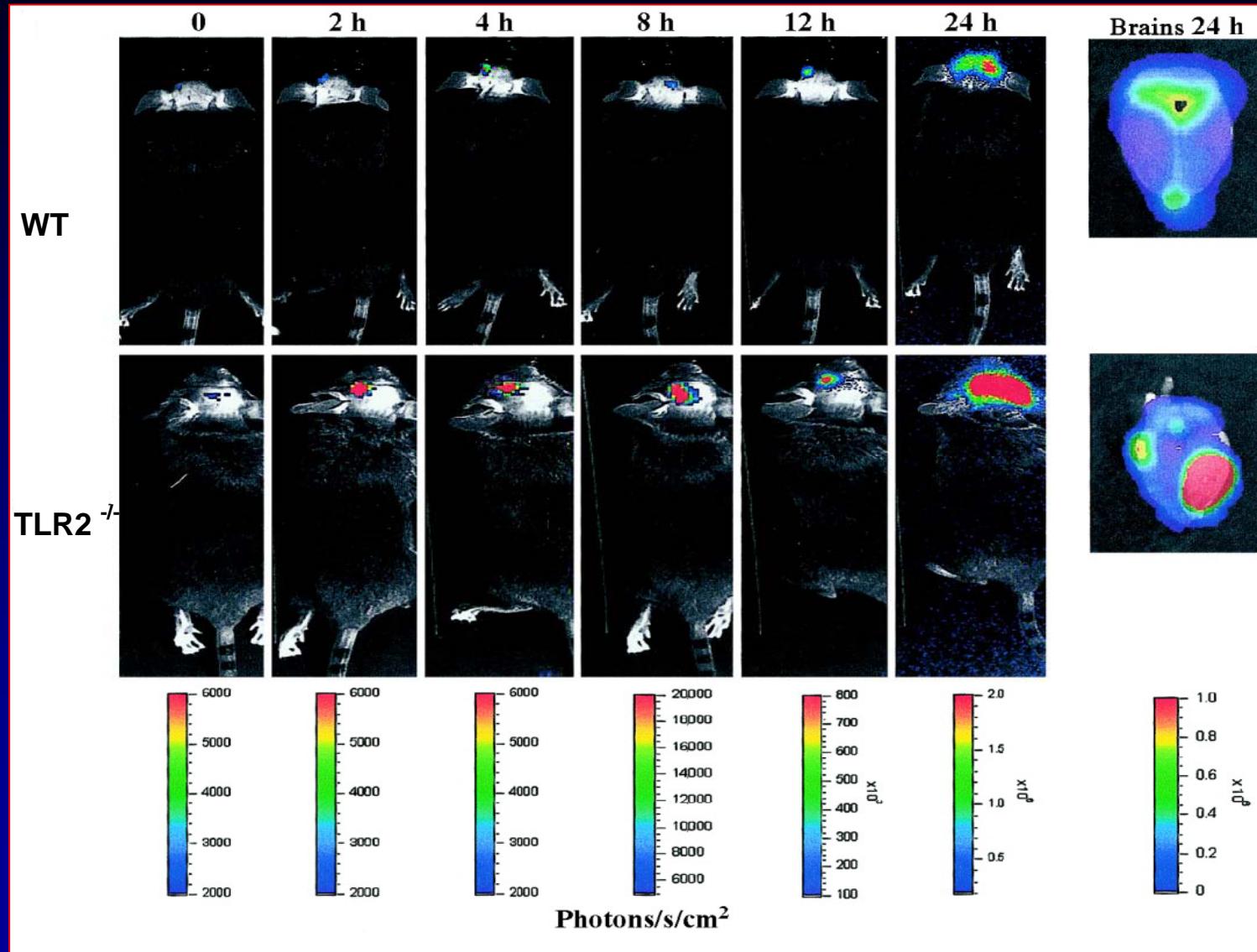
Monocyte or Dendritic cell



TLR2-Knockout Mice

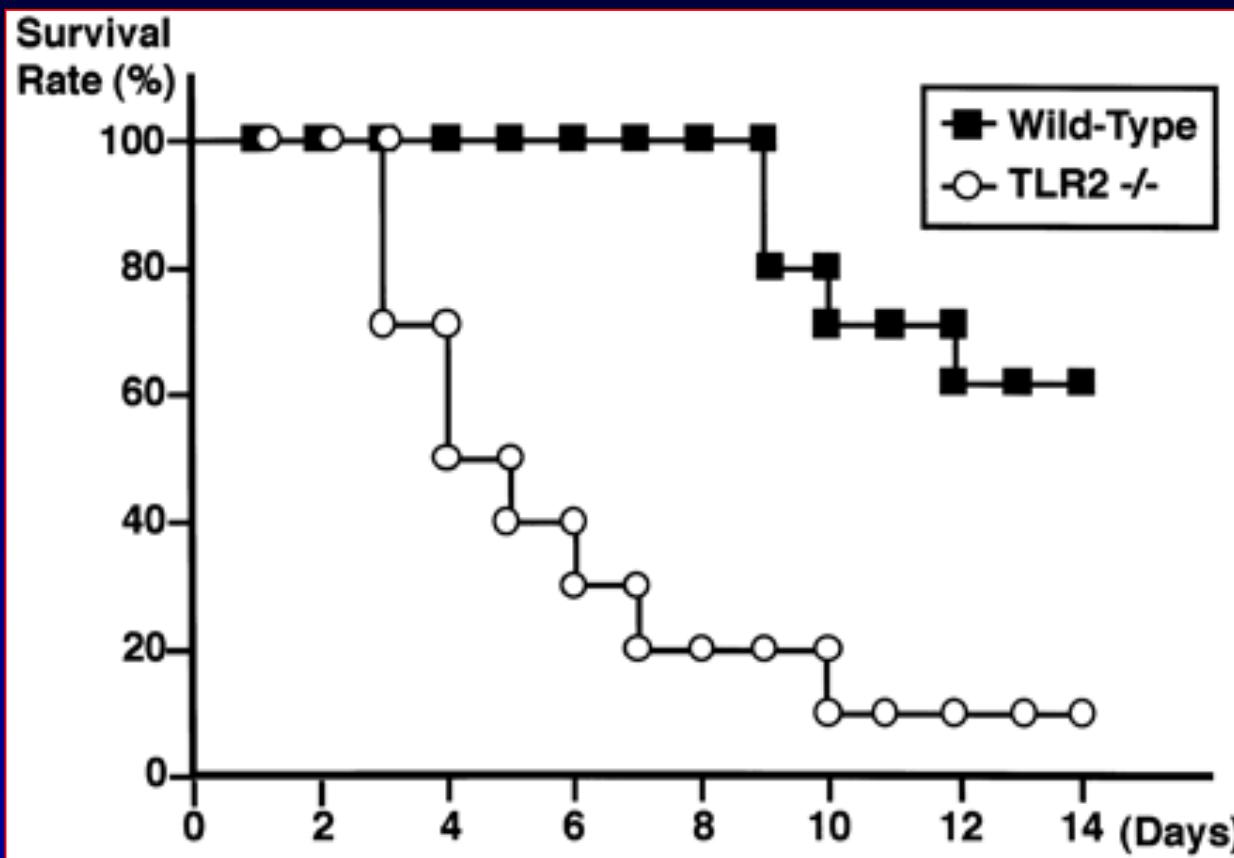


TLR2 and *Streptococcus pneumoniae* meningitis



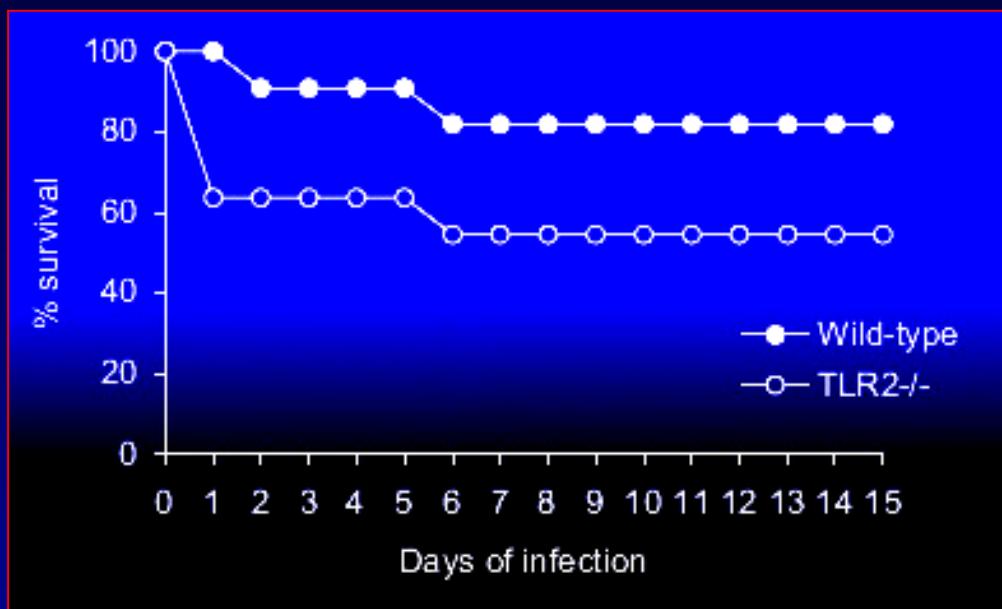
TLR2-deficient mice and Gram positive infections

IV challenge of live *Staphylococcus aureus*

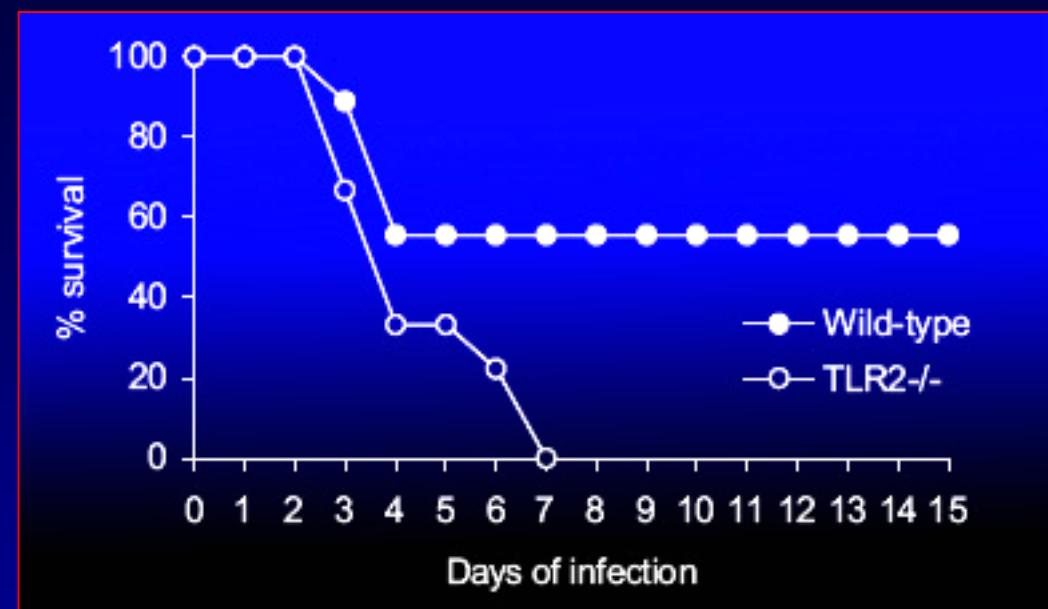


TLR2-deficient mice and Candida Infections

Candida albicans IP 50×10^6

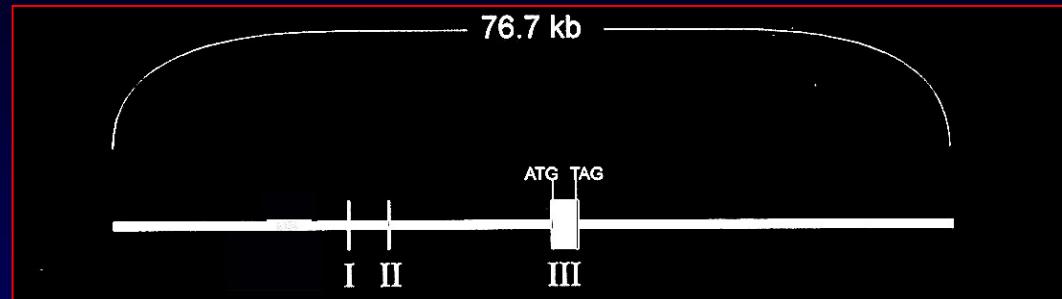


Candida albicans IV 10^6



TLR2 Polymorphisms in Humans

Tlr2 location: Chromosome 4q32



<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi>

<http://innateimmunity.net>

88 SNPs

- 5'UTR: 26 SNPs
- 3'UTR: 17 SNPs
- Intron: 29 SNPs
- Exon: 16 SNPs

Synonymous

Position rs number
35 5743697

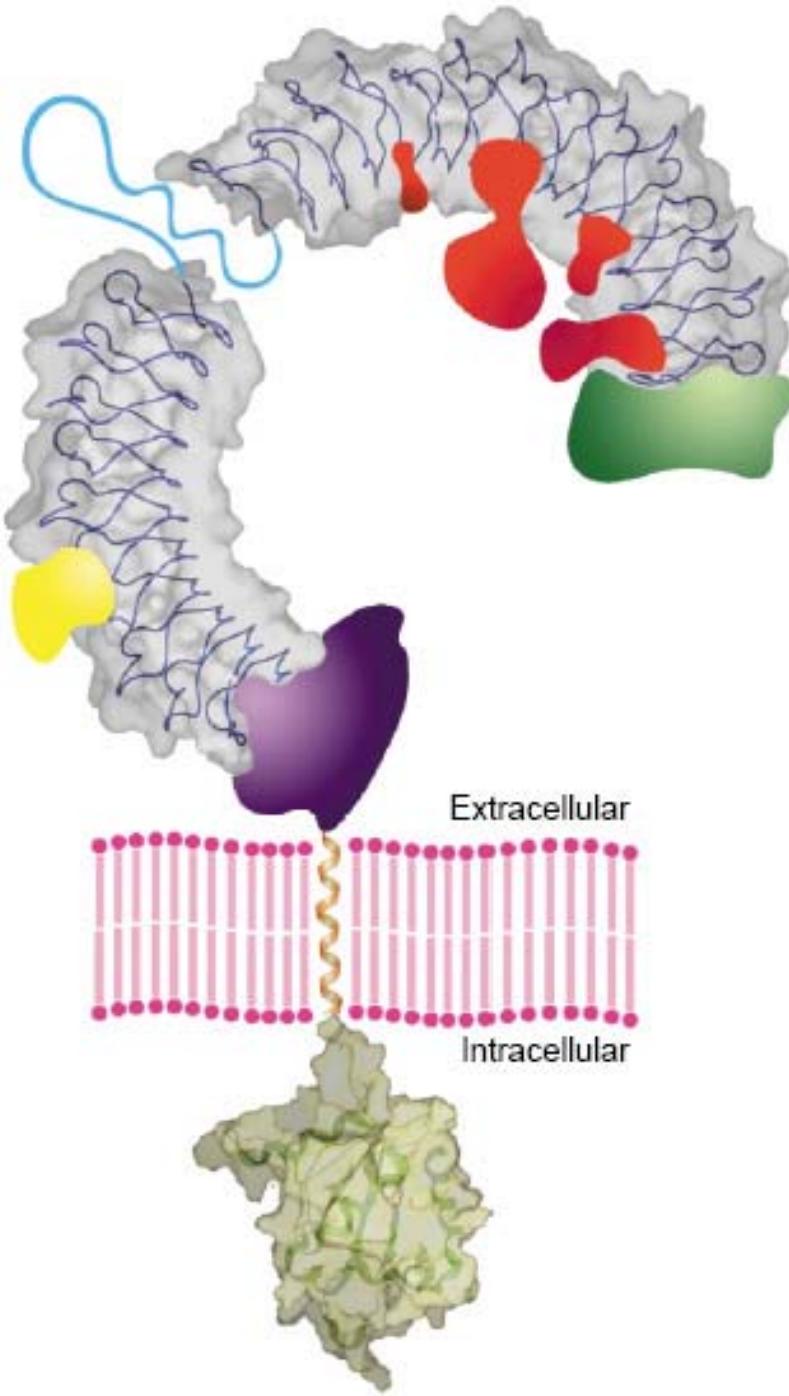
199 3804099
213 5743698

450 3804100

541 5743700
542 5743701

707 IIPGA-TLR2-31410

781 5743709



Non-synonymous

Position rs number

411(T/I) 5743699

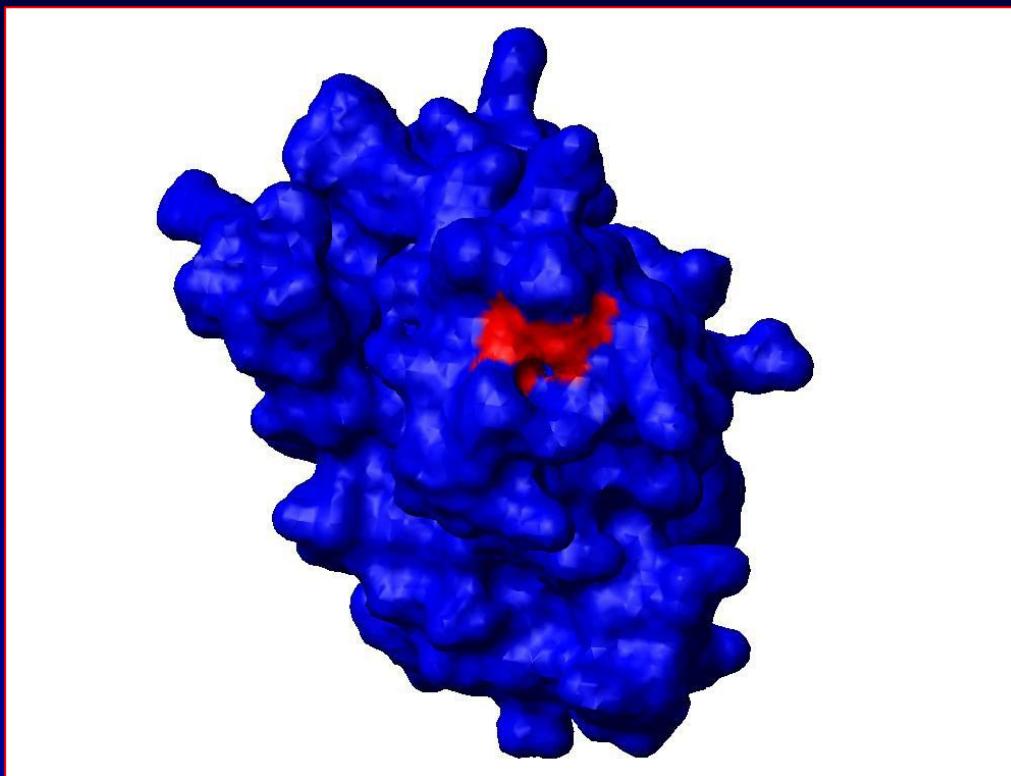
556 (I/T) 5743702

579 (R/H) 5743703

631 (P/H) 5743704
677 (R/W) 5743706

715 (Y/N) 5743707
715 (Y/Amb) 5743708
753 (R/Q) 5743708

Location of R753 in the TIR domain



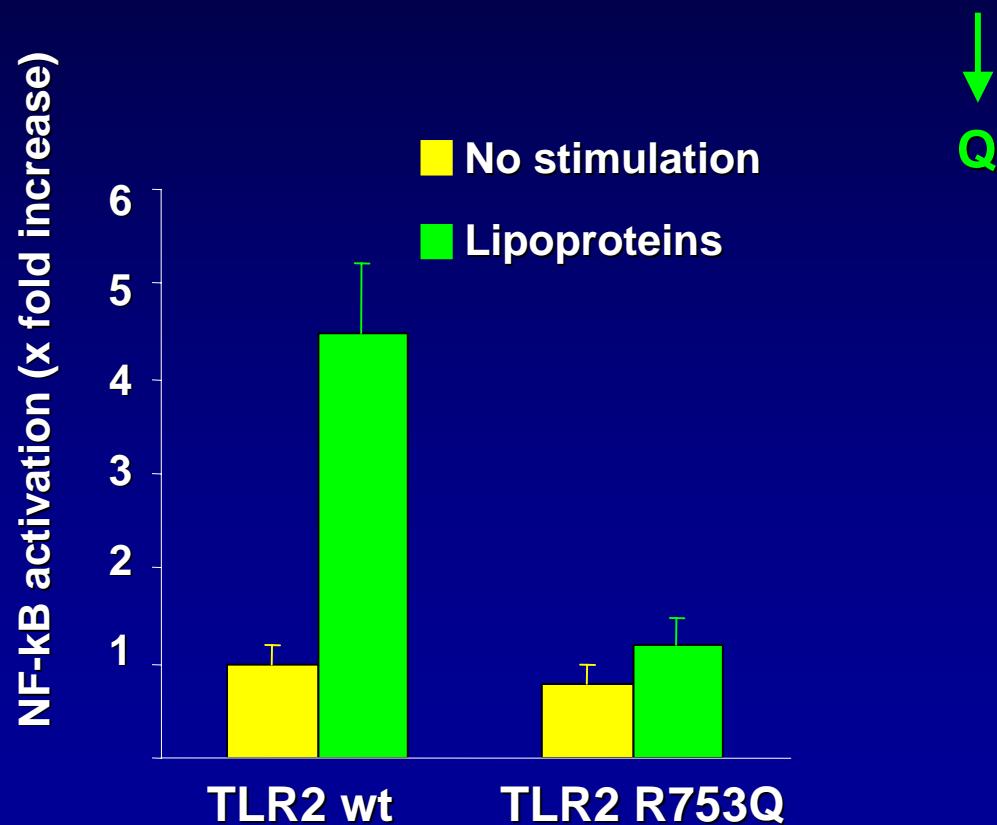
R753Q Polymorphism in the TLR2 gene

743

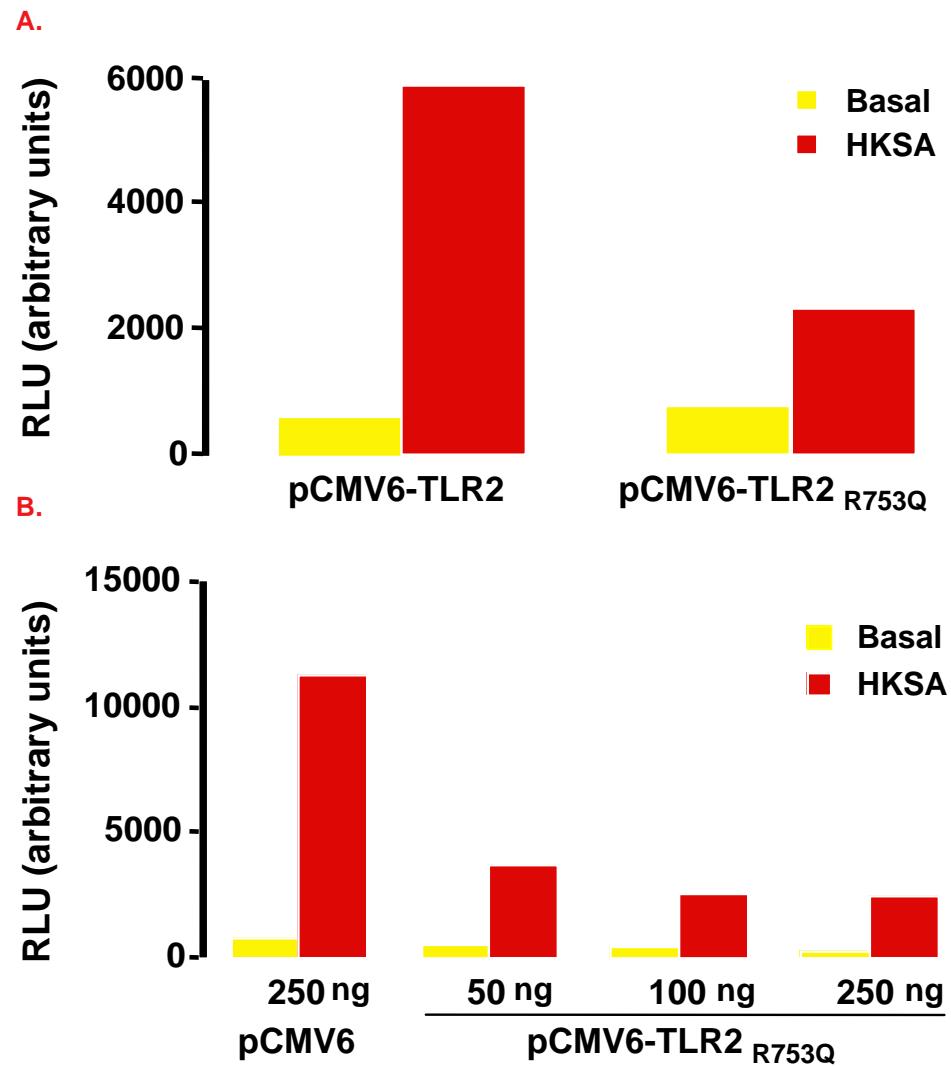
765

Human TLR2 KAIPQRPCKL**R**KIMNTKTYLEWP

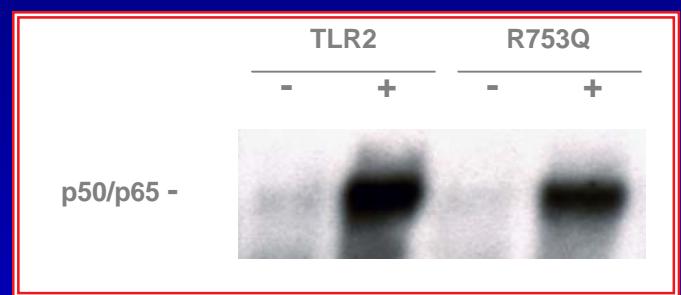
Mouse TLR2 KAIPQRPCKL**R**KIMNTKTYLEWP

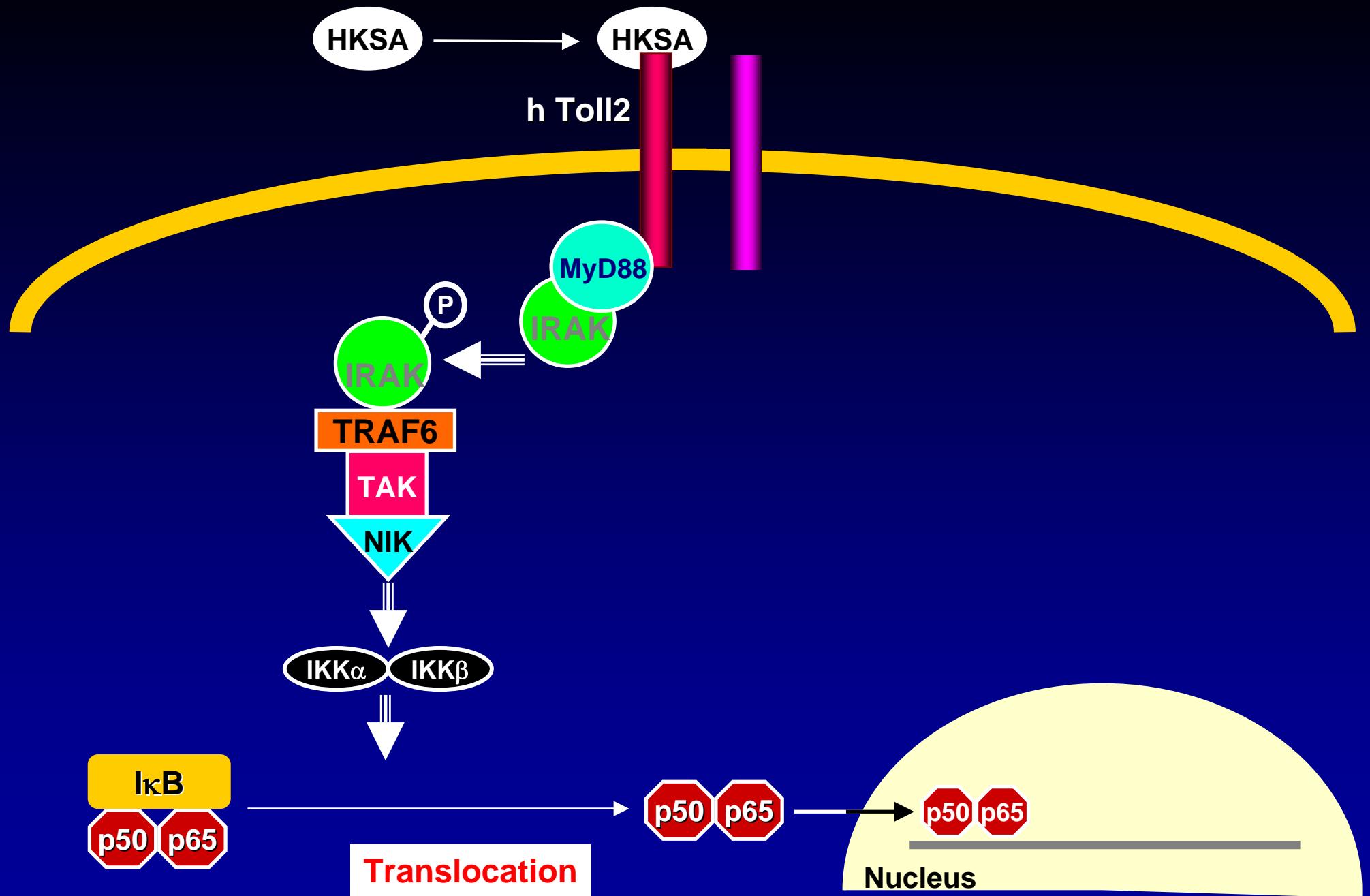


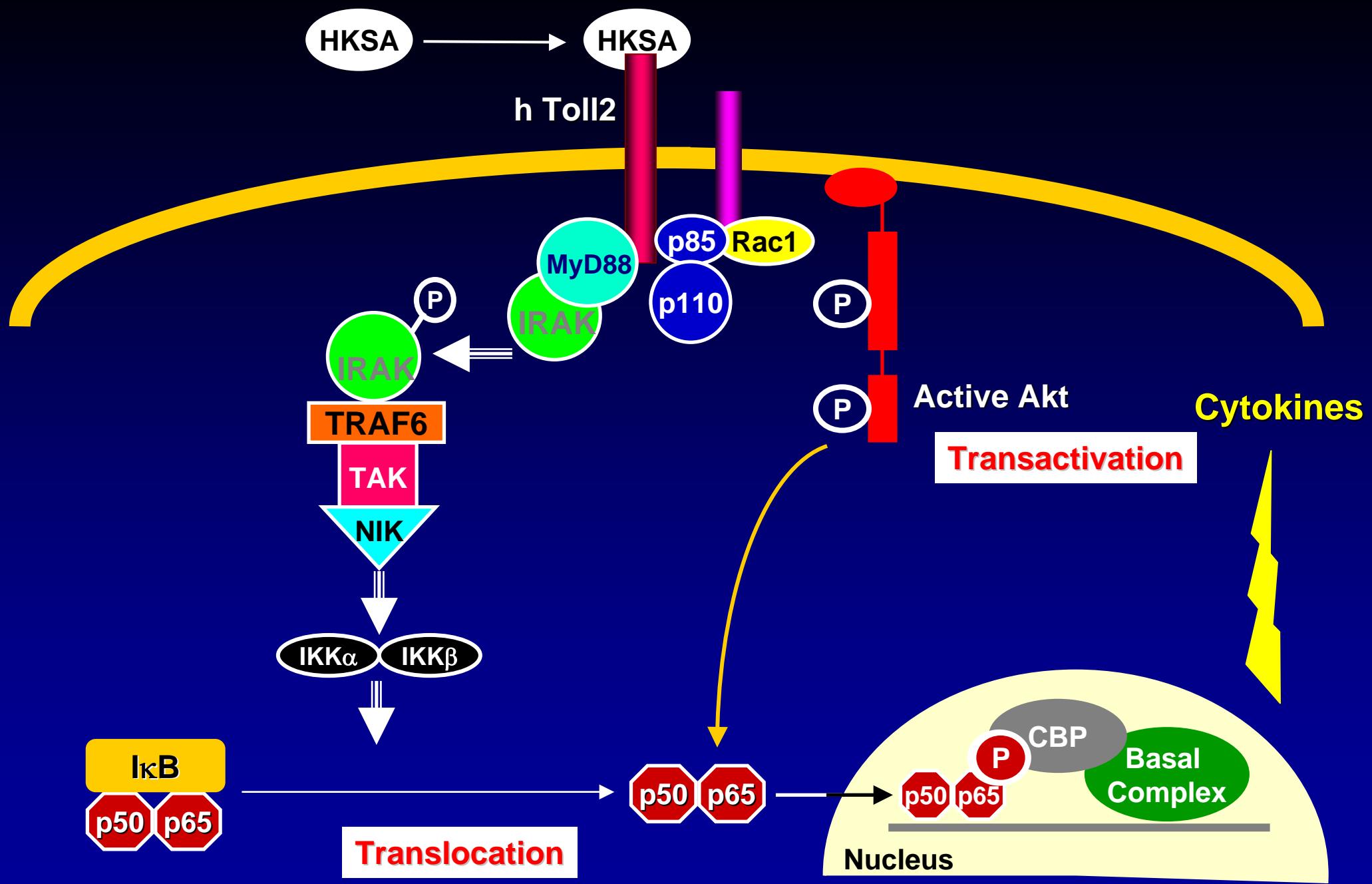
Dominant Negative Effect of TLR2 R753Q

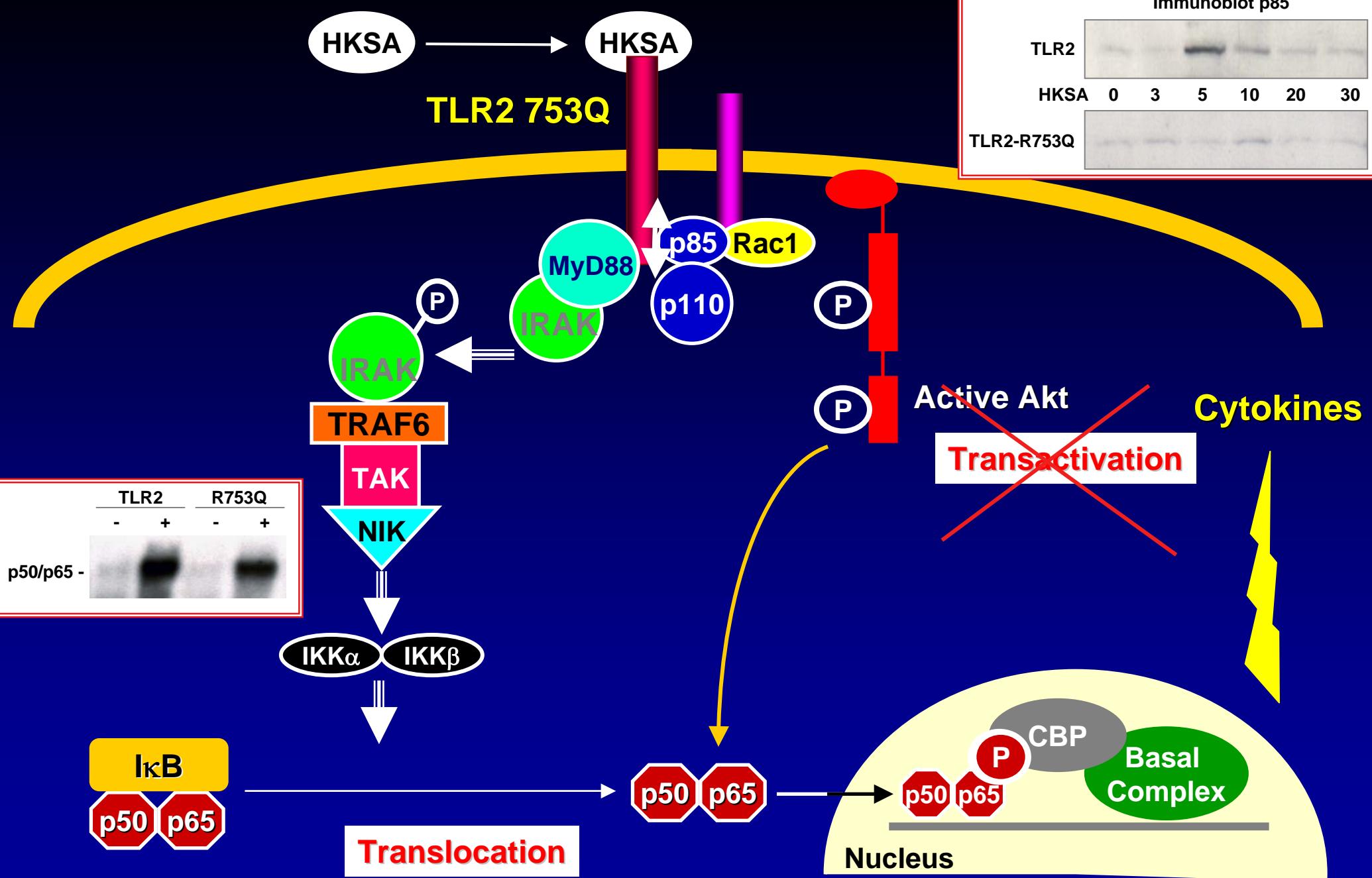


R753Q and NF- κ B translocation

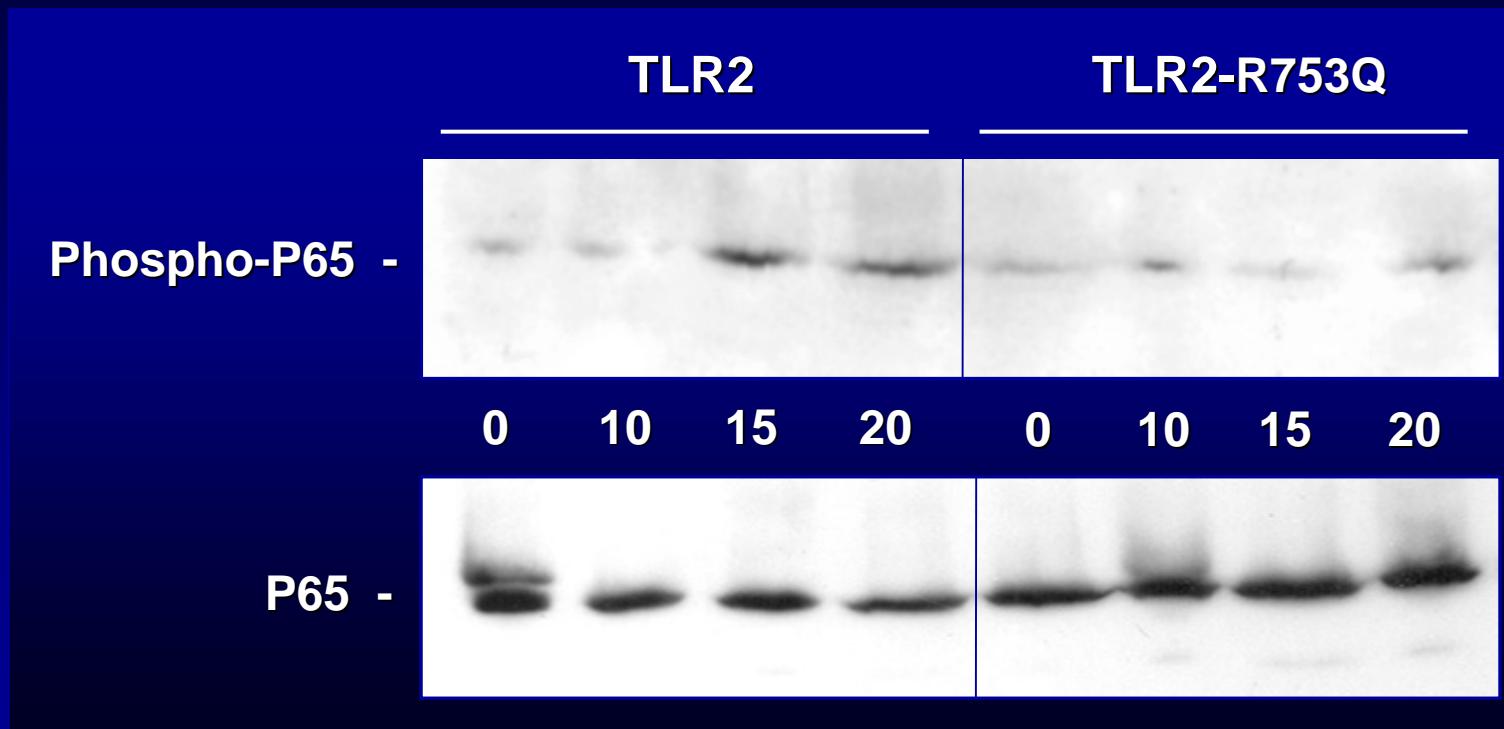








TLR2_{R753Q} and p65 phosphorylation



Imaging HKSA-induced PI-3K activation

TLR2

R753Q

QuickTime™ et un décompresseur
Cinepak sont requis pour visualiser
cette image.

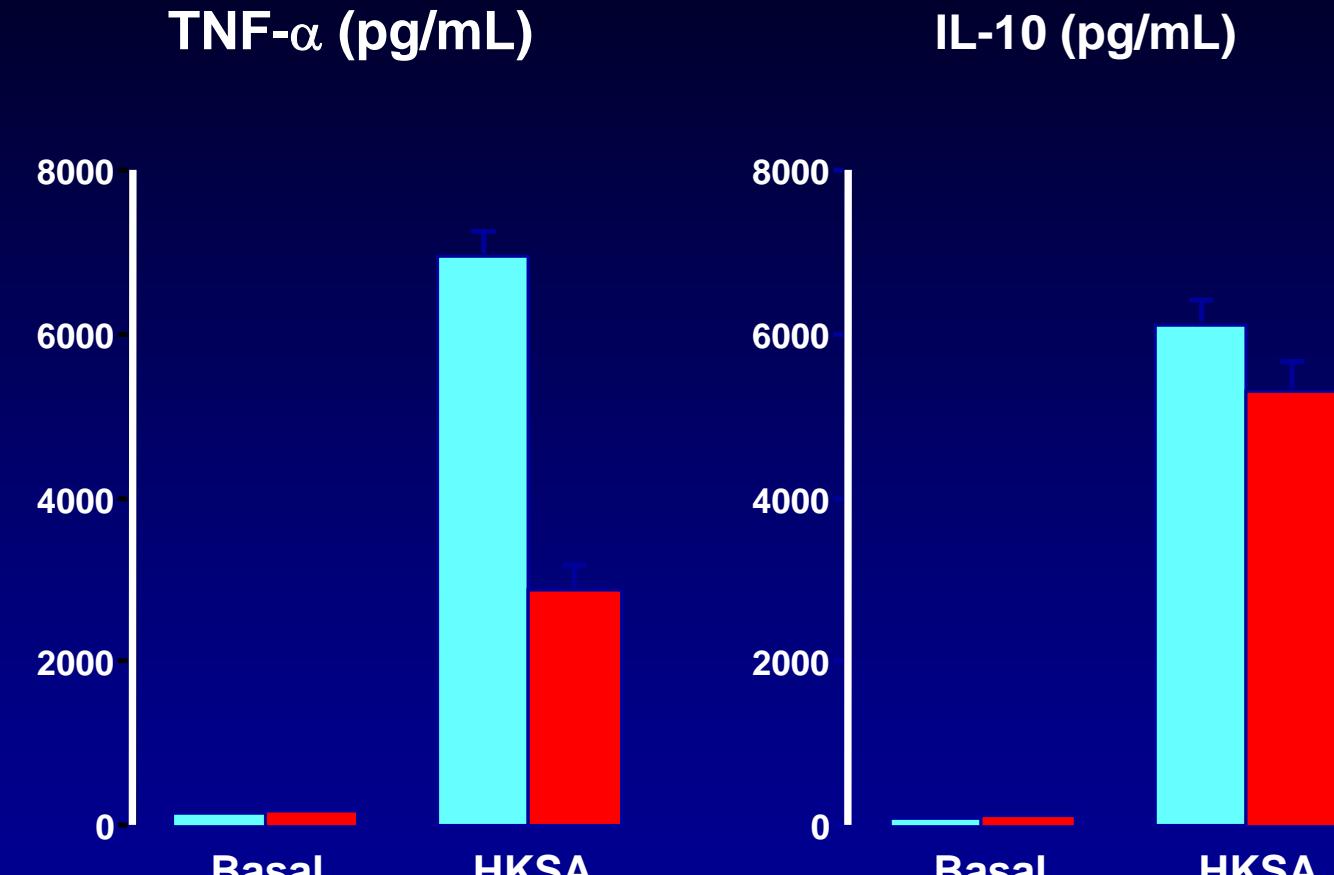
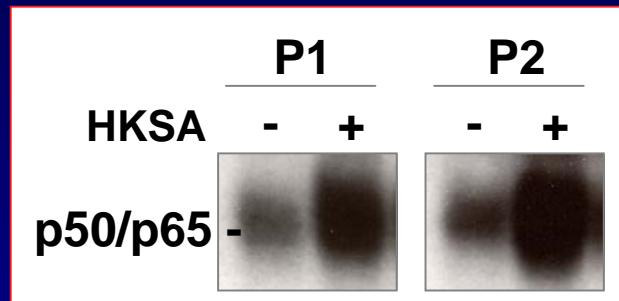
QuickTime™ et un décompresseur
Cinepak sont requis pour visualiser
cette image.

*TLR2 stably-transfected 293 cells
GFP-AKT-PH
HKSA*

TLR2 Polymorphisms in Humans



TLR2_{R753Q} and Cytokine Production



Monocytes from 8 TLR2wt Pts

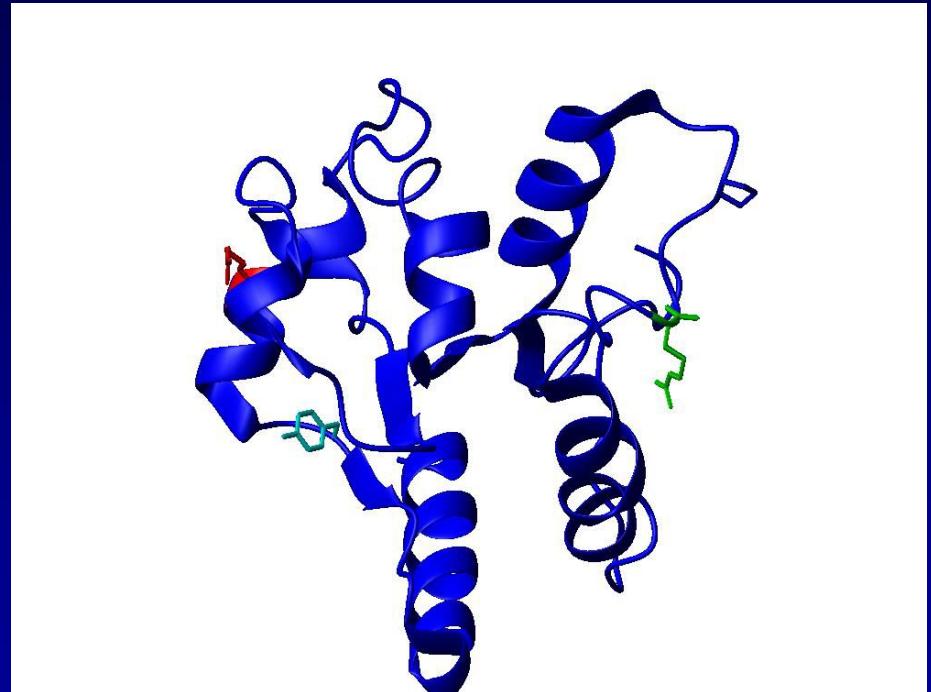
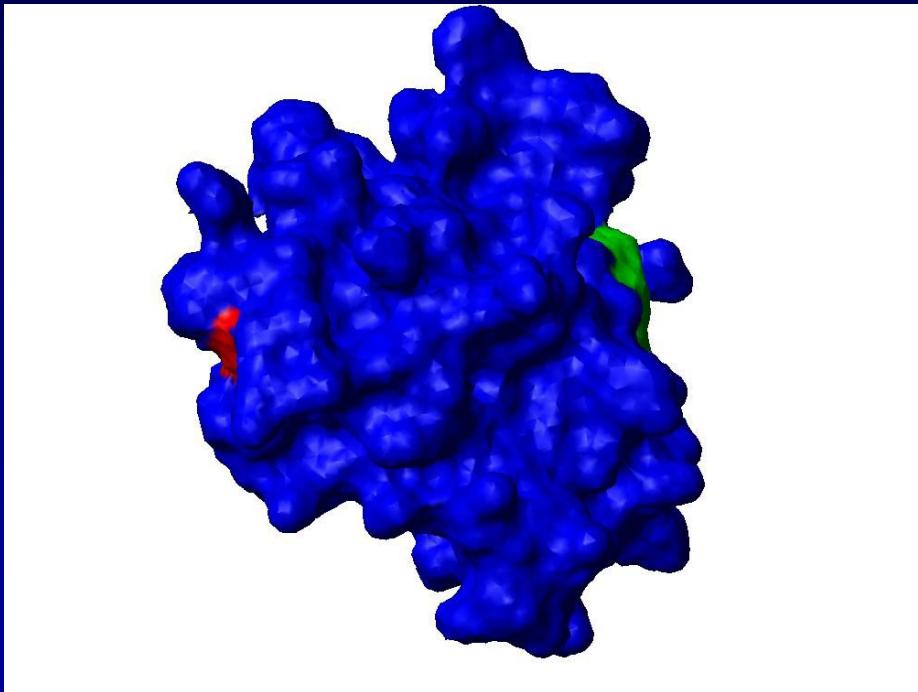
Monocytes from 10 TLR2_{R753Q} Pts

TLR2_{R753Q} in MICU

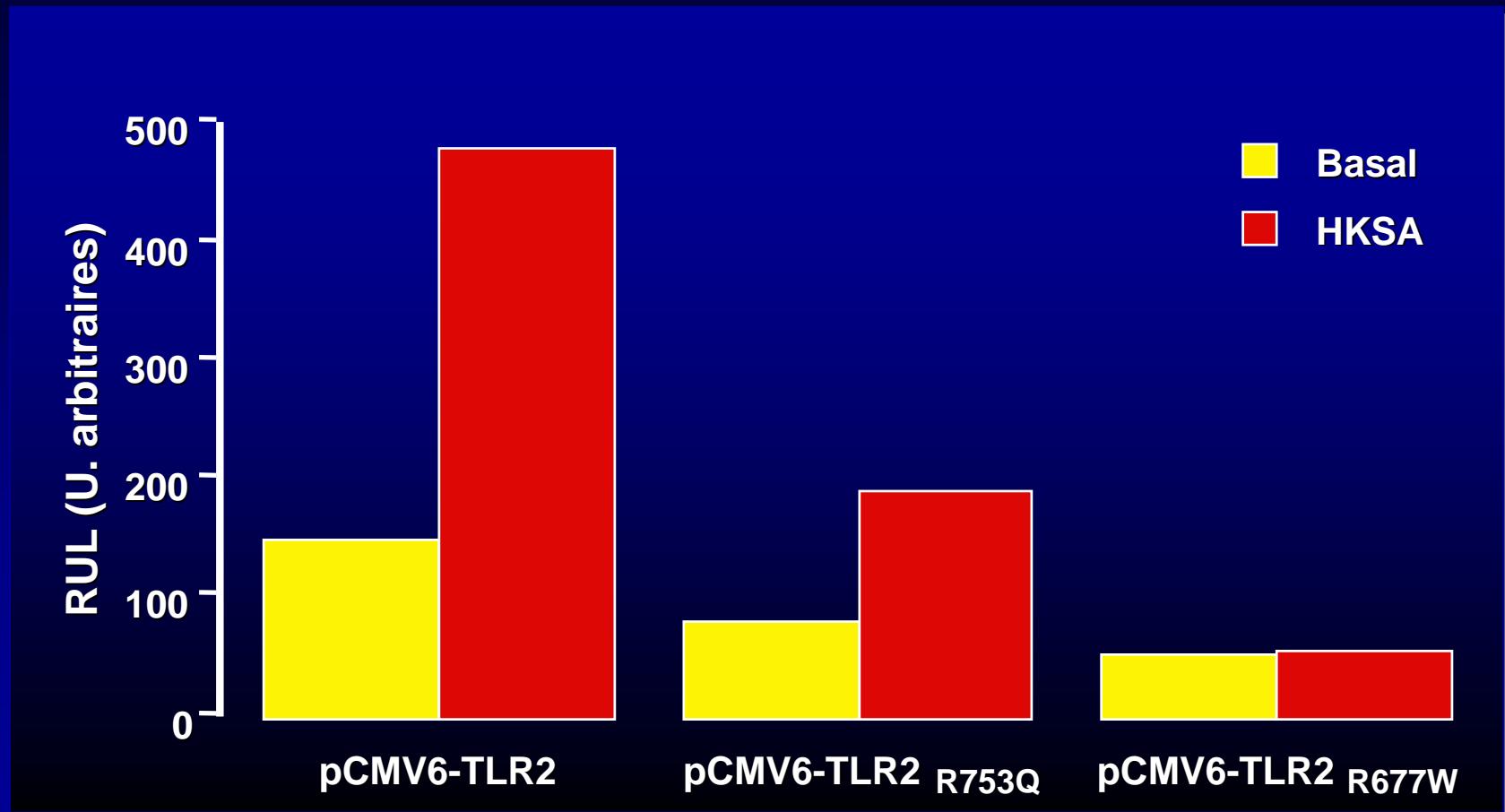
1103 Caucasian ICU Pts (322 SS) → 28 Pts TLR2_{R753Q} (2,5%)

- Age 47,2 ± 18
- SAPS 2 40,5 ± 19
- Survivors 23/28
- Infections 16/28 → 16 Septic Shock (5.1% of SS group)
- Origin of Infections
 - Pneumonia 10
 - Meningitis 4
 - Septicemia 5
 - Others 4
- Microorganisms
 - *S. pneumoniae* 8
 - *S. aureus* 5
 - *Candida sp.* 2 → 11.1% of Gram positive SS group
 - *Aspergillus sp.* 2
 - Others 6

Location of R753 and R677 in the TIR domain



R753Q & R677W inhibit NF-κB activation



Clinical Importance of TLR2_{R677W}

Association of TLR2 R677W with:

- susceptibility to tuberculosis in Tunisian patients

Ben Ali M; Clin Diagn Lab Immunol. 2004;11:625-6

- susceptibility to Lepromatous Leprosy

Kang TJ, FEMS Immunol Med Microbiol. 2001;31:53-8.

No association of TLR R677W with:

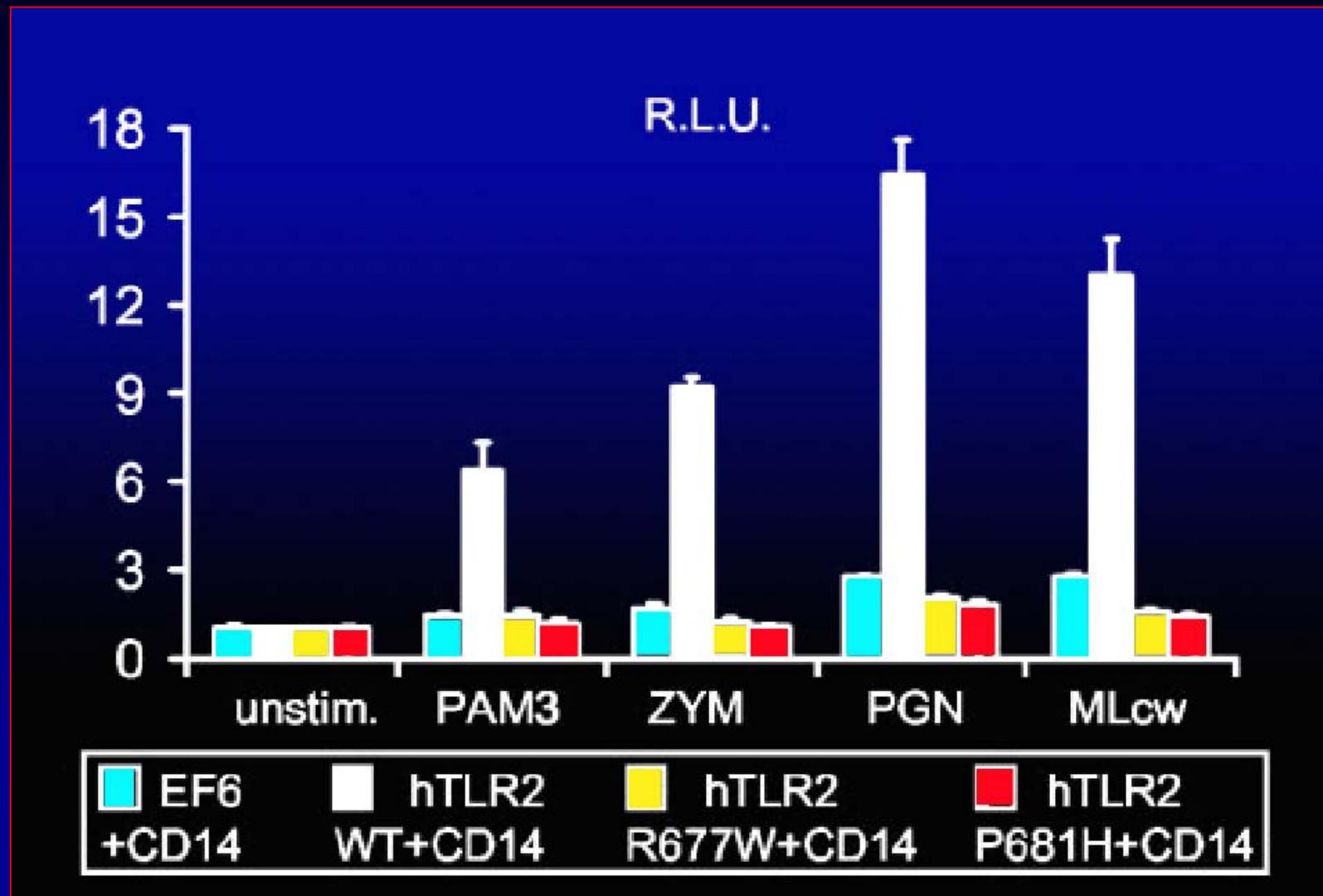
- chronic mucocutaneous candidiasis

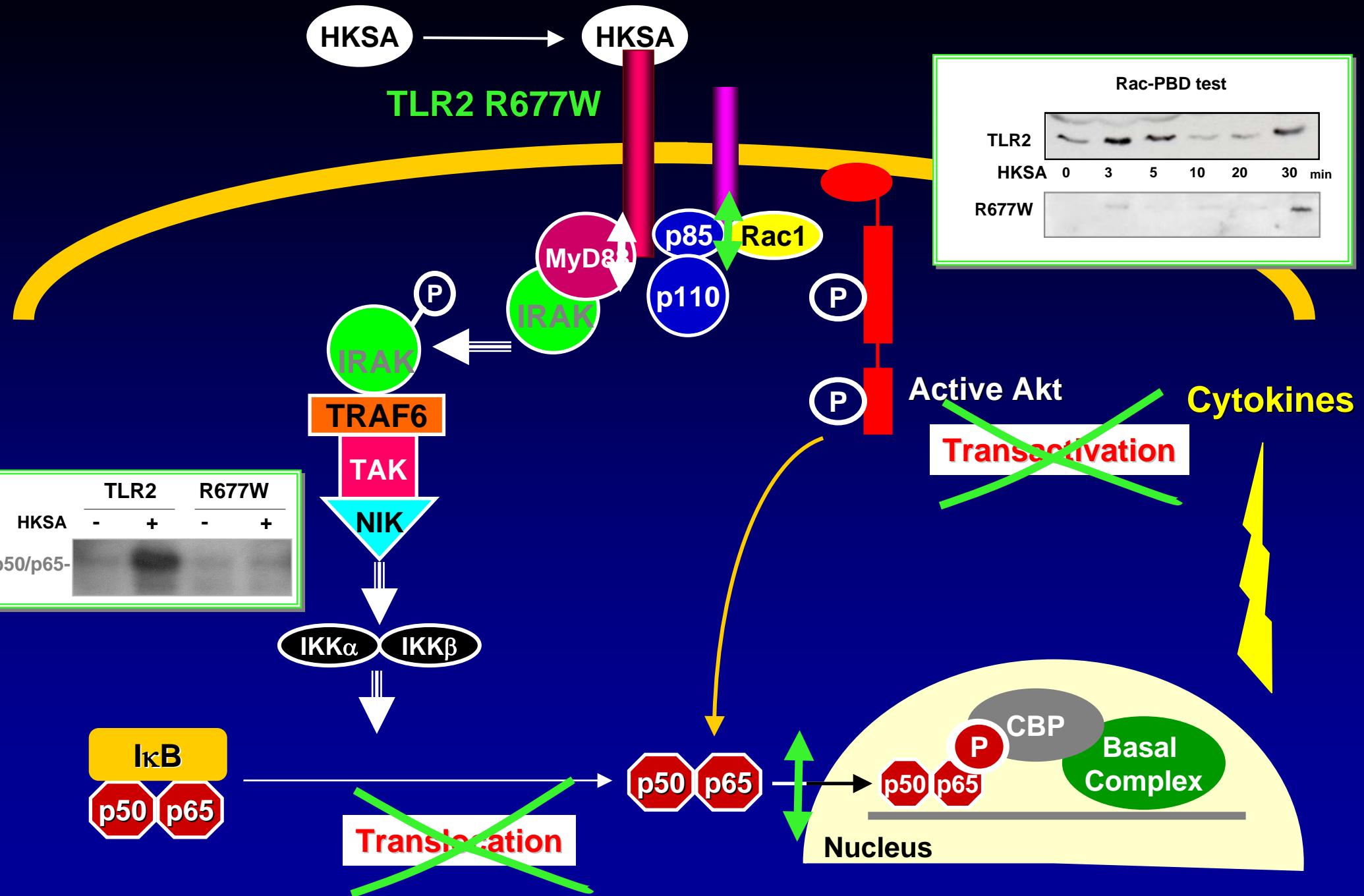
van der Graaf CA, Neth J med 2003:61:365-9

- lymphatic filariasis

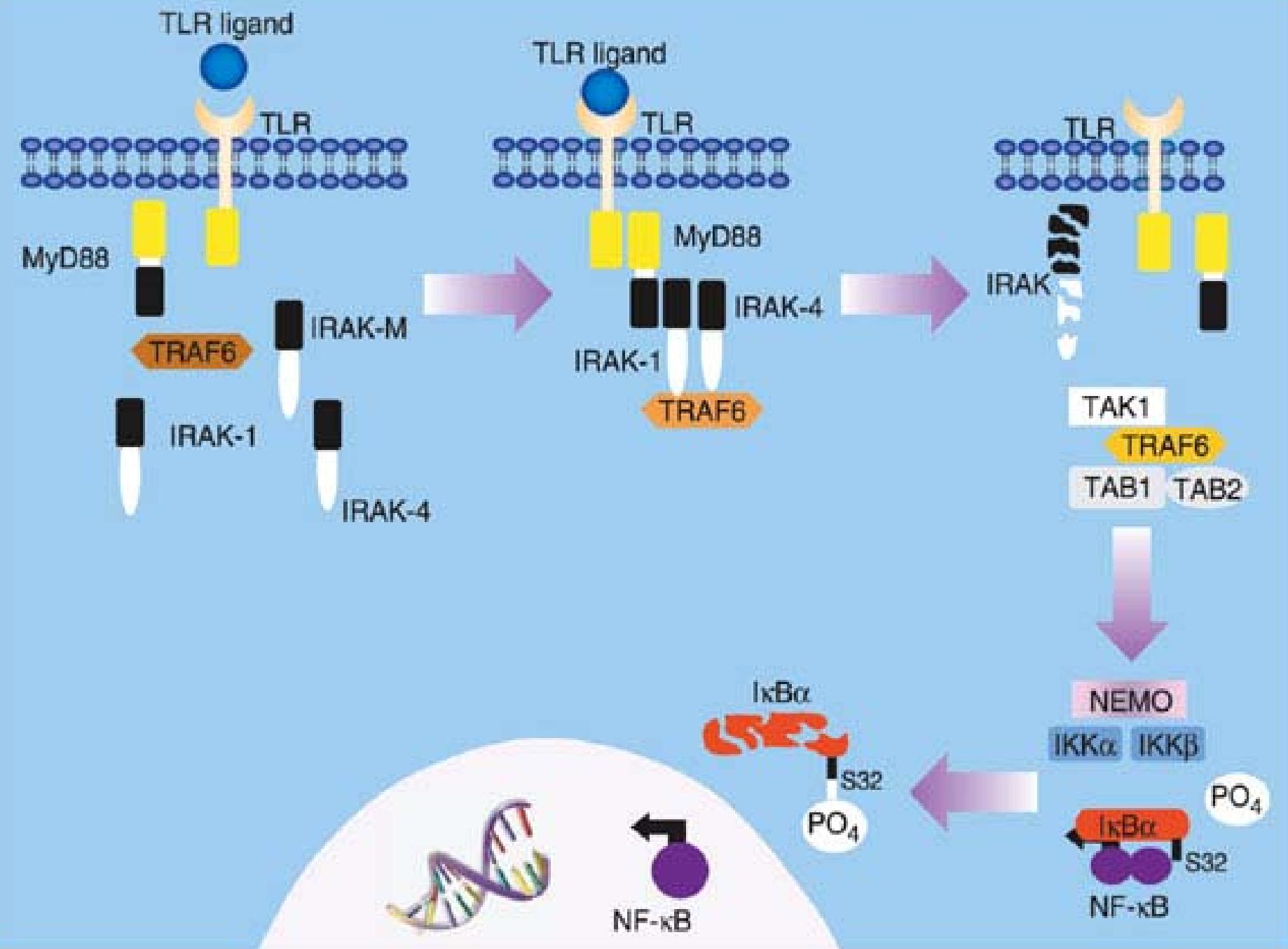
Hise AG, Genes Immun 2003; 4:524-7

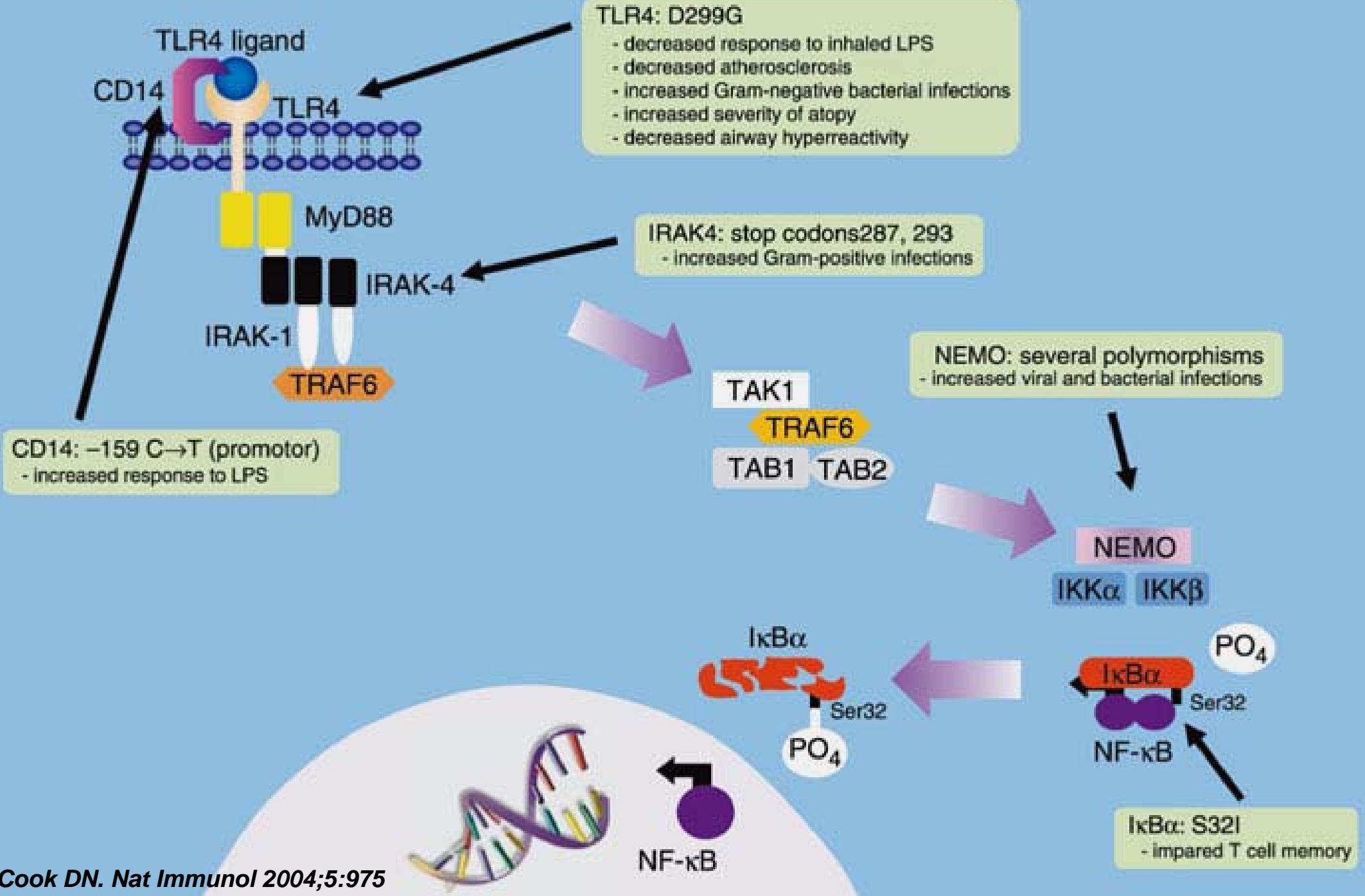
Polymorphism R677W in the *TLR2* gene





Polymorphisms of TLR Signalling Proteins



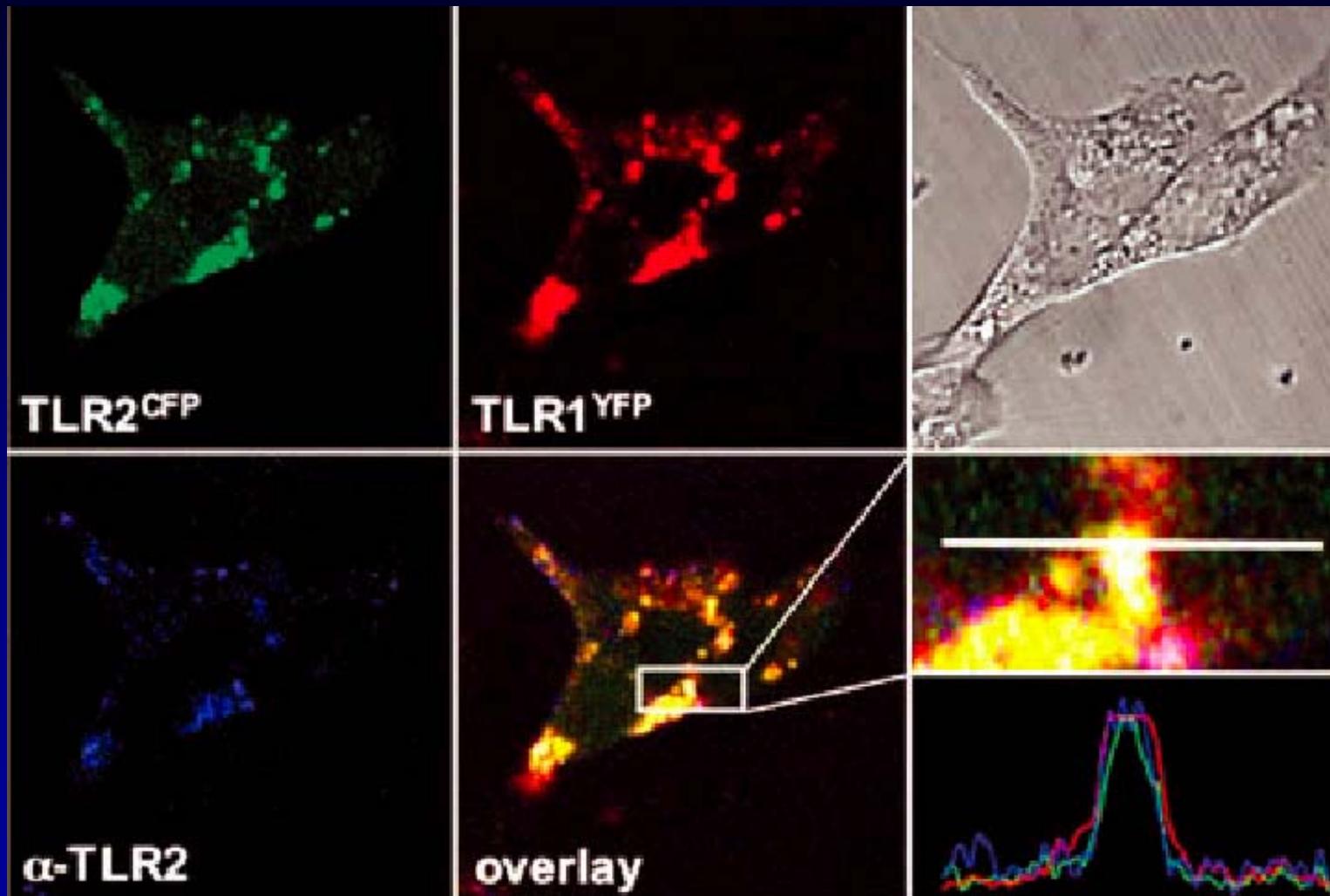


Conclusions and Perspectives

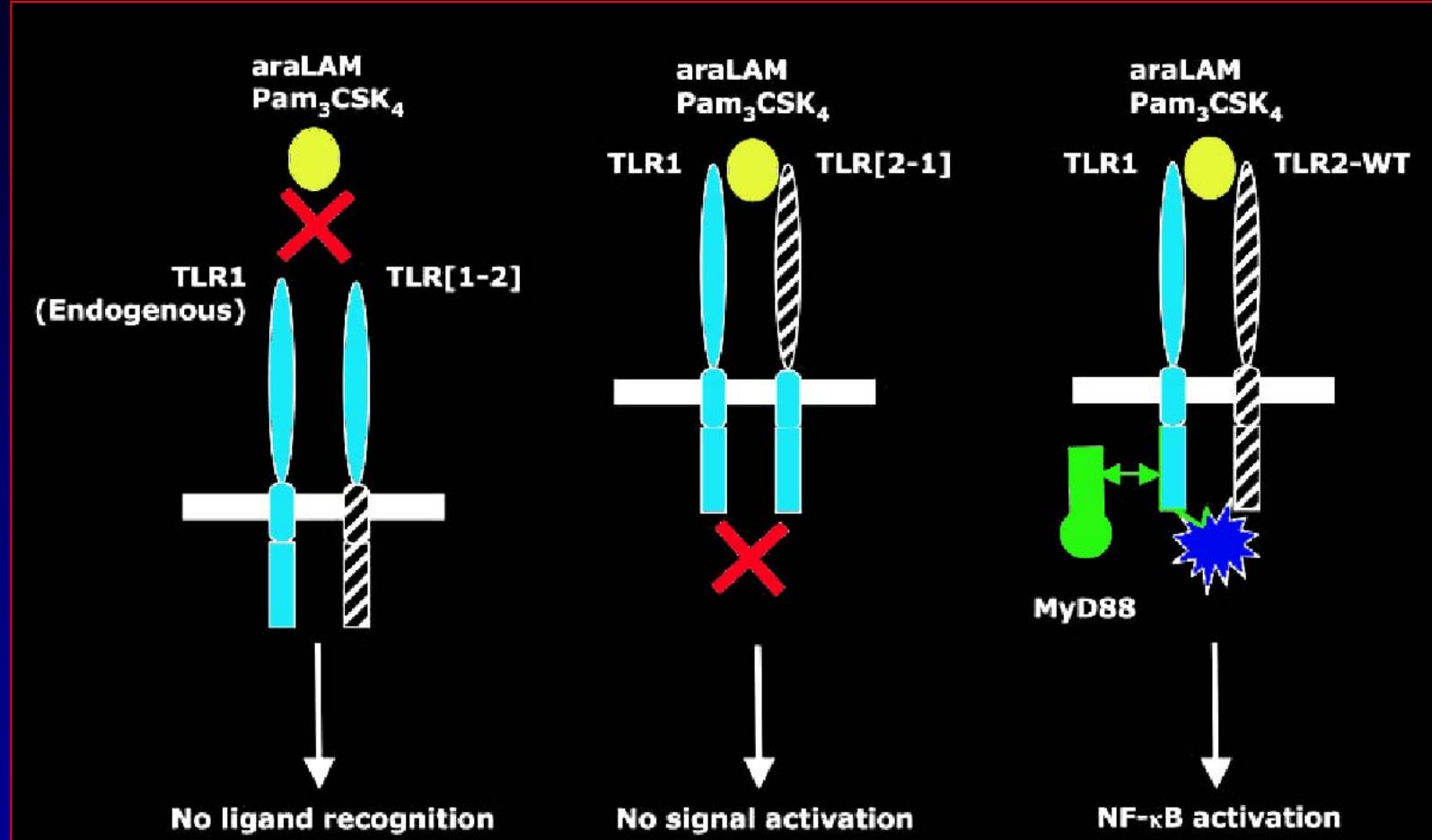
- TLR functional genomics might explain some inter-individual variabilities of innate immune response
- Functional genomics validates signal transduction in Humans
- Importance of TLR1 and TLR6 polymorphisms on TLR2 signalling

Surface co-localisation of TLR1 and TLR2

Surface antibody-patching of TLR2



Complementarities of TLR2 and TLR1 for signalling



TLR1: 77 SNPs

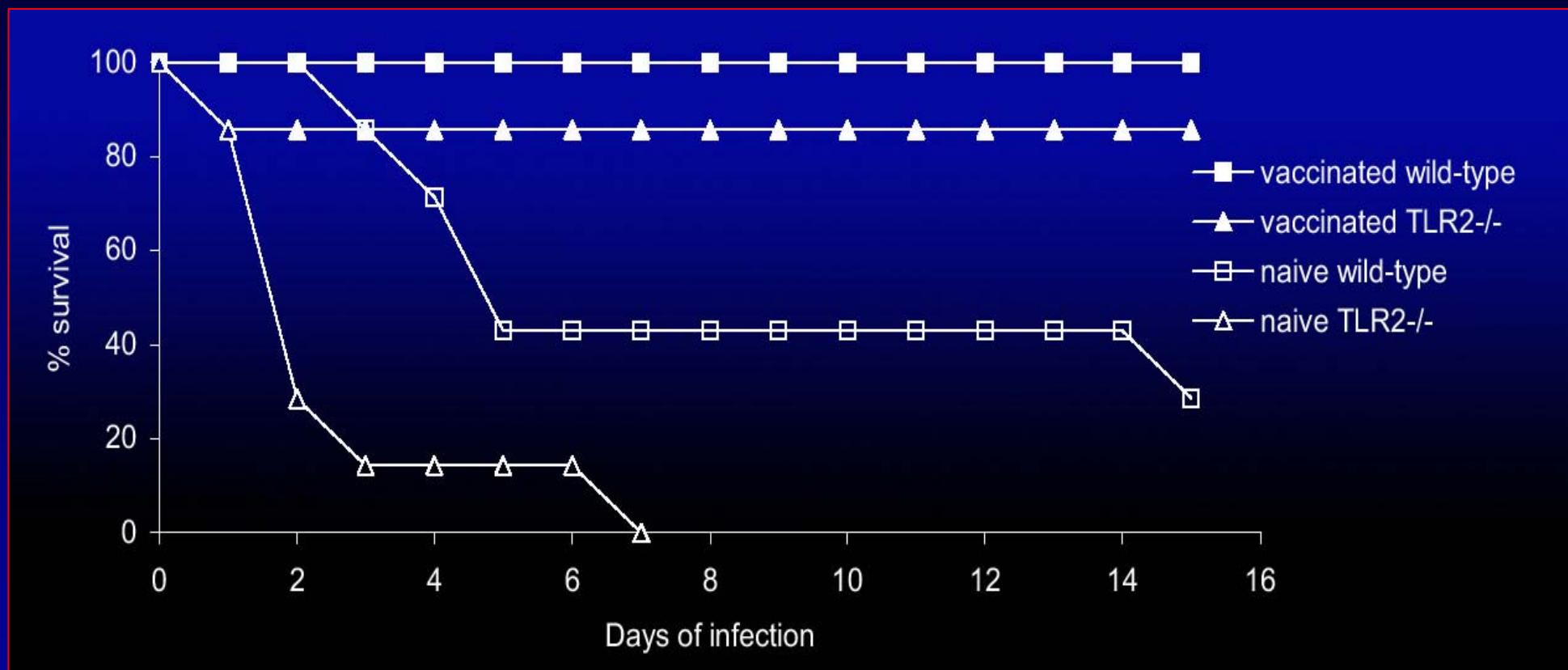
TLR6: 53 SNPs

Conclusions and Perspectives

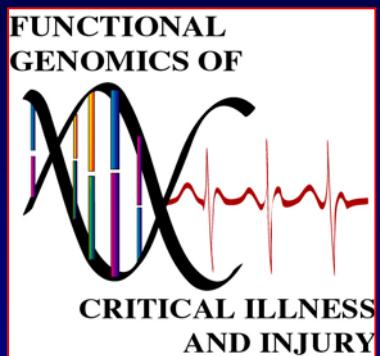
- TLR functional genomics might explain inter-individual variability of innate immune response
- Functional genomics validates signal transduction in Humans
- Importance of TLR1 and TLR6 polymorphisms on TLR2 signalling
- TLR2 polymorphism detection for severe sepsis prevention

Immunization of TLR2-deficient mice

IV infection with 10^6 virulent *C. albicans*

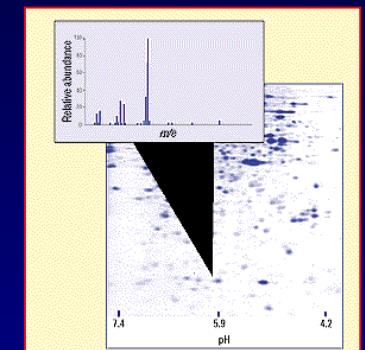


Clinique

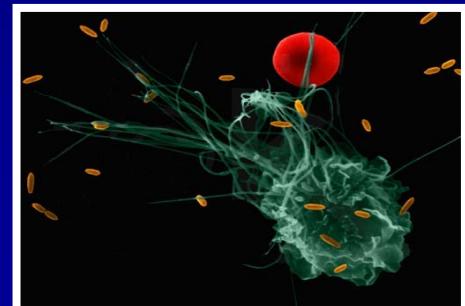


Diagnostic Pronostic Therapeutic

MARKERS



Génomique



Biology

Proteomic

Acknowledgments

Cochin Institute - Paris

CHICHE Jean-Daniel

DHAINAUT Jean-François

TEXEREAU Joelle

GRIMALDI David

ROGET Karine

ROUSSEAU Christophe

COMBA Béatrice

CHRABIEH Maya

Collaborations

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SCHWARTZ David

LORENZ Eva

University of Colorado, Denver USA

ABRAHAM Edward