

SINDROME URÉMICO HEMOLÍTICO ATÍPICO SUHa

FISIOPATOLOGÍA

DIAGNÓSTICO

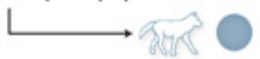
SUHa Y TRANSPLANTE

HERNÁN TRIMARCHI

2014



Mammals
5,600 species estimated
5,501 (98%) species discovered



Birds
10,500
10,064 (96%)



Reptiles
12,000
9,547 (80%)



Amphibians
15,000
6,771 (45%)



Fish
45,000
32,400 (72%)



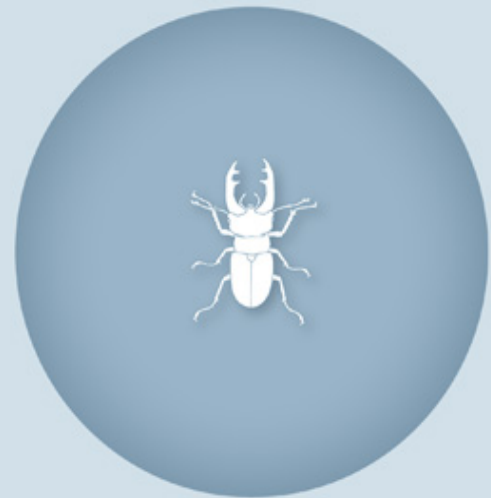
Crustaceans
150,000
47,000 (31%)



Mollusks
200,000
85,000 (43%)



Arachnids
600,000
102,248 (17%)



Insects
5,000,000
1,000,000 (20%)

REVIEW

Between a chicken and a grape: estimating the number of human genes

Mihaela Pertea and Steven L Salzberg*

Abstract

Many people expected the question 'How many genes in the human genome?' to be resolved with the publication of the genome sequence in 2001, but estimates continue to fluctuate.

Ever since the discovery of the genetic code, scientists have been trying to catalog all the genes in the human genome. Over the years, the best estimate of the number of human genes has grown steadily smaller, but we still do not have an accurate count. Here we review the history of efforts to establish the human gene count and present the current best estimates.

The first attempt to estimate the number of genes in the human genome appeared more than 45 years ago, while the genetic code was still being deciphered. Friedrich Vogel published his 'preliminary estimate' in 1964 [1], based on the number of amino acids in the alpha- and beta-chains of hemoglobin (141 and 146, respectively). Knowing that three nucleotides corresponded to each amino acid, he extrapolated to compute the molecular weight of the DNA comprising these genes. He then made several assumptions in order to produce his estimate: that these proteins were typical in size (they are actually smaller than average); that nucleotide sequences were uninterrupted on the chromosomes (introns were discovered more than 10 years later [2,3]); and that the entire genome was protein coding. All these assumptions were reasonable at the time, but later discoveries would reveal that none of them was correct. Vogel then used the molecular weight of the human haploid chromosomes to correctly calculate the genome size as 3×10^9 nucleotides, and dividing that by the size of a 'typical' gene, came up with an estimate of 6.7 million genes.

Even at the time, Vogel found this number 'disturbingly high', but no one suspected in 1964 that most human genes were interrupted by multiple introns, nor did anyone know that vast regions of the human genome would turn out to contain seemingly meaningless repetitive sequences. Since Vogel's initial attempt, many scientists have tried to estimate the number of genes in the human genome, using increasingly sophisticated molecular tools. Over the years, the number has gradually come down, in a process that has been humbling at times, as we realized that many other species - even plants - are predicted to have more genes than we do (Figure 1). An estimate of 100,000 genes appeared in the 1990 joint National Institutes of Health (NIH)/Department of Energy (DOE) report on the Human Genome Project [4]; this was apparently based on a very rough (and incorrect) calculation that typical human genes are 30,000 bases long, and that genes cover the entire 3-gigabase genome.

Many people, including many geneticists, expected that we would have a definitive gene count when the human genome was finally completed, and indeed one of the main surprises upon the initial publication of the human genome in February 2001 [5,6] was that the number had again dropped, quite precipitously. However, as we shall see, the publication of the human genome did not come anywhere close to producing a precise gene list or even a gene count, and in the years since the number has continued to fluctuate. As a result, even today's best estimates still have a large amount of uncertainty associated with them.

In order to count genes, we need to define what we mean by a 'gene', a term whose meaning has changed dramatically over the past century. For our discussion, we will restrict the definition of gene to a region of the genome that is transcribed into messenger RNA and translated into one or more proteins. When multiple proteins are translated from the same region due to alternative mRNA splicing, we will consider this collection of alternative isoforms to be a single gene. In this respect, our definition of a gene is equivalent to what may also be called a chromosomal locus. We will exclude non-protein-coding RNA genes (such as microRNAs (miRNAs) and small nuclear RNAs (snRNAs)), in part

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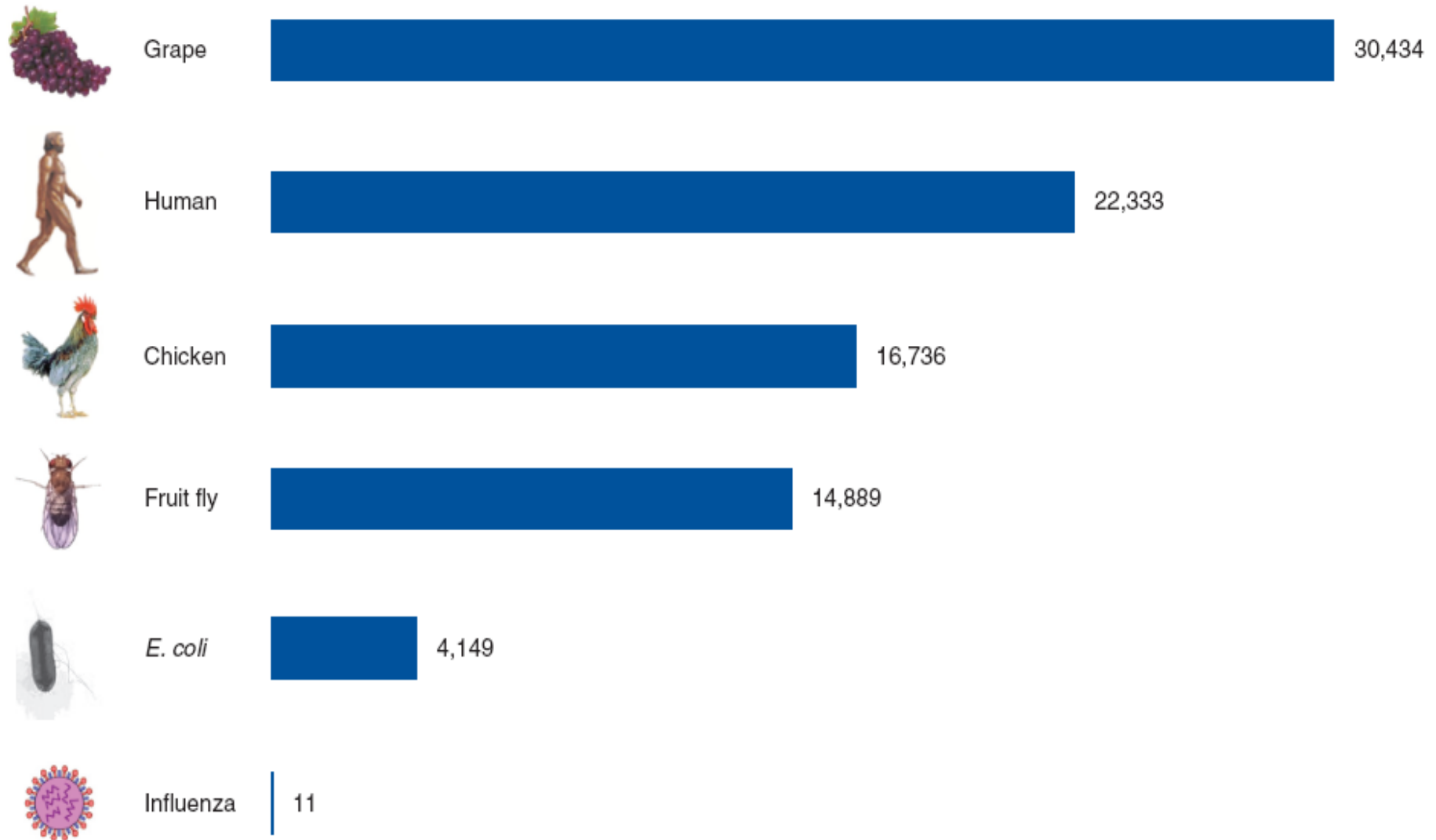


Figure 1. Gene counts in a variety of species. Viruses, the simplest living entities, have only a handful of genes but are exquisitely well adapted to their environments. Bacteria such as *Escherichia coli* have a few thousand genes, and multicellular plants and animals have two to ten times more. Beyond these simple divisions, the number of genes in a species bears little relation to its size or to intuitive measures of complexity. The chicken and grape gene counts shown here are based on draft genomes [50,51] and may be revised substantially in the future.

Fruit Fly

44%



Mouse

92%



85%

Yeast

26%



24%



Chimp

98%



47%

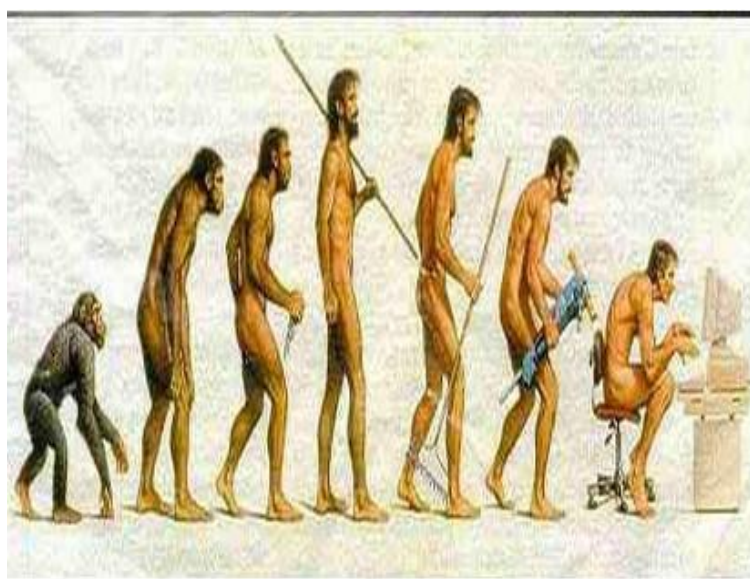


Plant

18%

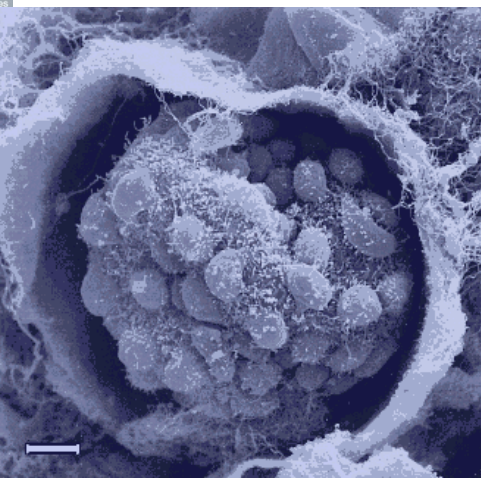
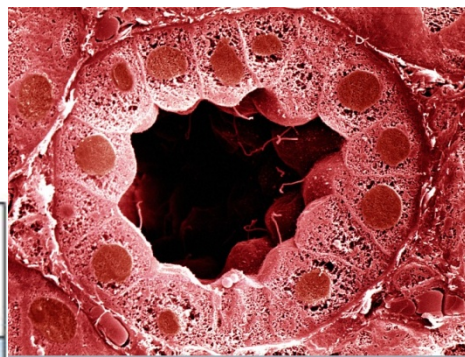
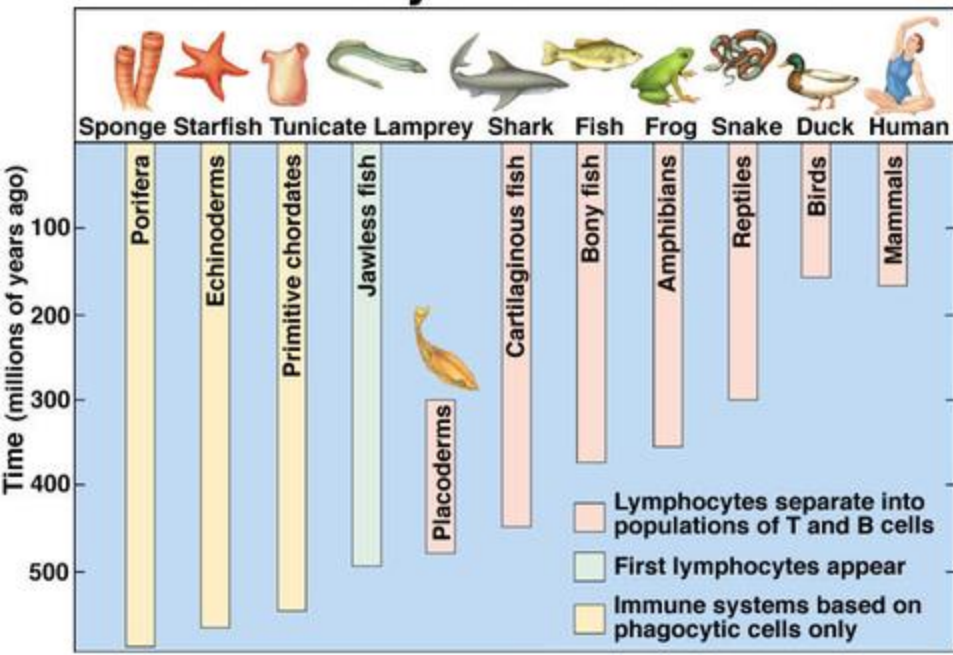


**What percent
of your genes
do you share?**



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Immune System Evolution



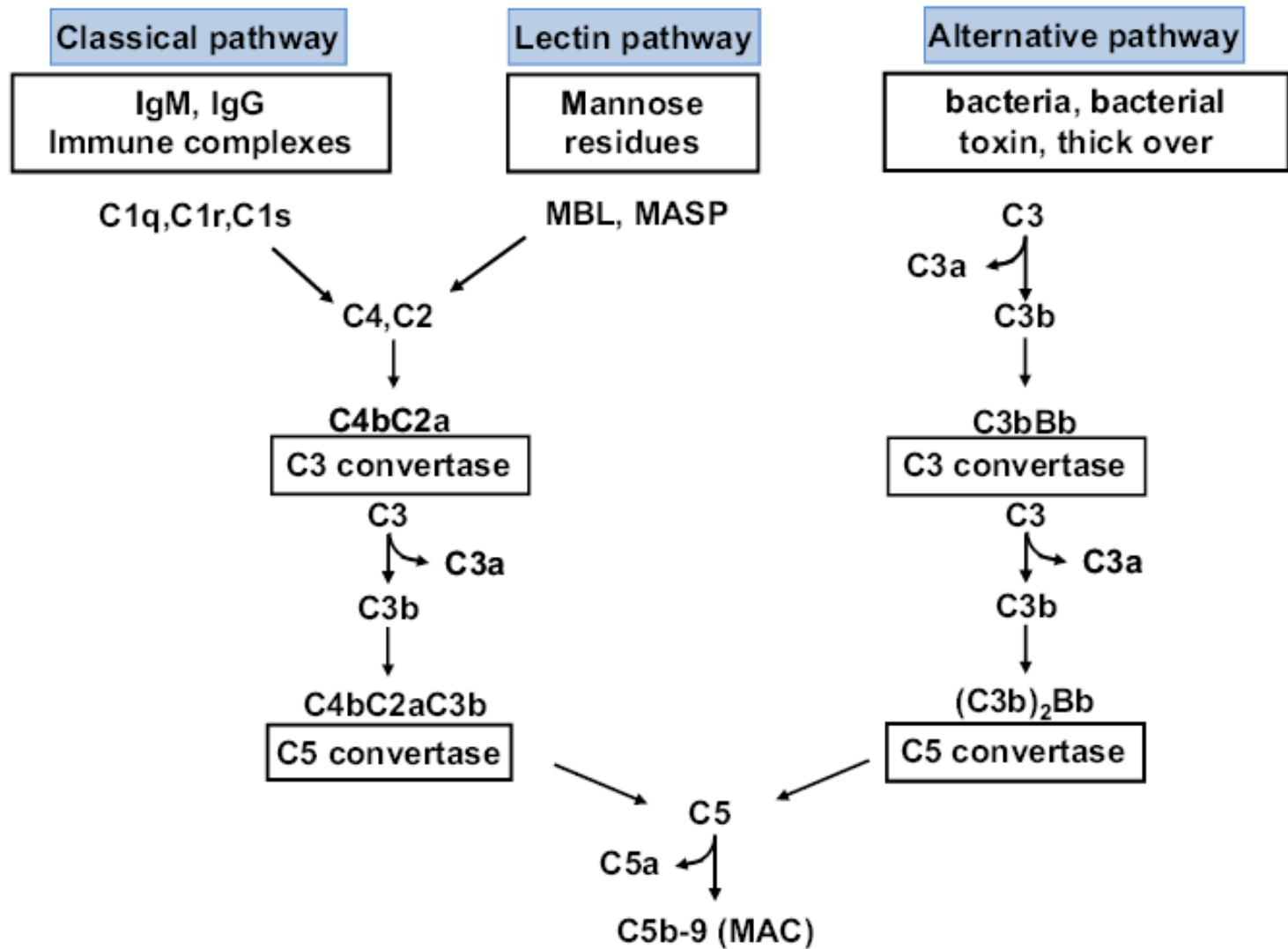
Overview of Complement Activation and Regulation

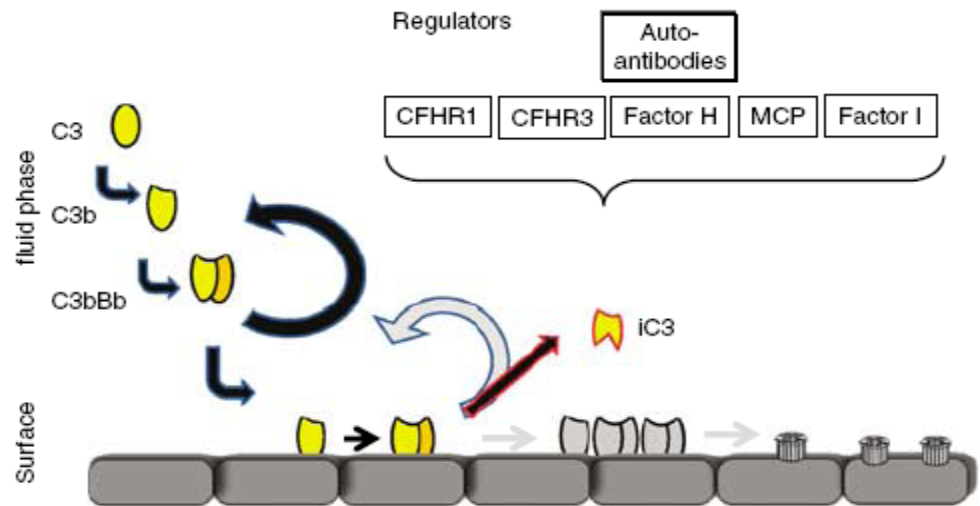
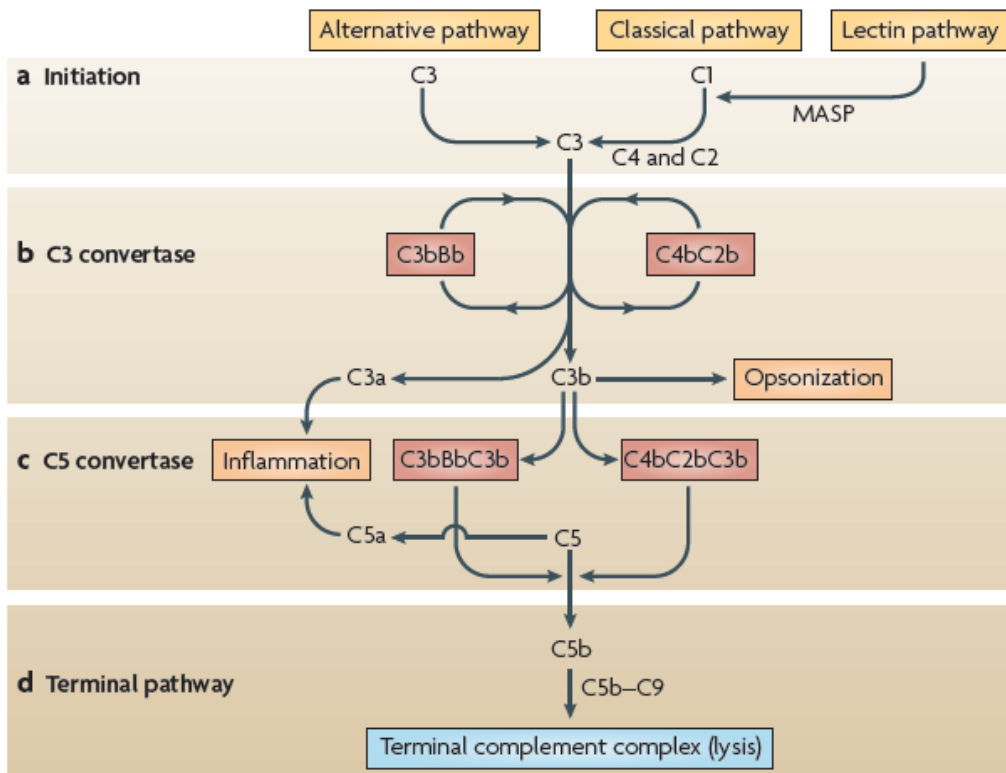
Marina Noris, PhD, and Giuseppe Remuzzi, MD

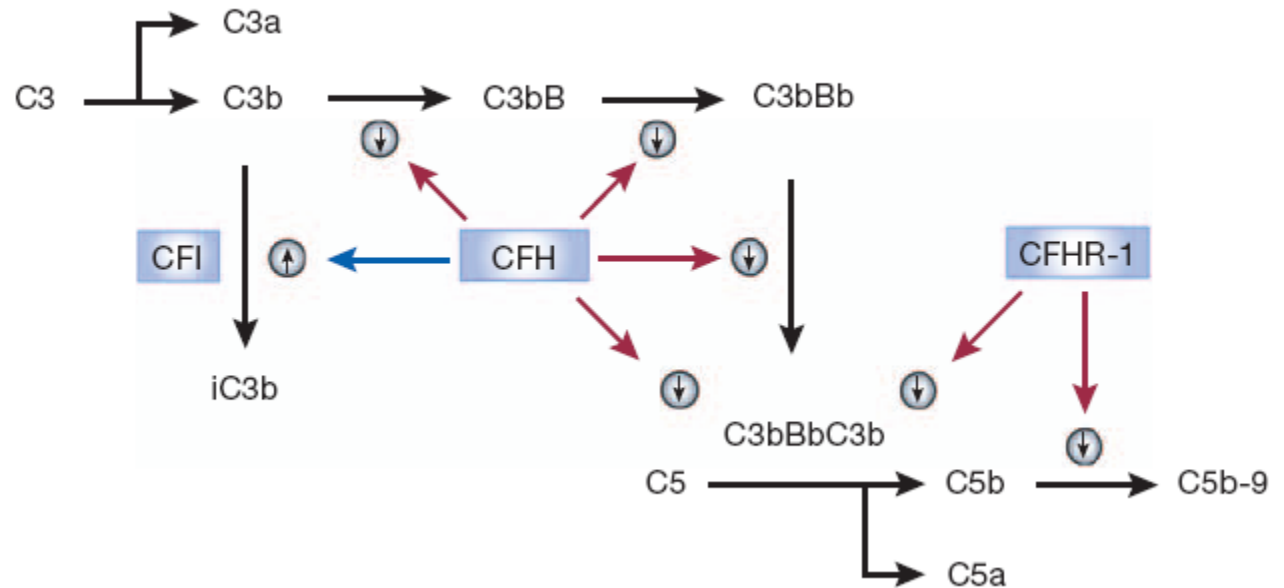
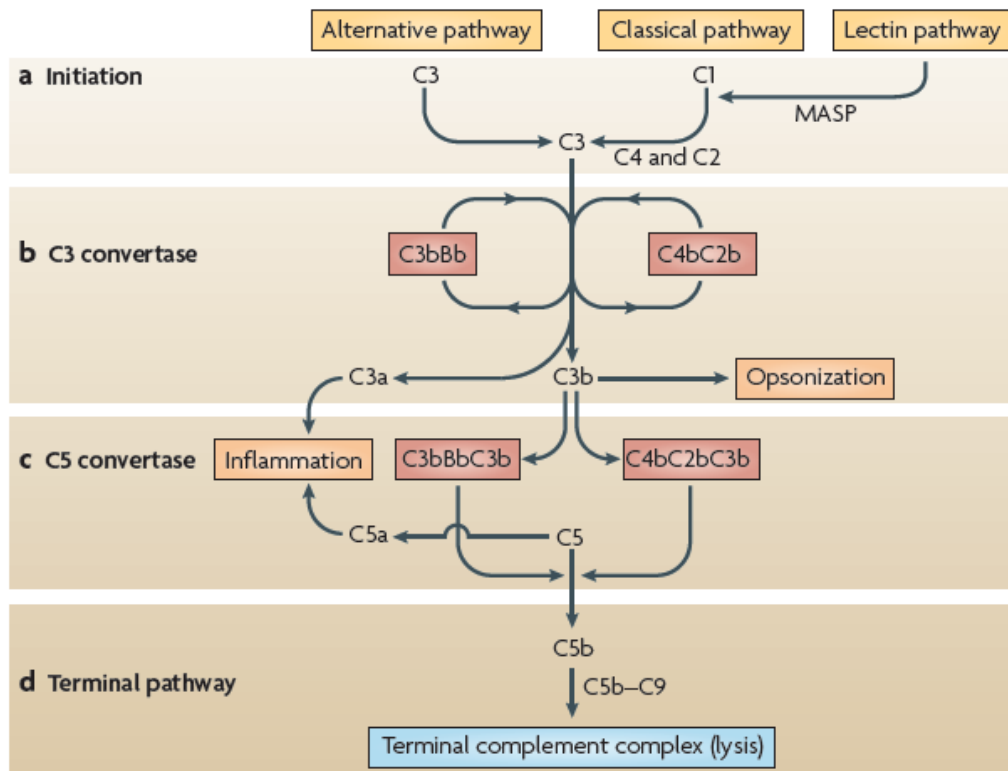
Table 1. The Main Physiologic Activities of the Complement System

Activity	Complement Protein Responsible for the Activity
Host defense against infection	
Oponization	Covalently bound fragments of C3 and C4 (C3b, C4b)
Chemotaxis and activation of leukocytes	Anaphylatoxins (C5a, C3a); anaphylatoxin receptors on leukocytes (C5aR, C3aR)
Lysis of bacteria and cells	Membrane-attack complex (C5b-9)
Interface between innate and adaptive immunity	
Augmentation of antibody response	C3b and C4b fragments bound to immune complexes and to antigens; CR1-4 receptors on B cells and APC
Enhancement of T-cell response to APC	C3a and C5a, C3aR and C5aR on T cells and APC
Reduction of Treg function	C3a and C5a, C3aR and C5aR on T cells and APC
Disposal of waste	
Clearance of immune complexes from tissues	C1q; covalently bound fragments of C3 (C3b) and C4 (C4b), CR1 on erythrocytes, CR1-4 receptors on phagocytes
Clearance of apoptotic cells	C1q; covalently bound fragments of C3 (C3b) and C4 (C4b), CR1 on erythrocytes, CR1-4 receptors on phagocytes

Abbreviations: APC, antigen presenting cells; Treg, regulatory T cells.







Los inhibidores naturales son necesarios para controlar el sistema del complemento

Proximal



Depuración de complejos inmunes
Opsonización Microbiana

C3

C3 + H₂O: siempre activo(crónico)
Amplificación

Anafilatoxina débil C3a

C3b

Inhibidores naturales:
Factor H,I, PCM

iC3b

Trombomodulina

C3-Convertasa

C5-Convertasa

C5

C5b C6 C7 C8 C9

C5a

Potente anafilatoxina
Quimiotaxia
Pro-inflamatoria
Activación leucocitaria
Activación endotelial
Pro-trombótica

C5b-9

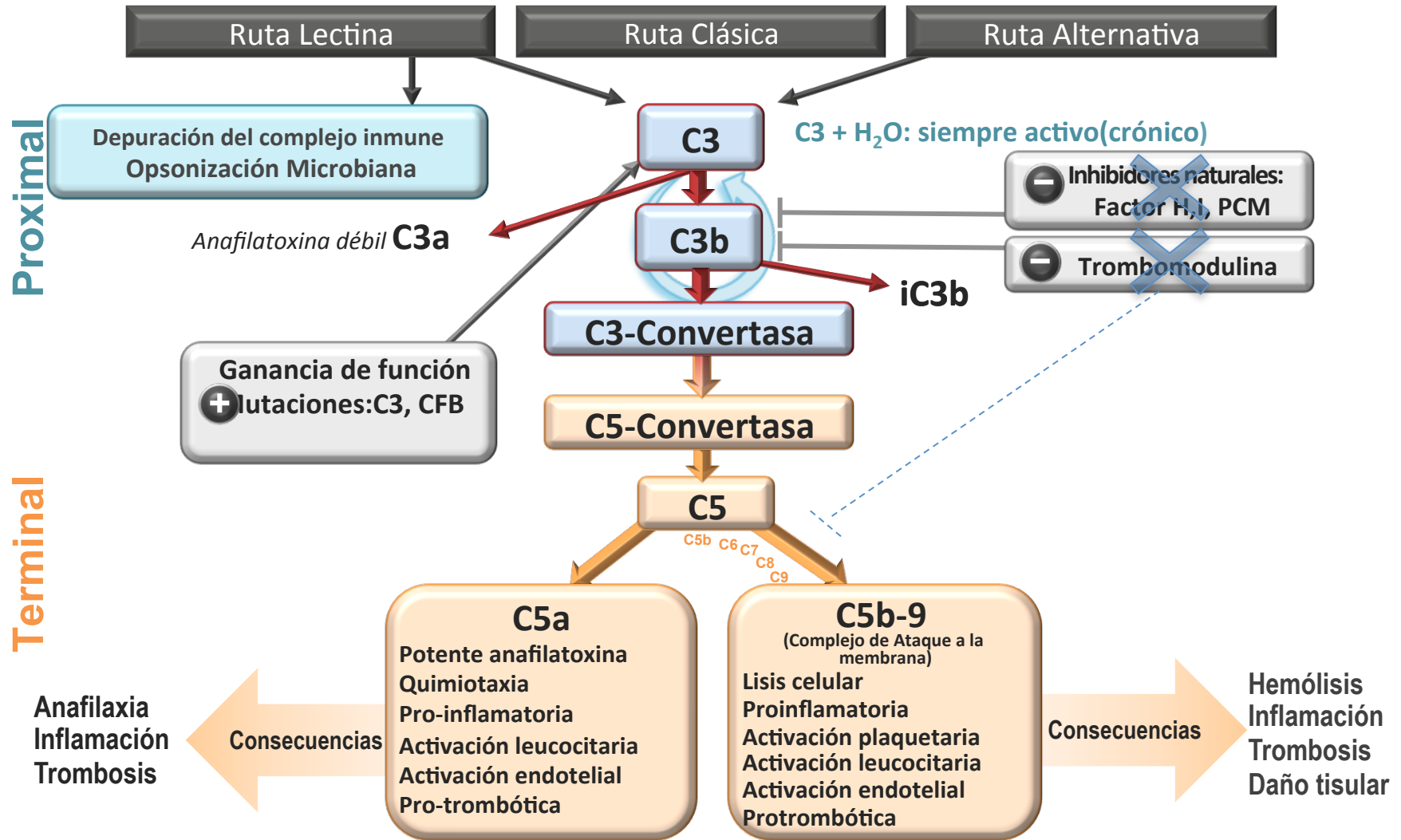
(Complejo de Ataque a la membrana)

Lisis celular
Proinflamatoria
Activación plaquetaria
Activación leucocitaria
Activación endotelial
Protrombótica

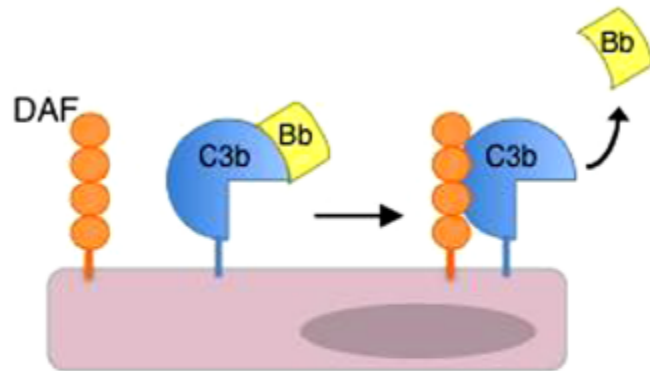
Terminal



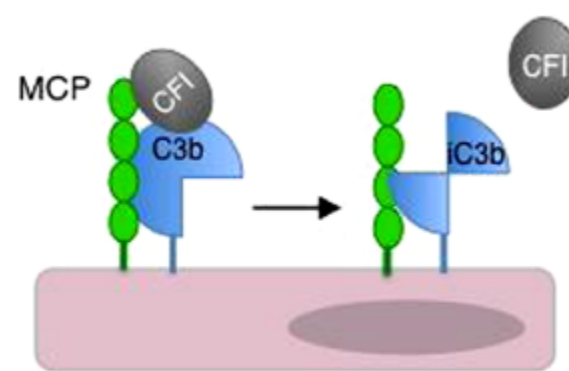
En el SHUa, la actividad crónica no controlada del complemento lleva daños severos



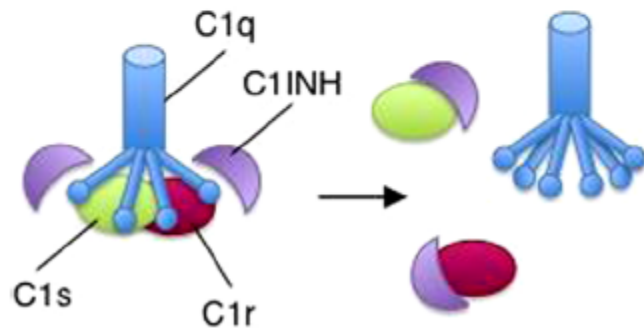
A- Decay-accelerating activity



B- Cofactor-mediated cleavage



C- C1 complex inactivation



D- MAC inhibition

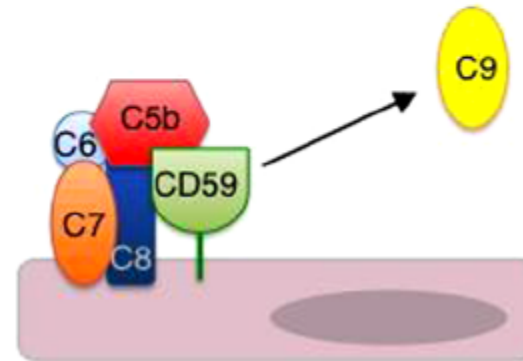


Figure 3. Mechanisms of complement regulation. (A) DAF (or CFH, CR1) destabilizes C3 convertases and accelerates the dissociation of C3bBb (depicted) and C4bC2a. (B) Cofactor activity: MCP (or CFH, CR1) binds to C3b and serves as a cofactor for CFI-mediated cleavage and inactivation of C3b (or C4b). (C) C1 complex inactivation. C1INH binds to C1r and C1s to inactivate the C1 enzyme complex. (D) MAC inhibition: CD59 inhibits C9 association with C5b-8 and prevents MAC (C5b-9) formation.

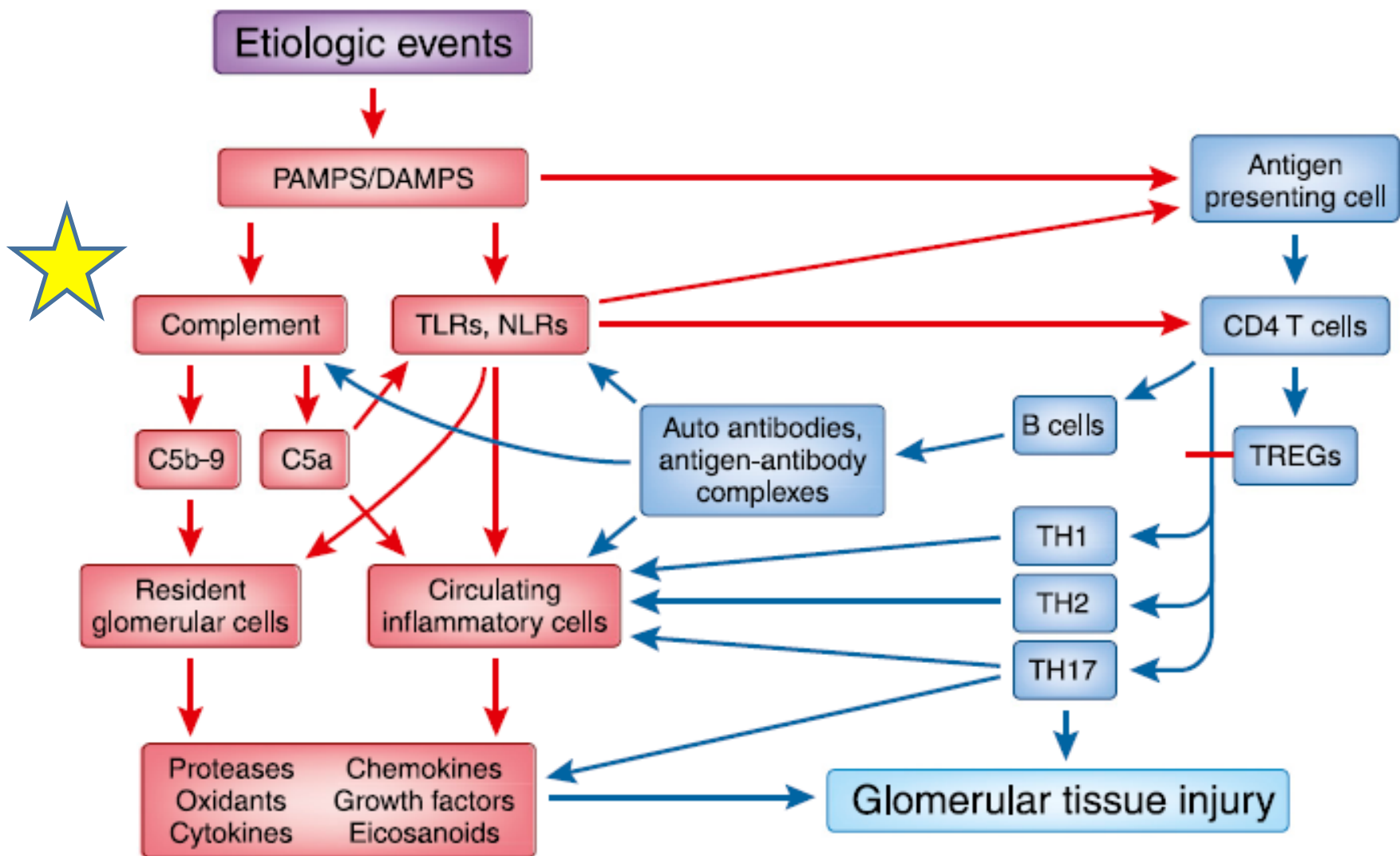


Figure 1. Complement activation and regulation. The proteins relevant to complement activation beginning with ICs in the classic pathway are shown. Regulators of complement activation are in the boxes adjacent to their site(s) of action. Classic pathway activation can recruit the alternative pathway; if intrinsic regulation is overwhelmed, activation and generation of C3a, C3b, C5a, and C5b-9 ensues, each of which has pathophysiologic relevance in kidney diseases. CPN, carboxypeptidase N.

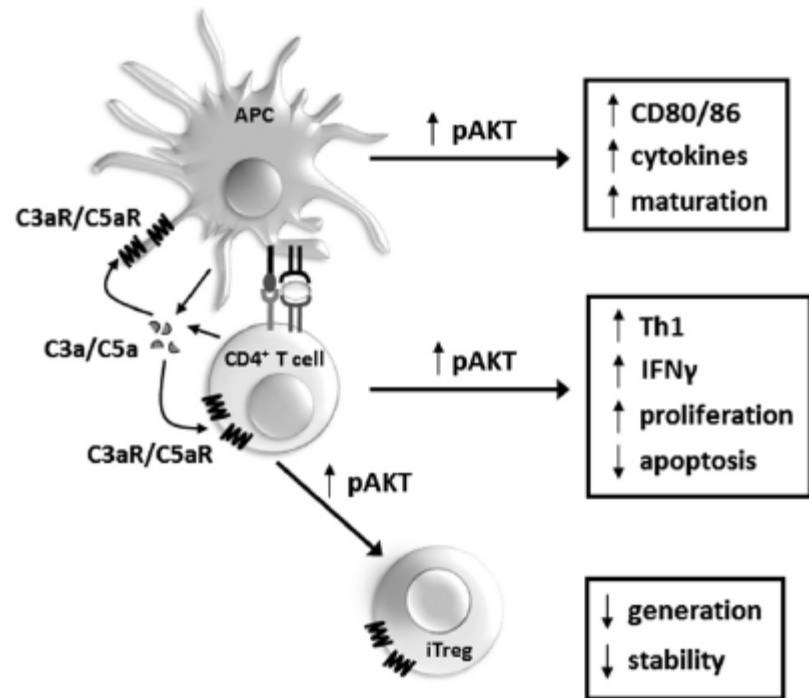


Figure 2. Schematic representation of complement-mediated effects on T cells and APCs. C3aR/C5aR signaling on both APC and T cells activates the AKT pathway by phosphorylation (among other pathways). AKT activation on the APC stimulates maturation, cytokine production, and B7 costimulatory molecule expression. AKT activation on the T cell directly promotes IFN- γ secretion, reduces susceptibility to apoptosis, and promotes cell proliferation and reduces iTreg generation and stability. In this manner, C3aR/C5aR stimulation directly and indirectly promotes T-cell maturation with an expanded effector repertoire. Modified with permission from Kwan et al.⁶⁴

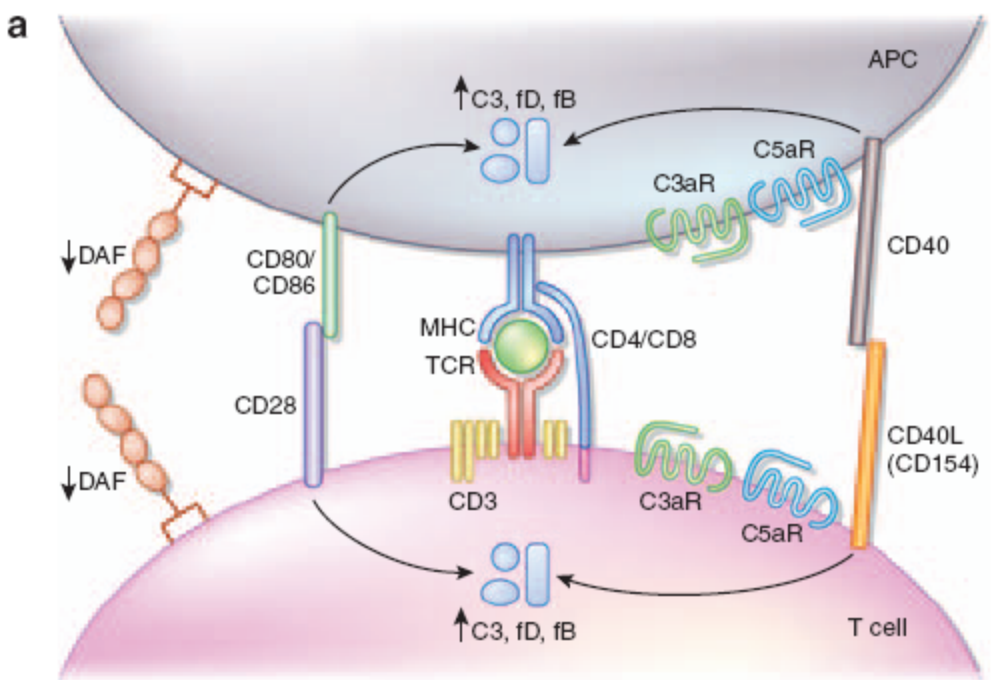
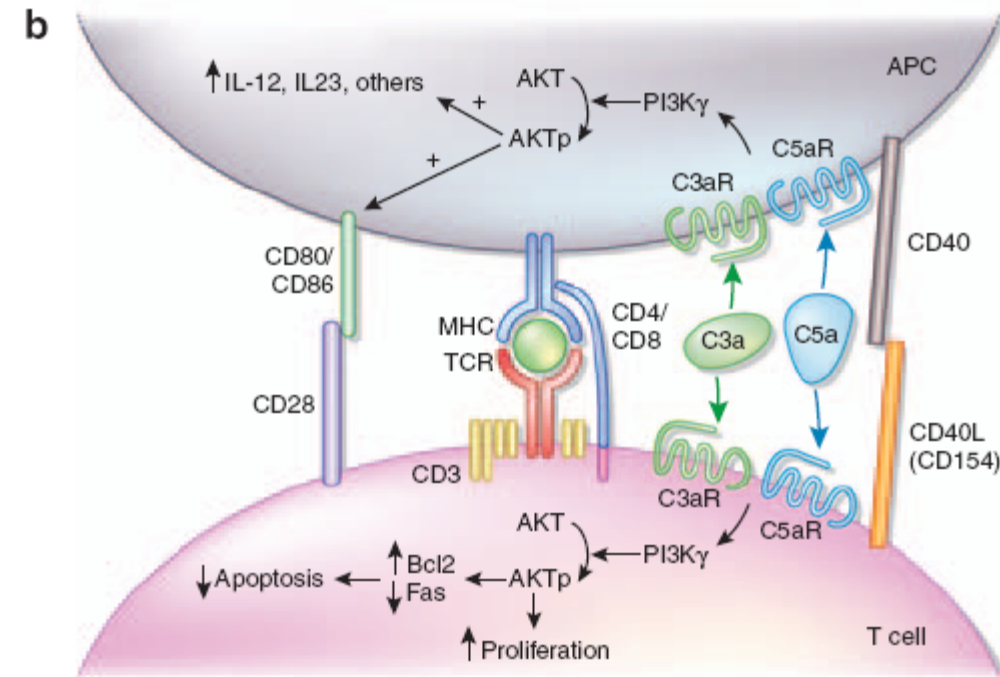


Figure 2 | Schematic depiction of how complement modulates T-cell immunity. Cognate T-cell-APC interactions result in the upregulation and release of alternative pathway complement components by both partners and in the downregulation of (a) cell-surface DAF, which permits local complement activation resulting in the production of (b) C3a and C5a. These split

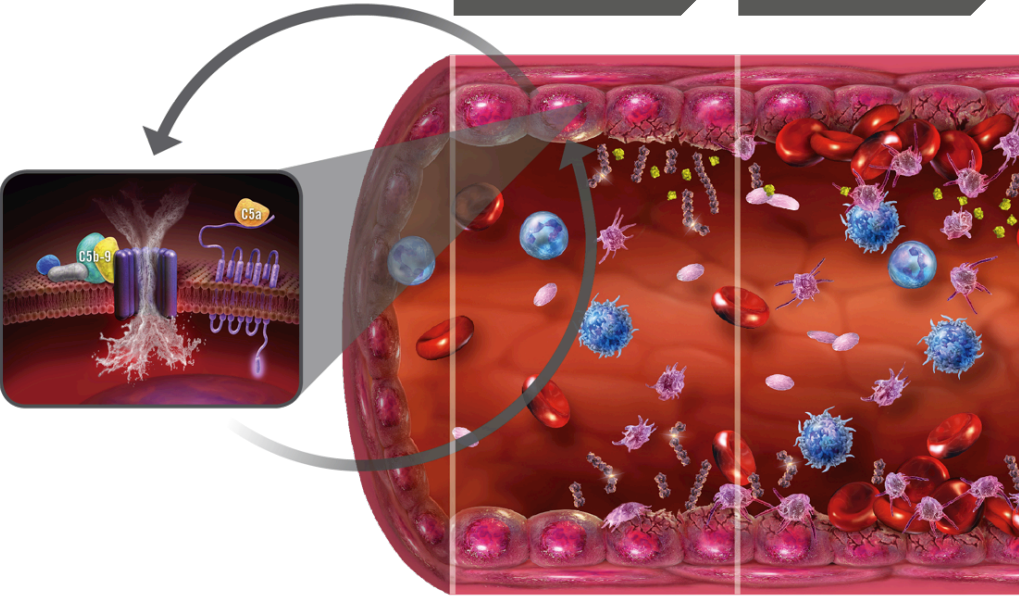


resulting in the production of (b) C3a and C5a. These split products bind to their G-protein-coupled receptors expressed on T cells, signaling through PI3K γ and AKT to induce proliferation and inhibit apoptosis, while simultaneously activating APCs to upregulate B7 and innate cytokine (for example, IL-12) production. APC, antigen presenting cell; DAF, decay-accelerating factor; IL-12, interleukin-12; PI3K γ , phosphoinositide 3-kinase- γ .

La actividad crónica no controlada del complemento resulta en un daño endotelial continuo y riesgo permanente de MAT

Actividad del complemento elevada al inicio

Actividad crónica del complemento



- El ensamblaje de múltiples complejos de C5b-9 en la superficie de las células endoteliales causa lesión endotelial y activación plaquetaria²⁻⁵
- La unión de C5a al receptor de C5a resulta en una disminución de las propiedades anti-complemento y anti-trombóticas del endotelio^{2,4,6,7}

glóbulo rojo

leucocito

plaqueta

leucocito activado

plaqueta activada

vWF

factores protrombóticos

esquistocito



La actividad crónica no controlada del complemento resulta en un daño endotelial continuo y riesgo permanente de MAT

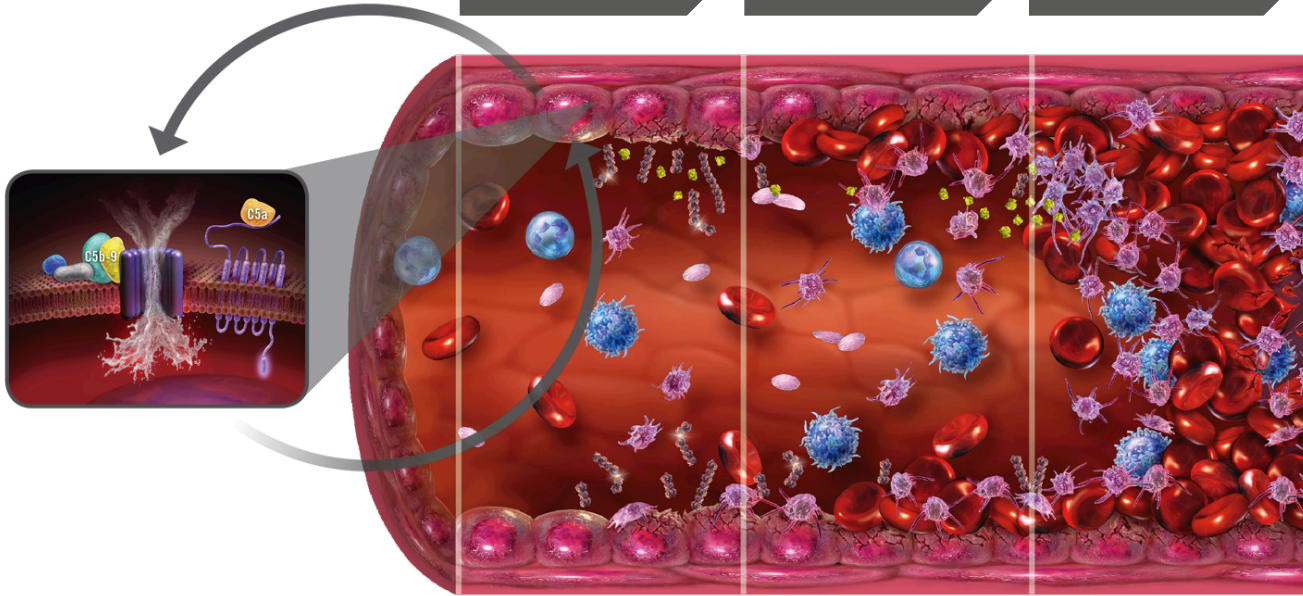
Actividad del complemento elevada al inicio

Actividad crónica del complemento

MAT mediada por el complemento

Células endoteliales interrumpidas:

- Liberan micropartículas activadoras del complemento, lo que resulta en un círculo vicioso de activación endotelial, amplificación del complemento y lesión endotelial permanente^{2,3}
- Liberan proteínas de coagulación pro-trombóticas, activan las plaquetas y reclutan leucocitos, lo que resulta en la formación de trombos en los vasos sanguíneos pequeños en todo el cuerpo²



glóbulo rojo

leucocito

plaqueta

leucocito activado

plaqueta activada

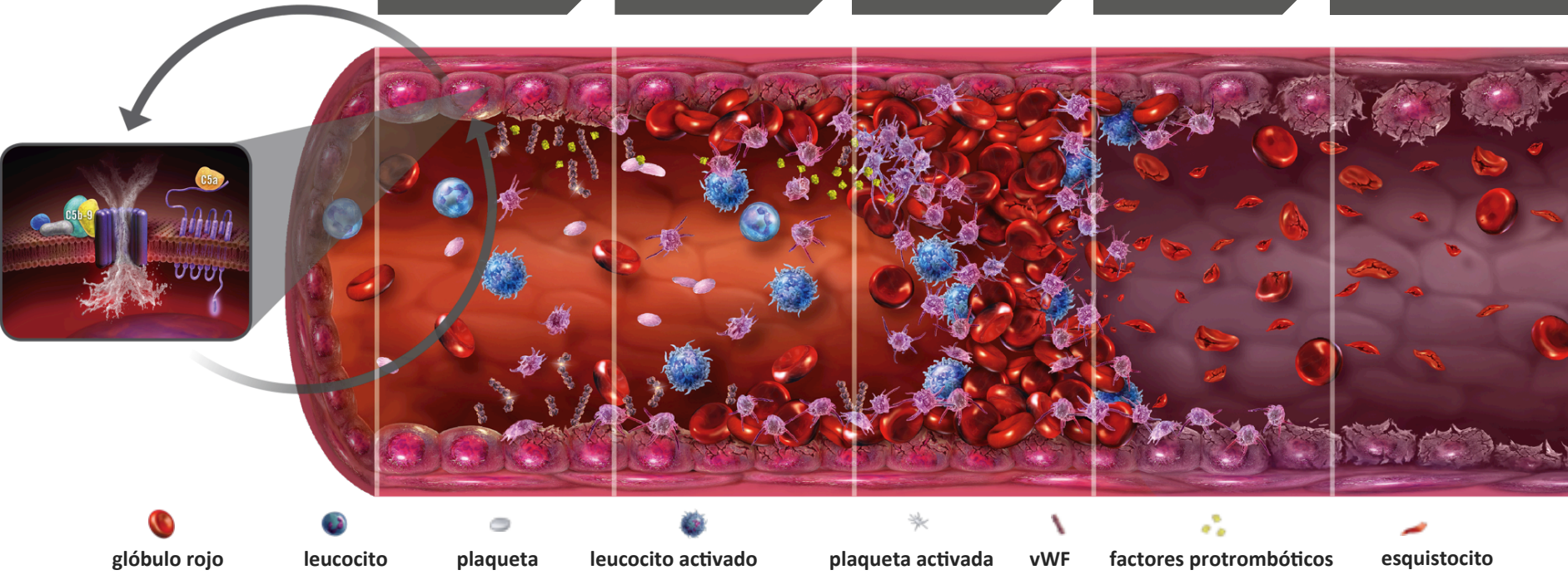
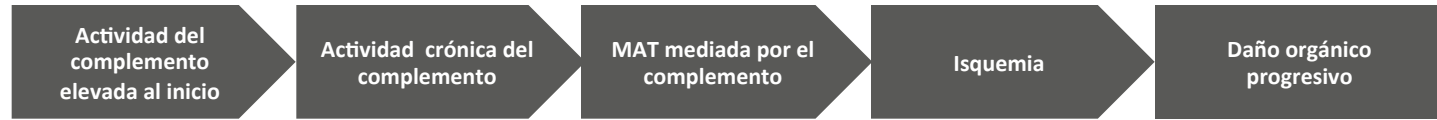
vWF

factores protrombóticos

esquistocito



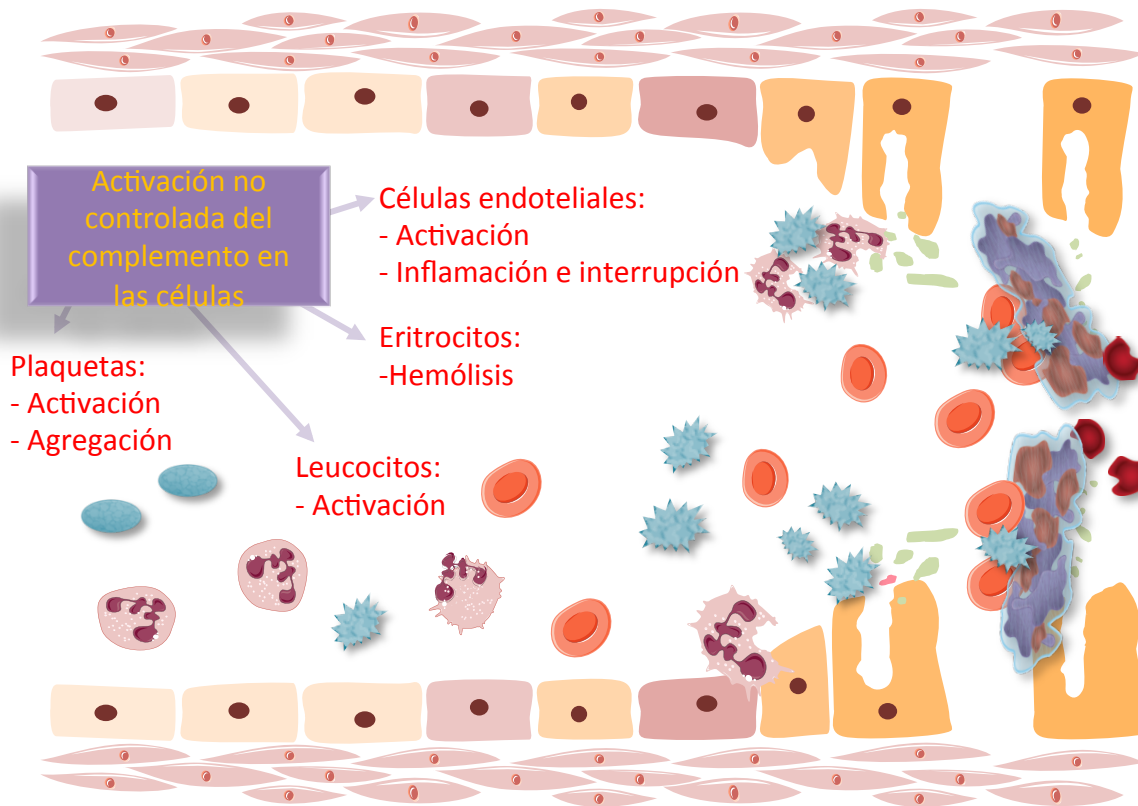
La actividad crónica no controlada del complemento resulta en un daño endotelial continuo y riesgo permanente de MAT



- La actividad no controlada del complemento causa lesión endotelial vascular permanente²⁻⁵
- Las lesiones resultantes de la MAT pueden progresar a daño multiorgánico irreversible²⁻⁵



Activación Crónica No Controlada del Complemento lleva a Daño endotelial y del órgano terminal



Consecuencias clínicas:

Consumo plaquetario
Hemólisis mecánica
Trombos vasculares
Oclusión de vasos
Inflamación
Isquemia



Complicaciones sistémicas multiorgánicas

Table 1 | A molecular and etiologic classification of thrombotic microangiopathy

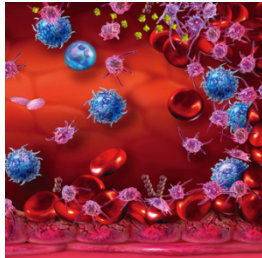
Renal failure: uncommon	Renal failure: common
Defective vWF proteolysis <ul style="list-style-type: none"> Mutations of ADAMTS13 Inhibitory antibodies of ADAMTS13 	Dysregulation of complement activation <ul style="list-style-type: none"> Mutations of CFH, IF, MCP, BF Autoantibodies of CFH
Tumor cell embolism	Shiga toxins (e.g. <i>E. coli</i> O157:H7)
Paroxysmal nocturnal hemoglobinuria	Neuraminidase (e.g. <i>S. pneumoniae</i>)
Infectious vasculitis (e.g. <i>C. difficile</i> , <i>R. rickettsii</i> , <i>B. anthracis</i>)	Drugs (e.g. calcineurin inhibitors, mitomycin, gemcitabine, quinine)
Idiopathic	Autoimmune disorders (e.g. SLE, scleroderma) BM/stem cell transplantation Miscellany (e.g. HELLP syndrome, surgery, pancreatitis) Idiopathic Graft rejection

Diferentes causas diferencian el SHUa de la PTT

MAT mediada por el complemento (SHUa)

Causa subyacente:

Actividad crónica no controlada del complemento¹⁻⁵



Los defectos genéticos en los activadores y/o inhibidores inducen la actividad crónica del sistema del complemento, causando daño celular endotelial y agregación plaquetaria continua¹⁻⁵

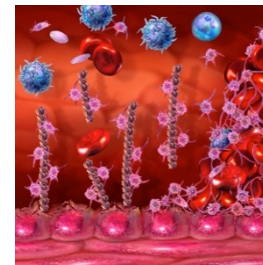
Objetivo del tratamiento:

Regular la activación crónica y no controlada del complemento

MAT mediada por la deficiencia severa de ADAMTS13 (PTT)

Causa subyacente:

Deficiencia severa de ADAMTS13 ($\leq 5\%$)⁶⁻¹⁰



Una actividad insuficiente de ADAMTS13 ($\leq 5\%$) deja el factor de von Willebrand sin escindir, lo que causa excesiva agregación plaquetaria^{8,7,11,12}

Objetivo del tratamiento:

Eliminar los auto-anticuerpos contra ADAMTS13



Differential Diagnosis for Thrombotic Microangiopathies (TMAs)

Thrombocytopenia^{1,7}
Platelet count <150,000
Or
>25% Decrease from baseline



Microangiopathic Hemolysis^{2,7}
Elevated LDH and/or
Decreased Haptoglobin and/or
Schistocytes and/or
Decreased Hemoglobin

Plus One or More of the Following:

Neurological Symptoms^{3,4,9,12}
Confusion^{3,4} and/or
Seizures^{9,12}

Renal Impairment^{5,6,7}
Elevated Creatinine⁶ and/or
Decreased eGFR^{6,7} and/or
Abnormal Urinalysis⁵

Gastrointestinal Symptoms^{7,8,9}
Diarrhea +/- Blood⁸ and/or
Nausea/Vomiting⁹ and/or
Abdominal Pain⁹ and/or
Gastroenteritis^{7,8}

Evaluate ADAMTS13 Activity and Shiga-toxin/EHEC*Test^{10,11}

≤5% ADAMTS13 Activity

>5% ADAMTS13 Activity

Shiga-toxin/EHEC Positive

TTP

aHUS

STEC-HUS

*Shiga-toxin/EHEC test is warranted in history/presence of GI symptoms.

1. Data on file. Alexion Pharmaceuticals, Inc. 2. Noris et al. *NEJM*. 2009;361:1676-1687. 3. Neuhaus et al. *Arch Dis Child*. 1997;76:518-21. 4. Noris et al. *JASN*. 2005;16:1177-1183. 5. Al-Akash et al. *Pediatr Nephrol*. 2011;26:613-619. 6. Sellier-Leclerc AL. *JASN*. 2007;18:2392-2400. 7. Caprioli et al *Blood*. 2006; 108(4)1267-7. 8. Noris M et al. *Clin J Am Soc Nephrol*. 2010;5:1844-1859. 9. Dragon-Durey et al. *J Am Soc Nephrol*. 2010;21:2180-2187. 10. Tsai H-M. *Int J Hematol*. 2010;91:1-19. 11. Bitzan M. *Semin Thromb Hemost*. 2010;36:594-610. 12. Davin et al. *Am J Kid Dis*. 2010;55:708-777.

La MAT sistémica mediada por el complemento afecta en forma sistémica

Renal: Más del 50% de los pacientes progresan a ERET¹

- Elevada creatinina^{2,3}
- Proteinuria⁴
- Edema,³ hipertensión maligna⁵
- Disminución en TFG⁶

SNC: Hasta 48% de los pacientes presentan síntomas neurológicos⁴

- Desorientación⁷
- Apoplejía⁷
- Encefalopatía⁵
- Convulsión⁴

Blood:

- Trombocitopenia¹
- Disminución en haptoglobina¹
- Elevada LDH¹
- Disminución en hemoglobina¹
- Esquistocitos¹

Visual:

- Oclusión ocular⁸



Cardiovascular: Hasta 43% de los pacientes experimentan síntomas cardiovasculares⁴

- Infarto del miocardio^{9,16}
- Hipertensión¹⁰
- Vasculopatía difusa⁶
- Gangrena periférica^{11,16}

Gastrointestinal: 37% de los pacientes experimentan síntomas GI¹²

- Diarrea¹³
- Colitis⁷
- Náusea/Vómito¹⁴
- Pancreatitis¹⁴
- Dolor abdominal⁷
- Gastroenteritis⁴
- Necrosis hepática⁴

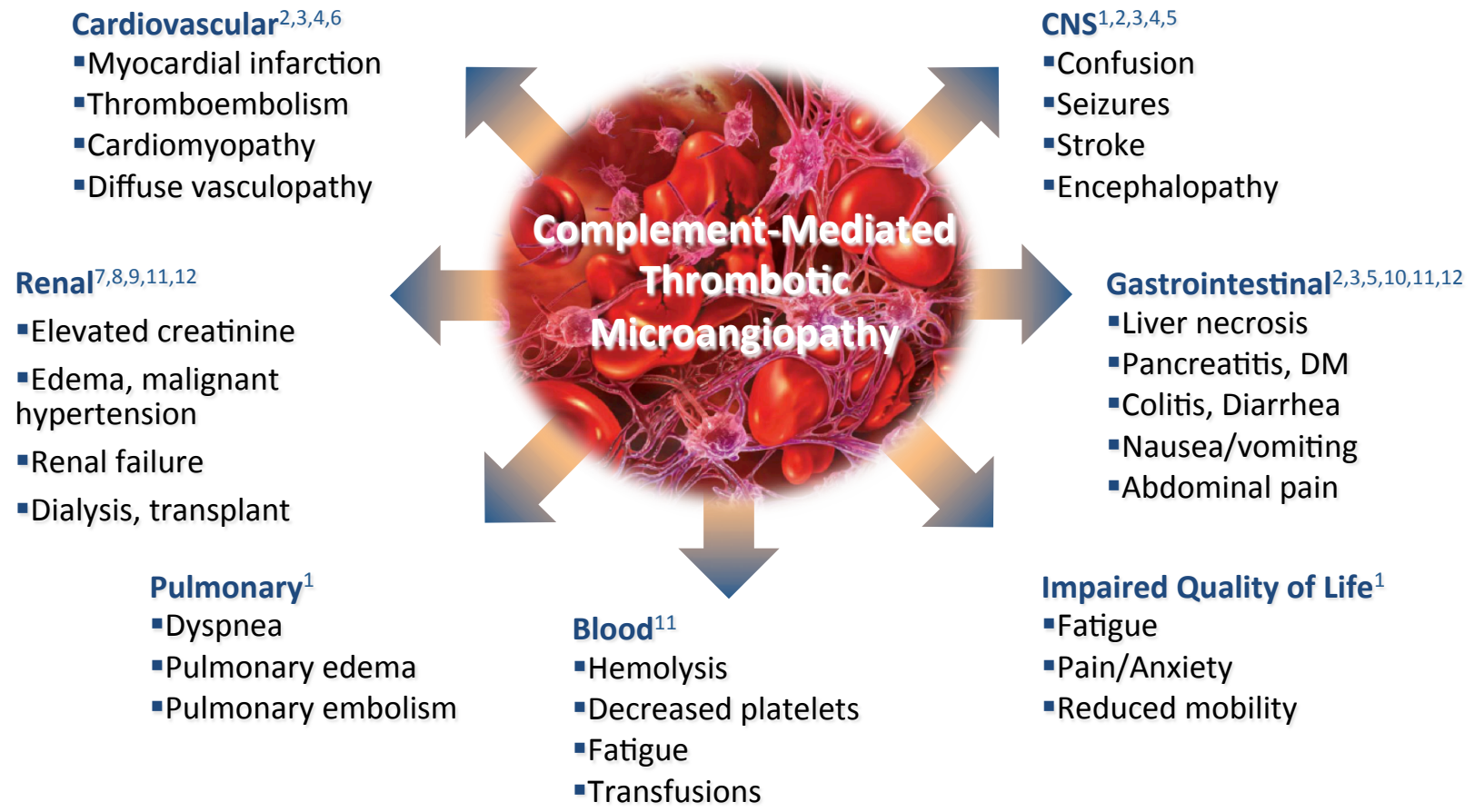
Pulmonar:

- Disnea⁹
- Hemorragia pulmonar¹⁵
- Edema pulmonar⁹

- Una evaluación clínica completa debe evaluar múltiples sistemas orgánicos



Complement-Mediated TMA Leads to the Morbidities and Mortality in aHUS



1. George et al. *Blood*. 2010;116:4060-69. 2. Hosler et al. *Arch Pathol Lab Med*. 2003;127:834-39. 3. Noris et al. *CJASN*. 2010;10:1844-59. 4. Neuhaus et al. *Arch Dis Child*. 1997;76:518-21. 5. Vesely et al *Blood*. 2003;102:60-8. 6. Sallee et al. *Nephron Dial Trans*. 2010; 25:2028-32. 7. Kose et al. *Semin Thromb Hemost*. 2010;36:669-72. 8. Davin et al. *Am J Kid Dis*. 2010;55:708-77. 9. Caprioli et al. *Blood*. 2006;108:1267-7. 10. Dragon-Durey et al. *J Am Soc Nephrol*. 2010;21:2180-87. 11. Loirat et al. *Pediatr Nephrol*. 2008;23:1957-72. 12. Stahl et al. *Blood*. 2008;111:5307-15.

Seminars in NEPHROLOGY

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Introduction: Complement-Mediated Kidney Diseases

Table 1. Triggers of aHUS

Trigger	Reference
Non-Stx toxin diarrheal illnesses	51,94,95
Norovirus	161,162
<i>Campylobacter upsaliensis</i>	163
<i>Clostridium difficile</i>	164
Respiratory infections	51
<i>Bordetella pertussis</i> infection	10,165
<i>Streptococcus pneumonia</i>	166
<i>Haemophilus influenzae</i>	10
Other bacterial	
<i>Fusobacterium necrophorum</i>	167
Viral illnesses	
Varicella	168
Cytomegalovirus	169
Influenza H1N1	170
Hepatitis A	171
Hepatitis C	172
Human immunodeficiency virus	173
Coxsackie B virus	174
Epstein–Barr virus	175
Dengue	176
HHV6	177
Human parvovirus B19	178
Parasites	
<i>Plasmodium falciparum</i>	179
Pregnancy	51,98,180

Drugs	
Cisplatin	181
Gemcitabine	182
Mitomycin	183
Clopidogrel	184
Quinine	185,186
Interferon-alfa, -beta	187,188
Anti-vascular endothelial growth factor	189
Campath	190
Cyclosporin tacrolimus	191
Ciprofloxacin	192
Oral contraceptives	193–195
Illicit drugs (eg, cocaine, heroin, ecstasy)	196
Autoimmune	
Anticardiolipin	197
C3Nef	198
Systemic lupus erythematosus	199
Vaccination	
Hepatitis B	10
Bone marrow transplantation	200
Malignancy (gastric, breast, prostate, lung, colon, ovarian, pancreatic, lymphoma)	201
Combined methylmalonic aciduria and homocystinuria	202

Table 2. Complement Regulatory Proteins in Human Beings and Their Functions

Regulator	Function	Location
C1 inhibitor (C1-INH)	Inactivates C1r and C1s, MASP-1, and MASP-2	Plasma
MCP	Cofactor for factor I–mediated cleavage of C3b and C4b	Membrane-bound
DAF	Destabilizes C3/C5 convertases of the CP and AP (decay accelerating activity)	Membrane-bound
CR1	Decay accelerating activity as well as cofactor activity for factor I–mediated cleavage of C3b and C4b	Membrane-bound
C4 binding protein (C4BP)	Binds to C4b; decay accelerating and cofactor activity	Plasma
Factor H	Binds to C3b; has decay accelerating activity of the AP C3 and C5 convertases and cofactor activity	Plasma
Thrombomodulin	Increases CFH cofactor activity, activates TAFI-mediated C3a and C5a inactivation	Membrane-bound
Factor I	Degrades C3b and C4b aided by cofactors	Plasma
CD59	Blocks the C9 association with C5b-8 to prevent C5b-9 formation on host cells	Membrane-bound
S-protein (vitronectin)	Binds to C5b-7 and inhibits C9 polymerization	Plasma
Clusterin (SP-40,40)	Binds to C5b-7 and inhibits generation of C5b-9	Plasma

Abbreviation: TAFI, thrombin activatable fibrinolysis inhibitor.

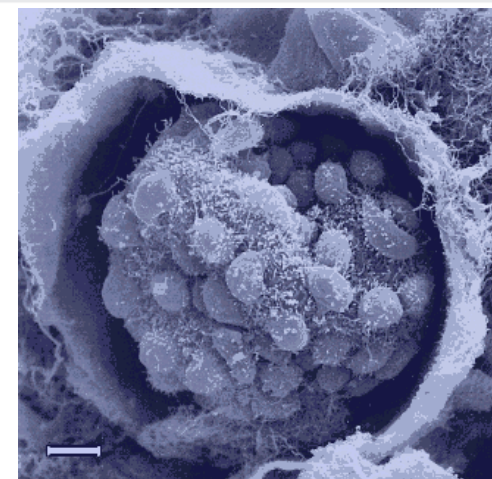
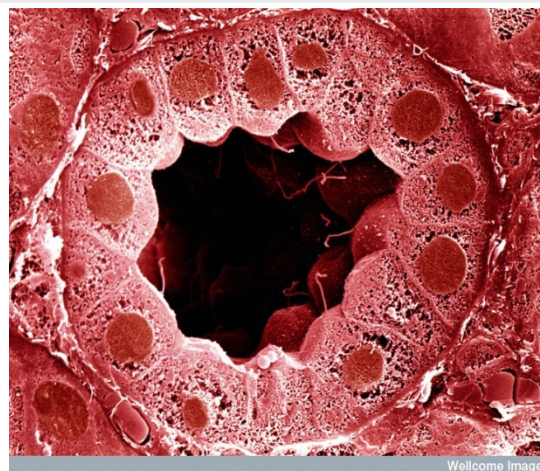
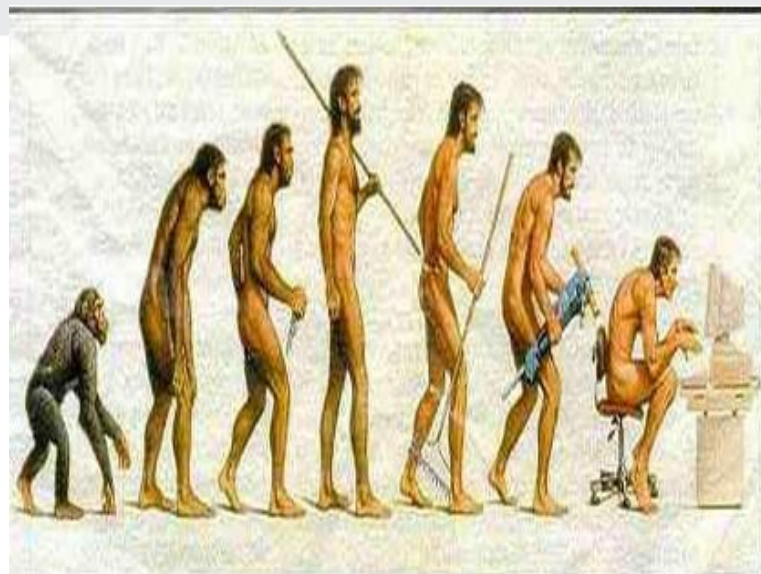
Table 2. Summary Data for Genetic Mutations in aHUS

Mutations	CFH [†]		MCP		CFI		C3		THBD						
	Ped	Ad	Ped	Ad	Ped	Ad	Ped	Ad	Ped	Ad					
Reference	49	51	49	51	49	51	49	51	49	51					
Percentage	27.5	24	9.3	7	8.4	4	8.4	4	0	5					
Type I mutation	56%	14% [†]	91%	88% [†]	42%	9% [†]	-	-	N/A	0% [†]					
Type II mutation	44%	86% [†]	9%	12% [†]	58%	91% [†]	-	-	N/A	100% [†]					
Homozygous	1.8%	4%	2.8%	1%	0%	0%	0%	0%	N/A	0%					
Heterozygous	25.7%	20%	6.5%	6%	8.4%	4%	8.4%	4%	N/A	5%					
Low C3 levels	70%	52%	47%	0%	11%	27%	60%	50%	20%	70%	85%	73%	N/A	N/A	50%
ESRF	52% [‡]	65% [‡]	53% [§]	17% [‡]	63% [‡]	6% [§]	17% [‡]	83% [‡]	60% [§]	43% [‡]	63% [‡]	67% [§]	N/A	N/A	23% [§]
Death	11% [‡]	2.5% [‡]	23% [§]	0% [‡]	0% [‡]	0% [§]	33% [‡]	0% [‡]	0% [§]	0% [‡]	0% [‡]	0% [§]	N/A	N/A	31% [§]
Death/ESRF	63% [‡]	68% [‡]	77% ^c	17% [‡]	63% [‡]	6% [§]	50% [‡]	83% [‡]	60% [§]	43% [‡]	63% [‡]	67% [§]	N/A	N/A	54% [§]

Table 3. Summary of the Main Complement-Associated Renal Diseases

Disease	Pathogenesis	Complement Pathway
Lupus nephritis	Anti-DNA antibodies, accumulation of apoptotic cells	CP
Post-streptococcal glomerulonephritis	Antibody mediated, circulating or planted antigens	CP
Goodpasture syndrome	Anti-GBM antibodies	CP
IgA nephropathy	Deposition of polymeric IgA	CP/AP
ANCA-associated vasculitis	Antibodies directed against neutrophil components	CP/AP
Membranous nephritis	Antibody-antigen complexes subepithelially	CP AP/LP
MPGN I	Immune complexes, C3NeF, complement gene mutations	CP/AP
C3 glomerulopathies	C3NeF, complement gene mutations	AP
STEC-HUS	Shiga-toxin mediated endothelial injury/activation	AP
aHUS	Complement gene mutations, anti-CFH antibodies	AP
Tubulointerstitial injury in proteinuric progressive glomerulopathies	Proteins (including complement components) abnormally ultrafiltered by the glomeruli	AP
I/R injury	Ischemic tissue injury, oxygen radicals	AP/LP

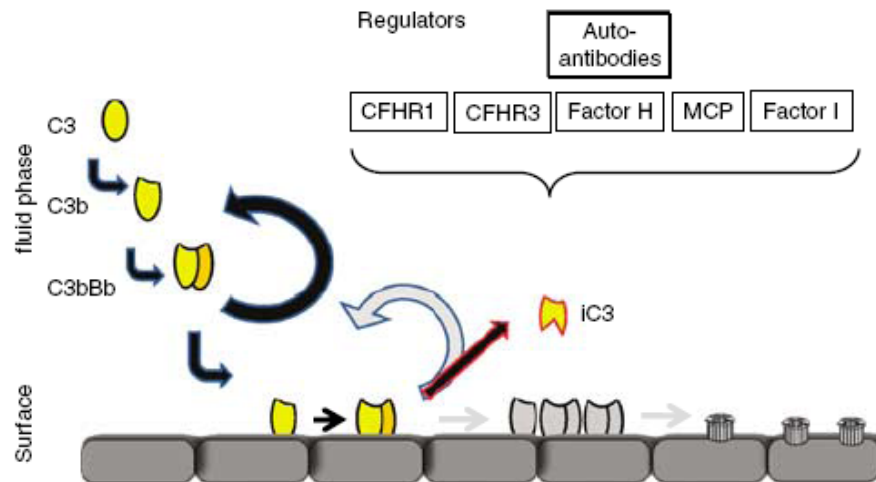
Seminars in Nephrology, Vol 33, No 6, November 2013, pp 479–492



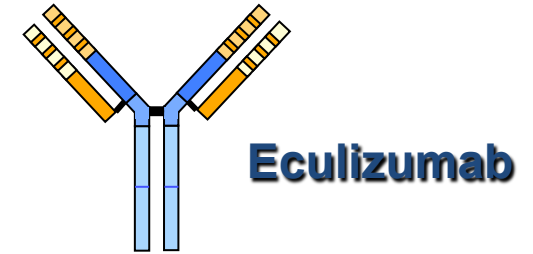
Desórdenes del Complemento

- 30% mutaciones del gen que codifica la porción soluble del factor H (FH)
- 10% autoanticuerpos contra FH (mas frecuente en niños), asociado a deficiencia de la proteína relacionada al factor H
- 10% mutaciones del CD46 (MCP)
- 10% mutaciones del factor I (FI)
- Mutaciones activadoras del factor B y C3

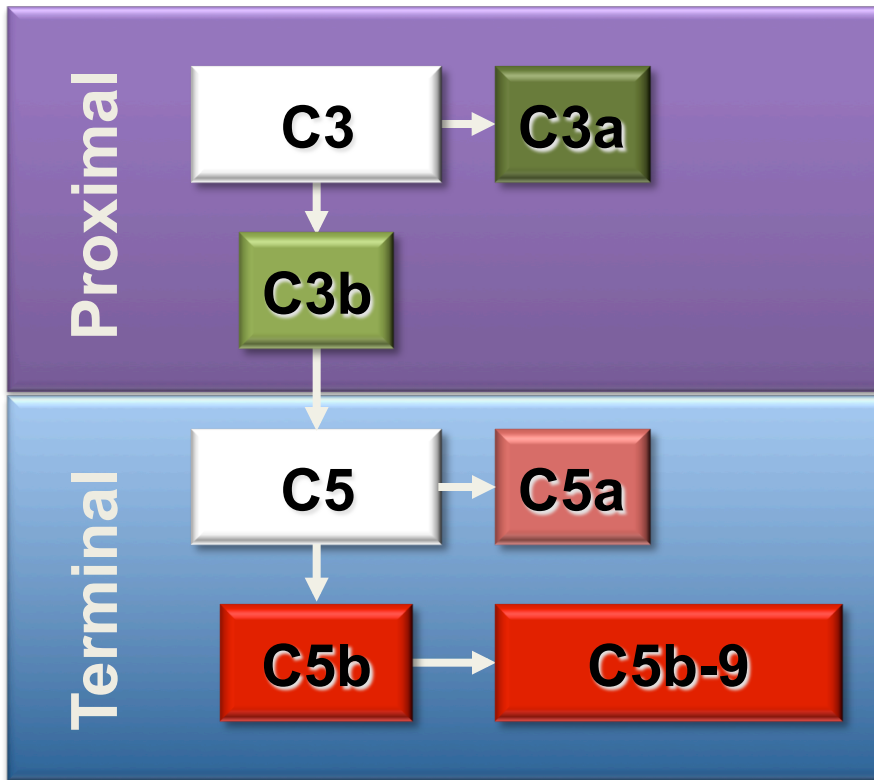
LAS MUTACIONES O POLIMORFISMOS DE MÁS DE UNO DE ESTOS GENES AUMENTAN LAS POSIBILIDADES DE SUH ATIPICO



El eculizumab bloquea la fase terminal de activación del complemento



Complement Cascade



- Soliris binds with high affinity to C5
- Terminal complement - C5a and C5b-9 activity blocked
- Proximal functions of complement remain intact
 - Weak anaphylatoxin
 - Immune complex clearance
 - Microbial opsonization

Novel roles of complement in renal diseases and their therapeutic consequences

Takehiko Wada¹ and Masaomi Nangaku¹

¹*Division of Nephrology and Endocrinology, University of Tokyo School of Medicine, Bunkyo-ku, Tokyo, Japan*

Table 1 | Representative abnormalities in complement leading to renal disease

Components/related molecules	Diseases/phenotypes	Species	Notes
Complement C3	C3 glomerulopathy (DDD) aHUS	Human	Mutation (923ΔDG) Mutations
Factor H	C3 glomerulopathy (DDD/C3GN) aHUS	Human	Mutations Mutations
Factor I	C3 glomerulopathy (C3GN) aHUS	Human	Mutations Mutations
MCP	aHUS	Human	Mutations
Factor B	aHUS	Human	Mutations
CFHR5	Familial C3 glomerulopathy (CFHR5 nephropathy)	Human	Mutation (internal duplication)
CFHR3-1	Familial C3 glomerulopathy	Human	Mutation (hybrid gene)
CFHR1/3	IgA nephropathy aHUS	Human	Combined deletion Combined deletion
Factor B autoantibody	C3 glomerulopathy (DDD)	Human	Positive in serum
Factor H autoantibody	C3 glomerulopathy (DDD/C3GN)	Human	Positive in serum
C3Nef	C3 glomerulopathy (DDD/C3GN)	Human	Positive in serum
Bb (activated factor B)	HUS ANCA-associated vasculitis	Human	Plasma level ↑ Plasma level ↑
Soluble C5b-9	HUS TTP ANCA-associated vasculitis	Human	Plasma level ↑ Plasma level ↑ Plasma level ↑
C3a	ANCA-associated vasculitis TTP	Human	Plasma level ↑ Plasma level ↑
C5a	ANCA-associated vasculitis	Human	Plasma level ↑
C1q/C1qR	C1q nephropathy	Human	Positive in glomeruli
Properdin	TI injury due to massive proteinuria	Rat	Binding to tubular heparan sulfate
C5	ANCA-associated vasculitis	Mouse	Deficient mice were protected from disease
Factor B	ANCA-associated vasculitis	Mouse	Deficient mice were protected from disease
C3aR	TI inflammation IRI	Mouse	Deficient mice were protected from disease Deficient mice were protected from disease
C5aR	IRI	Mouse	Deficient mice were protected from disease
Factor H	IRI	Mouse	Deficient mice were protected from disease
C5b-9	IRI	Mouse	Deficient mice were protected from disease
CD59	IRI	Mouse	Deficient mice were protected from disease

Table 1. Most common complement profiles and autoimmune features in GN

Disease	Serum C Profile	Autoimmune Features
Poststreptococcal GN	AP or MBL normal C1q, low C3-C9	Anti-C1q, IgG AECA*, anti-DNA, ANCA, protein disulfide Isomerase (PDI), cardiac myosin
IgAN	Normal	Antiglycan, endothelial cell, mesangial cell, IgG, C1q
Anti-GBM nephritis	Normal	Anti-GBM, ANCA (20%), anti-C1q
ANCA-positive GN	Normal	Anti-MPO, PR3, cPR3, NET, DNA, endothelial cell, ? LAMP2
Lupus nephritis	CP, low C1q-C9	Anti-dsDNA, annexin, MPO, PR3, nucleosome, IgG, C1q, C1s, C1-INH, C4, cardiolipin, MBL, NET, H-ficolin, C3Nef
MPGN I	CP, low C1q-C9	Anti-C3 Nef, C4 Nef, C1q
MCD/FSGS	Normal	None
Membranous nephropathy	Normal	Anti-PLA2R, DNA, NEP, aldose reductase, SOD2, C1q
DDD	AP, normal C1q, low C3-C9	Anti-C3Nef, C4 Nef, CFH, factor B, C1q
C3 nephropathy	AP, normal C1q, low C3-C9	C3Nef, CFH, factor B

CP, classic pathway; AP, alternative pathway; MBL, mannose binding lectin pathway; LAMP2, lysosomal membrane protein 2.

C3 glomerulopathy: what's in a name?

Vivette D. D'Agati¹ and Andrew S. Bomback²

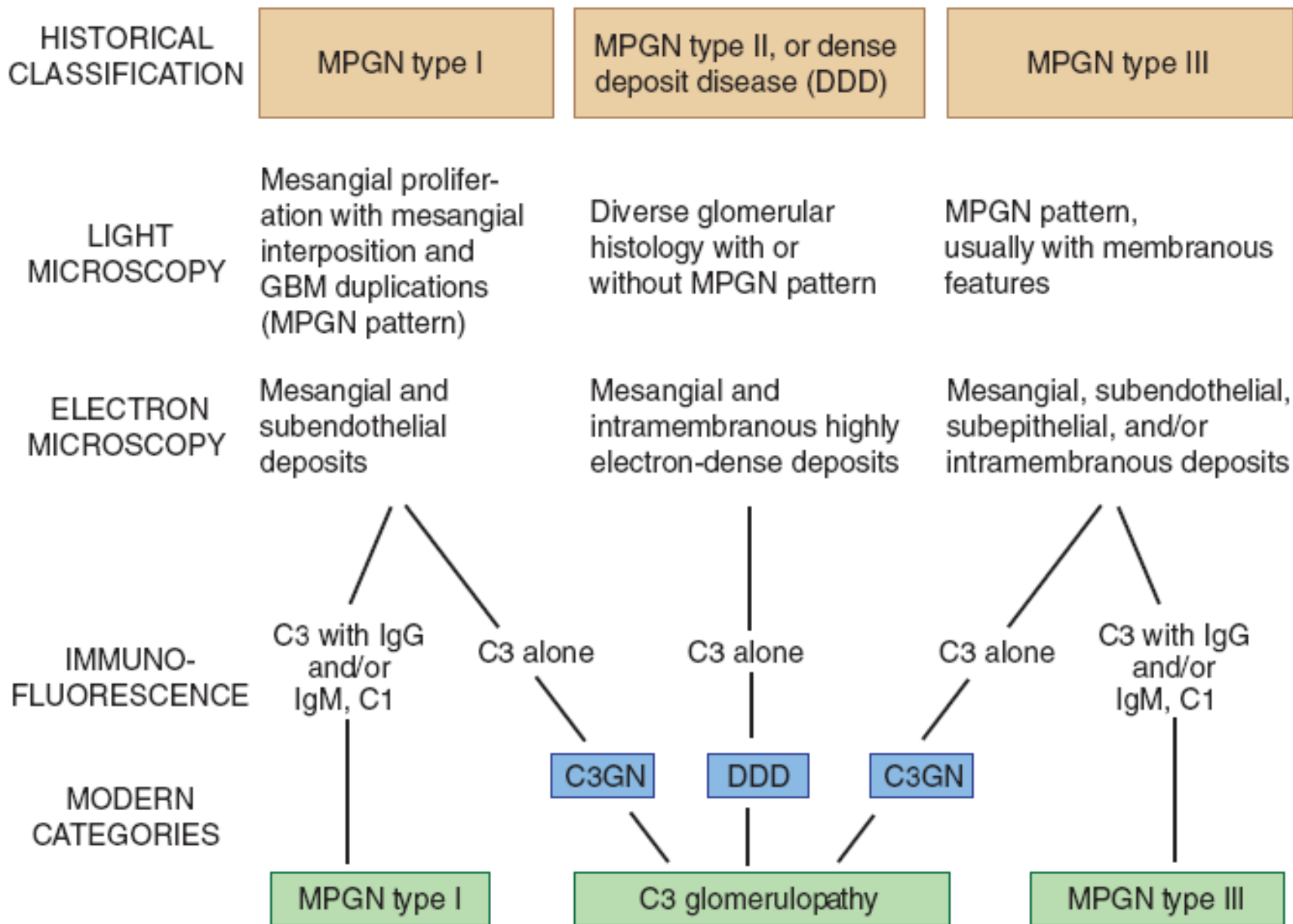
Kidney International (2012) **82**, 379–381. doi:10.1038/ki.2012.80

GLOMERULOPATÍA POR C3

DDD

Glomerulonefritis x C3

CFRH5



Use of eculizumab for atypical haemolytic uraemic syndrome and C3 glomerulopathies

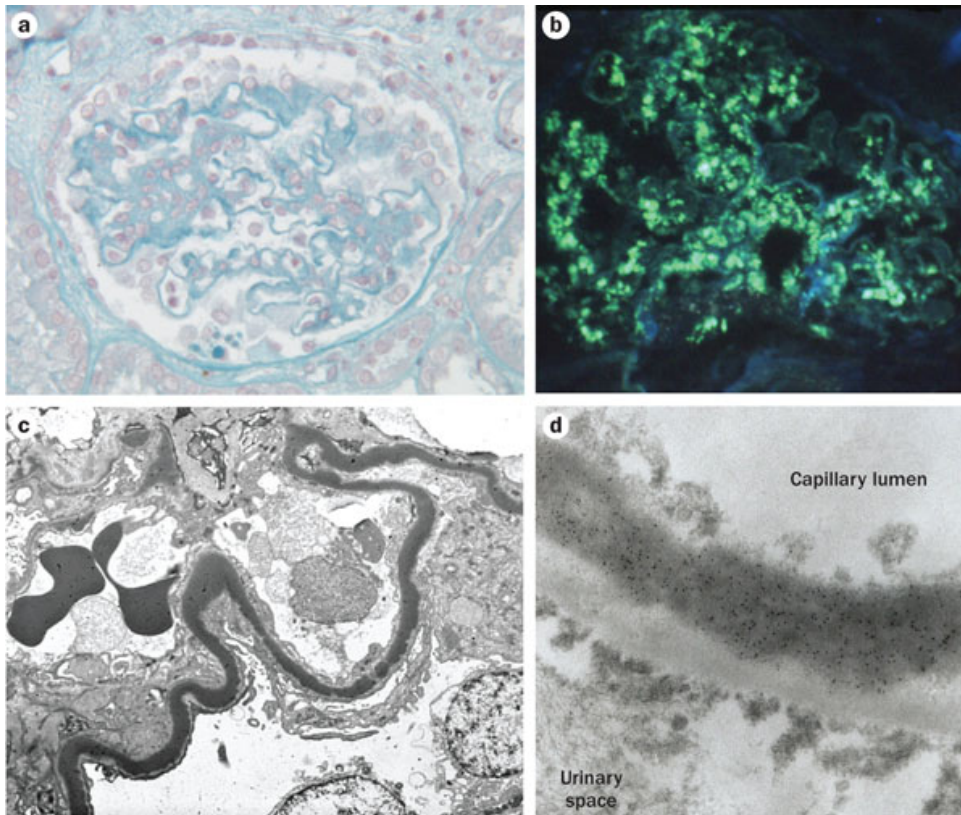
Julien Zuber, Fadi Fakhouri, Lubka T. Roumenina, Chantal Loirat and Véronique Frémeaux-Bacchi on behalf of the French Study Group for aHUS/C3G

Zuber, J. et al. *Nat. Rev. Nephrol.* **8**, 643–657 (2012)

NO ES TRATAMIENTO DE PRIMERA LÍNEA Y ES OFF-LABEL AL AÑO 2014

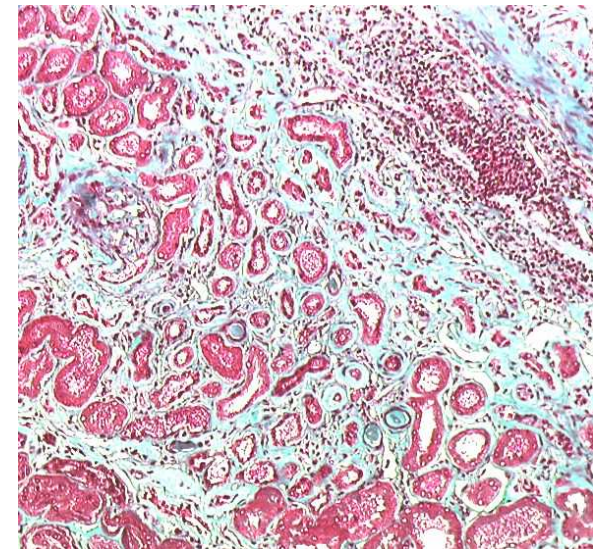
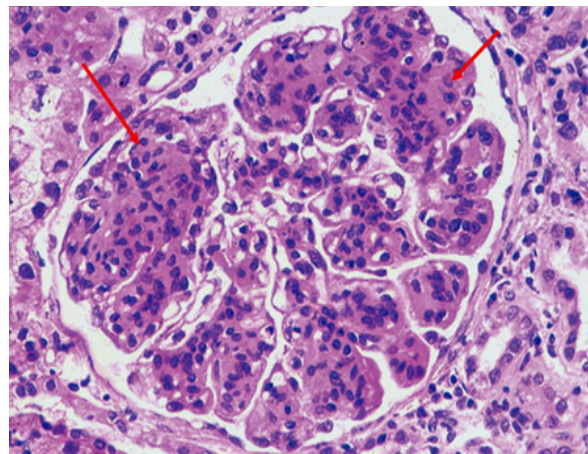
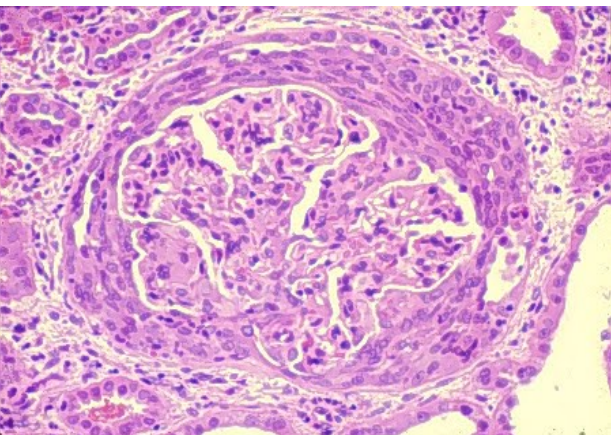
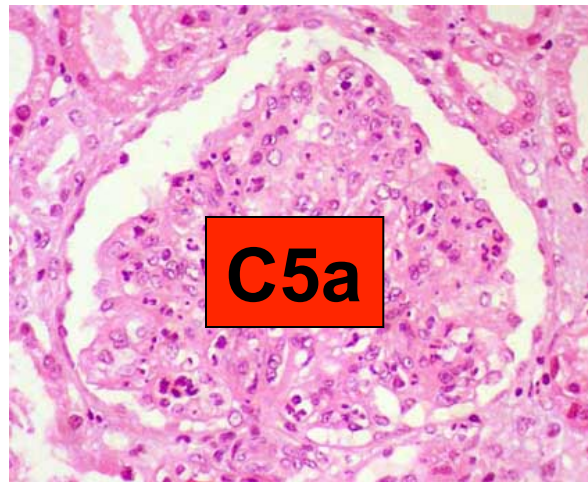
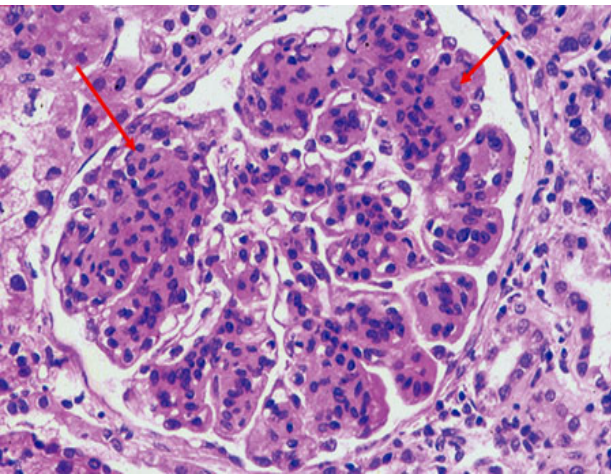
El término 'glomerulopatía por C3 abarca un espectro heterogéneo de nefropatías con base inmunológica que comparten un rasgo histopatológico:
Los depósitos glomerulares de C3.

La disregulación de la vía alterna del complemento y la subsecuente siembra glomerular de los productos de degradación de la fracción C3 factor, sobre todo de C3d, son los eventos primarios que llevan al desarrollo de las glomerulopatías por C3.



Las lesiones glomerulares de tipo inflamatorio y necróticas (expansión mesangial y proliferación endocapilar y extracapilar), que son en general gatilladas por la liberación de C5a, juegan un rol mayor en la progresión que lleva a la fibrosis y a la disfunción del riñón.

Las semilunas y en menor grado la proliferación mesangial, y no el tipo de glomerulopatía por C3, determinan el riesgo de enfermedad renal terminal y el riesgo de recurrencia en el injerto.



Los blancos de tratamiento en la glomerulopatías por C3 pueden dirigirse a la lesión inicial de los depósitos granulares glomerulares de C3 y/o a los cambios glomerulares inflamatorios subsecuentes.

La inhibición de la parte final de la vía del complemento a nivel del componente C5 atenúa los cambios inflamatorios glomerulares pero no alteran a los depósitos de C3 o el desarrollo de cambios en las paredes capilares

No hay drogas que bloqueen específicamente a la convertasa de C3 de la vía alterna.

Pero existe el bloqueo de la vía común final del complemento con el anticuerpo anti-C5, el eculizumab, el cual puede ser una terapia potencial para las glomerulopatías por C3.

La terapia anti-C5 ataca al componente inflamatorio de la glomerulopatía por C3, el factor C5a.

Sin embargo, las tinciones para C3 y para C5b–9 permanecen sin cambios en las biopsias post-eculizumab, indicando que el eculizumab no puede acelerar el clearance del complejo C5b–9 anterior al tratamiento.

Más aún, la inflamación glomerular y los cambios estructurales pueden prolongar la vida media de la fracción C5b–9 en el tejido renal.

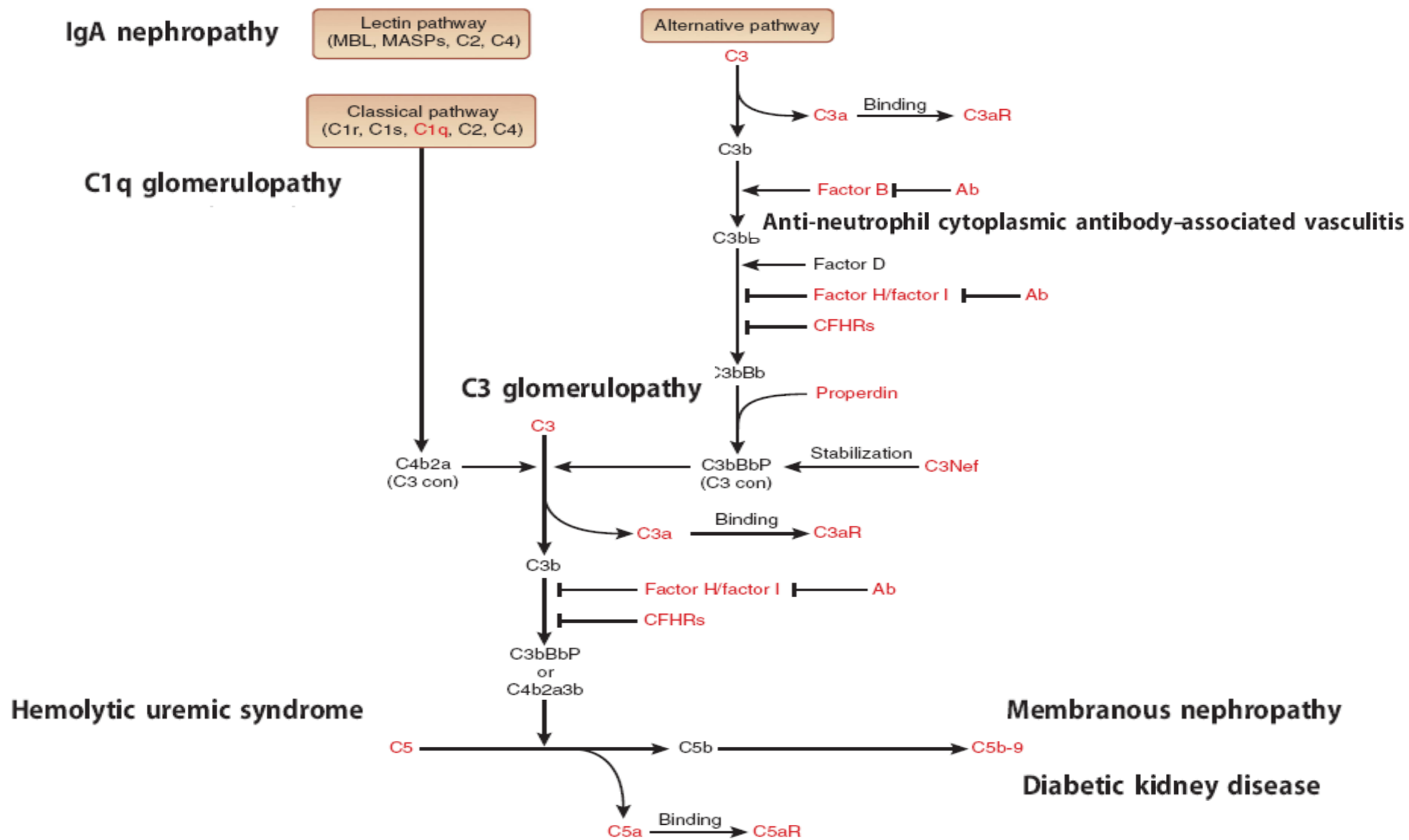


Figure 1 | Complement components and related molecules implicated in abnormal activation. The pathways of complement activation are depicted, with particular emphasis on the alternative pathway. The molecules highlighted in red are the complement components and the related molecules specifically discussed in this review. Ab, antibody; C3 con, C3 convertase; C3Nef, C3 nephritic factor; C3aR/C5aR, C3a receptor/C5a receptor; CFHRs, complement factor H-related proteins; MASPs, mannose-binding protein-associated serine proteases; MBL, mannose-binding lectin.

C + IgS

PENSAR EN VÍA CLÁSICA

C3

PENSAR EN VÍA ALTERNA

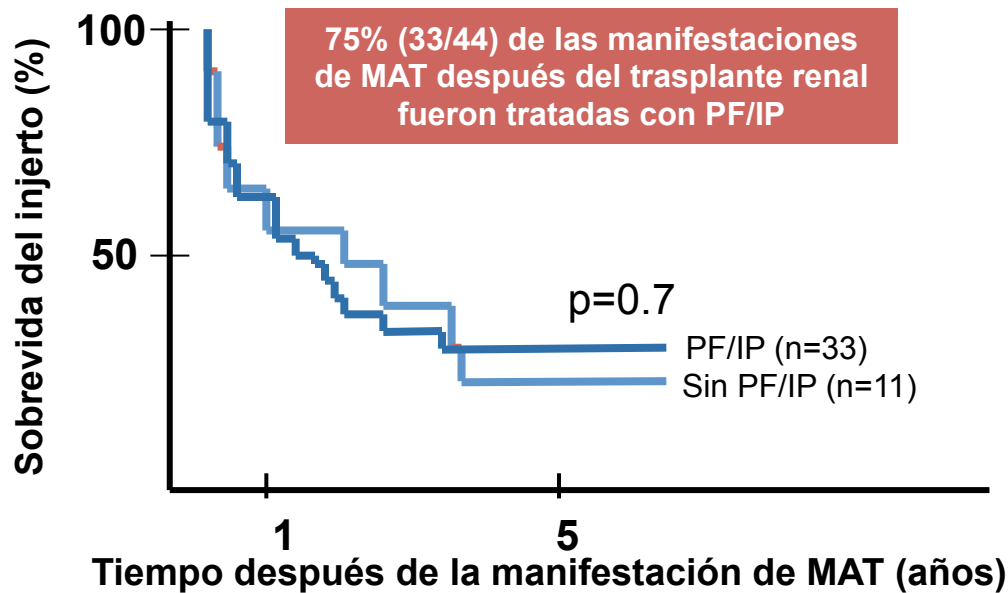
C4

PENSAR EN VÍA DE LAS LECTINAS

SINDROME URÉMICO HEMOLÍTICO ATÍPICO
Y
TRANSPLANTE RENAL

La PF/IP falló en mejorar la sobrevida del injerto en pacientes con SHUa posterior al trasplante renal¹

- En la mayoría de los reportes, la PF/IP falló en la prevención de la pérdida del injerto²⁻⁵
- No hubo mejoría en la sobrevida del injerto en los pacientes con SHUa posterior al trasplante renal a pesar de PF/IP en la cohorte de Francia (N=44)¹



Modificado de Le Quintrec et al. *AJT* 2013



La eficacia del eculizumab ha revolucionado el manejo y el pronóstico del SUHa y ha abierto la posibilidad del trasplante renal en los sujetos con SUHa.

Si bien el trasplante renal con donante fallecido es la opción preferida en los pacientes con SUHa, el trasplante vivo no-relacionado puede ser considerado en cada caso puntual.

El caso del donante vivo relacionado es más complejo pues el SUHa pudo haber pasado inadvertido en el donante y puede desenmascarse luego de la nefrectomía por el stress quirúrgico, por lo que no es la opción ideal

El riesgo de recurrencia del SUHa en el post-transplante depende básicamente de la anomalía genética del factor del complemento involucrado.

En este sentido los estudios genéticos son mandatorios.

Y servirán para ajustar a medida la estrategia terapéutica para cada caso de transplante renal en particular

Pacientes con alto riesgo de recurrencia deben recibir en forma profiláctica el eculizumab, incluyendo una dosis de 1200 mg antes de la cirugía y una dosis adicional de 900 mg dentro de las 24 horas de la reperfusión.

Pacientes con riesgo moderado pueden recibir plasma o una dosis profiláctica de eculizumab, dependiendo de la accesibilidad a la droga.

Duración del tratamiento profyláctico con eculizumab post transplante?

De por vida en los de alto riesgo de recurrencia.

Se puede discontinuar en el subgrupo de moderado riesgo a los 12 meses post-transplante.

Estas recomendaciones deben ser validadas en el futuro

El trasplante hepatorenal es efectivo en la cura el SUHa por las mutaciones en el factor H, factor I , C3 y CFB.

Si bien el procedimiento se ha tornado más seguro luego de la introducción del plasma pre-conditioning y de las técnicas quirúrgicas, sigue teniendo sus riesgos.

Tener en cuenta los costos de los tratamientos a instituir y los riesgos-beneficios en cada caso

El trasplante renal no trata la causa subyacente del SHUa

Proteína afectada	Resultado del Trasplante renal ¹
Factor H	Porcentaje de pacientes con MAT permanente: 80-90%
CFHR1, R3	Porcentaje de pacientes con MAT permanente: 20%
MCP	Porcentaje de pacientes con MAT permanente: 15-20%
Factor I	Porcentaje de pacientes con MAT permanente: 70-80%
Factor B	MAT permanente en un caso publicado
C3	Porcentaje de pacientes con MAT permanente: 40-50%
THBD	MAT permanente en un caso publicado

Más del 90% de los pacientes con SHUa en otra cohorte experimentaron pérdida del injerto, la mayoría en el primer año²



Candidates for renal transplantation with aHUS-related ESRD

Deceased-donor renal transplantation

Living-donor renal transplantation

Recipient risk assessment

Living non-related donor

Living related donor

HC, complemento

Low risk of recurrence

- Isolated MCP mutation
- Long-term negative anti-CFH antibody

Moderate risk of recurrence

- Isolated CFH mutation
- No identified mutation
- Mutation with unknown effect
- Persistent low-titre anti-CFH antibody

High risk of recurrence

- Previous early recurrence in the same individual or within the family
- Mutations in CFH, NAHR in CFH region, gain-of-function mutations in C3 and CFB

Donor risk assessment

Low risk

The donor does not harbour the mutation found in the recipient that has an indisputable role in the disease pathogenesis

High or moderate risk

- The donor shares a genetic susceptibility factor to aHUS with the recipient
- No mutations have been identified in either the donor or the recipient

No prophylaxis

Prophylactic eculizumab or PE*

Prophylactic eculizumab‡

PE or eculizumab-conditioned CLKT‡

Living-related donor RTx may be permitted

Living-related donor RTx should not be performed

Eculizumab – Approved Dosing Schedule in aHUS

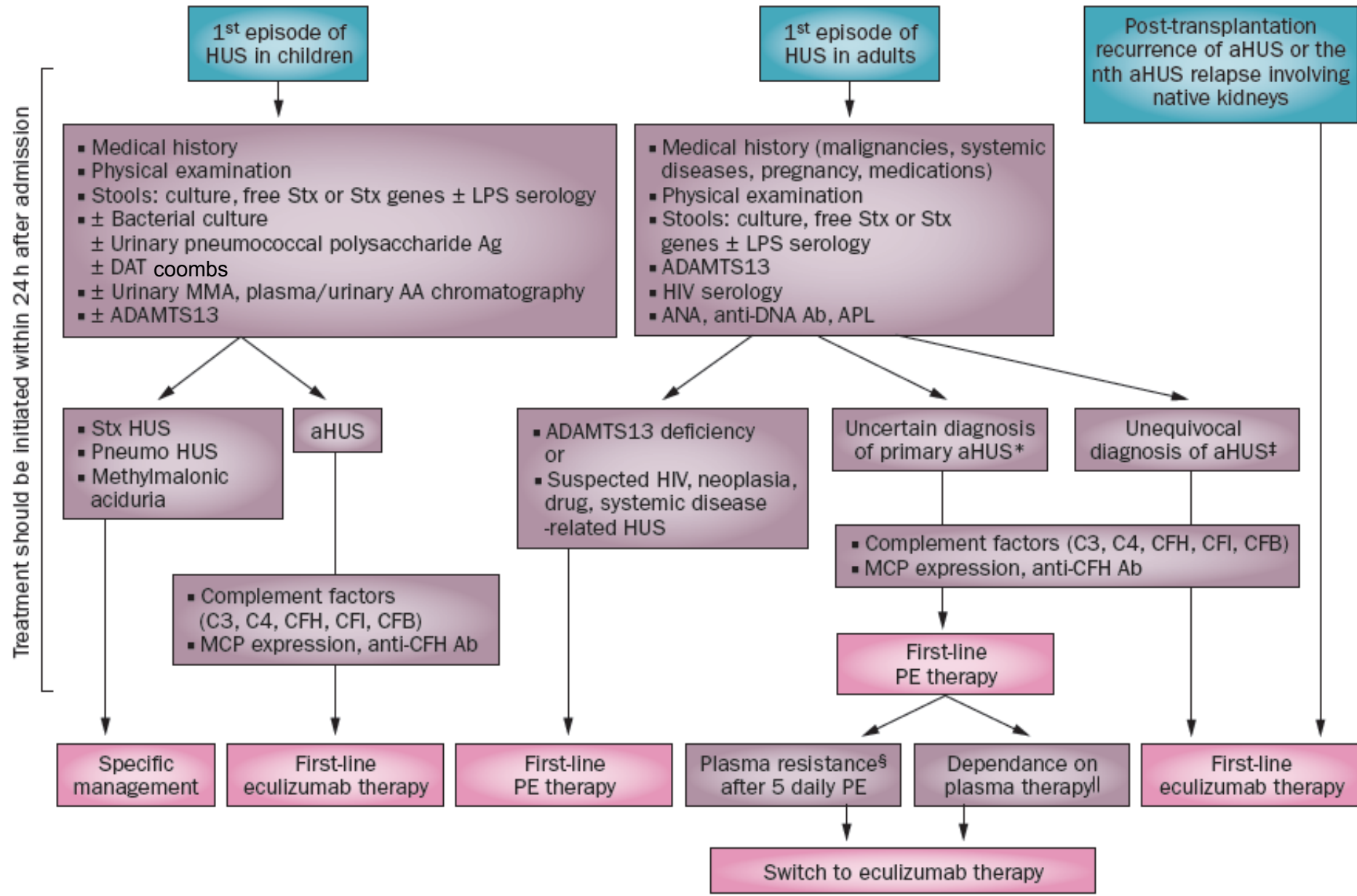
For patients ≥ 18 years of age, Soliris therapy consists of:

	Induction	Maintenance
	900 mg weekly x 4 doses	1200 mg at week 5; then 1200 mg every 2 weeks

For patients < 18 years of age, administer Soliris based upon body weight, according to the following schedule:

Patient Body Weight	Induction	Maintenance
40 kg and over	900 mg weekly x 4 doses	1200 mg at week 5; then 1200 mg every 2 weeks
30 kg to less than 40 kg	600 mg weekly x 2 doses	900 mg at week 3; then 900 mg every 2 weeks
20 kg to less than 30 kg	600 mg weekly x 2 doses	600 mg at week 3; then 600 mg every 2 weeks
10 kg less than 20 kg	600 mg weekly x 1 dose	300 mg at week 2; then 300 mg every 2 weeks
5 kg to less than 10 kg	300 mg weekly x 1 dose	300 mg at week 2; then 300 mg every 3 weeks

ALGORITMO DE DIAGNÓSTICO Y TRATAMIENTO DEL SUHa



- **NO ESPERAR EL ESTUDIO GENÉTICO PARA COMENZAR TRATAMIENTO**
- **ESTUDIO GENÉTICO CON IMPACTO A FUTURO (PLANIFICACIÓN DE TX)**
- **DIAGNÓSTICO CLÍNICO**
- **40% CURSAN CON DIARREA (SUH); 40% SON ADULTOS: A CUALQUIER EDAD**
- **80% CON C3 NORMAL; CFH NORMAL EN 87% DE CASOS**
- **PUEDE ACOMPAÑAR A OTROS CUADROS: LES, MALIGNIDAD, EMBARAZO**
- **TRATAMIENTO: CUANTO ANTES, MEJOR**
- **PLASMAFERESIS Y/O INFUSIÓN DE PLASMA (60% ÓBITO; 40% PROGRESAN A HD)**
- **RITUXIMAB**
- **ECULIZUMAB**
- **SUSPENSIÓN INMEDIATA DE PLASMAFERÉISIS , FUNCIÓN RENAL MEJORA EN GRAL A LA 5TA SEMANA, DURACIÓN DE TRATAMIENTO NO ESTABLECIDA; COSTO**

Some kind of happiness is measured out in miles



*You can talk to me
If you're lonely, you can talk to me*

Hey Bulldog Lennon & McCartney 1968